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GenCore version 4.5

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OM protein - protein search, using sw model

Run on: February 21, 2002, 16:26:14 ; Search time 12.75 Seconds

(without alignments)

131.438 Million cell updates/sec
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Title: US-08-753-851-1
Perfect score: 123
Sequence: 128
Scoring table: BLOSUM62
Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 4240

Minimum DB seq length: 0 Maximum DB seq length: 22 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	ribosomal protein	pyrB leader peptid	gene HEXA protein	manganese peroxida	hypothetical prote	Ig H chain V-D-J r	heat-stable entero	manganese peroxida	defensin AMP2 - Da	major fat-globule	capsid protein VP5	neurotoxin-associa	intracrystalline c	, mu-conotoxin GIIIA	mu-conotoxin GIIIB	. mu-conotoxin GIIIC	40K iron-repressed	T-cell receptor be	Ig H chain V-D-J r	antibiotic GE2270	calmodulin, vasoac	small granule S2 c	Ig heavy chain CDR	microbial serine p	arylsulfatase A -	Ig H chain V-D-J r	T-cell receptor al		cytochrome c551 -
QI	A34835	B39845	154351	S65435	T06383	PH1598	A54534	S65434	S66222	D48394	PQ0544	867990	A56894	MXKN1	MXKN2	MXKN3	A41833	PH0942	PH1632	A61210	C44101	PC1309	PT0248	PS0087	I54283	PH1611	PH0779	C37520	A36727
DB	7	7	~	~	~	7	~	~	N	~	7	7	~	-		-	~	7	~	7	7	7	7	7	~	~	7	7	7
% Query Match Length	17	19	21	19	11	14	17	19	20	15	20	20	20	22	22	22	22	6	11	13	15	19	20	20	20	12	15	17	17
% Query Match	26.8	22.8			21.1				6	19.5	o.	6		19.5	6	6	19.1	ъ.	18.7		ъ.	œ	œ.		18.7		17.9	17.9	17.9
Score	33	28	$\sim$	26.5	26	25	25	24.5	24.5	24	24	24	24	24	24	24	23.5	23	23	23	23	23		23	23	22	22	22	22
Result No.	п	7	m	4	5	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	.25	56	27	28	29

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0; Gaps

Query Match

22.8%; Score 28; DB 2; Length 19;
Best Local Similarity 66.7%; Pred. No. 9.6e+02;
Matches 4; Conservative 0; Mismatches 2; Indels

17 CCKAFN 22

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follitropin inhibi	Ig H chain V-D-J r	kallikrein (PK-120	hypothetical 2.4K	aspartylglycosamin	opacity protein P.	opacity protein P.	T-cell receptor be	somatostatin - spo	Ig H chain V-D-J r	25K kidney and gal	osteonectin - rat	sodium-translocati	proteasome chain L	alpha-macroqlobuli	TcR delta chain V-	
A27486	PH1621	S50175	C31182	137144	S16364	S16365	PH0746	A60622	PH1601	E58501	A34572	S66364	G02018	S70612	A49254	
7	2	2	7	2	7	7	7	7	7	2	7	7 2	2	2	7	
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17.9	17.9	17.9	17.9	17.9	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	
22	22	22	22	22	21	21	21	21	21	21	21	21	21	21	21	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

	RESULT 1
	ribosomal protein L34 - Pseudomonas aeruginosa (tragment)
	C; Species: Pseudomonas aeruginosa
_	C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Jun-1993
	C; Accession: A34835
	Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990
	A; Title: Pseudomonas chromosomal replication origins: a bacterial class distinct from
	A; Reference number: A34835; MUID:90160310
	A, Accession: A34835
	A Molecule type: DNA
_	A residues: 1-17 < YEEP
	A)CLOSS references: GB:M30125
_	C; Genetics:
	A; Gene: route and a control of the
_	C) Superiamily: Escrietichia coll ilbosomal procein 1534
_	C;Keywords: protein blosynthesis; ribosome
	26.8%;
_	Sal Similarity 58.3%; Pred. No. 1.6e+UZ;
	Matches /; Conservative 1; Mismatches 4; Indeis 0; Gaps 0;
	Qy 3 KNGRYSISRTEA 14
	Db 6 KNGRQVLSRRRA 17
	RESULT 2
	559840
	Pyrb leader peptilde - bacillus subtilis C.cnocies Bacillus enhtilis
	C:Date: 20-Mar-1992 #sequence revision 20-Mar-1992 #text change 12-Dec-1997
	C; Accession: B39845 · ·
	R;Quinn, C.L.; Stephenson, B.T.; Switzer, R.L.
	A/Title: Functional organization and nucleotide sequence of the Bacillus subtilis pyr
	A; Meterence number: A39845; MUID:91225016
	A ACCESSION: A BYSEAD A SCHAIUS: DIED IMIDARY
	A; Molecule types DNA
	A; Residues: 1-19 <qui></qui>
	A;CTOSS-Teleferences; GB:MM9/5/ C:Gunarfamily: unassidned leader nentides
	Cloudertaining, unassigned reader peptities

; 0

Gaps

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Length 11

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A; Molecule type: mRNA
A; Residues: 1-11 < DEW>
A; Cross-references: EMBL:U12735; NID:9530086; PIDN:AAA67718.1; PID:9530087
A; Experimental source: strain Dare; seed
                                                                                                                                  Score 26; DB 2; I
Pred. No. 1.2e+03;
1; Mismatches 1;
                                                                                                                                  21.18;
60.08;
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75.0%;
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ilarity 57.1%;
Conservative
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                                                                                                                                                                                3; Conservative
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 4; Conserv
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1 CAKDGYY 7
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C;Species: Glycine max (soybean)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000
C;Accession: T06383
R:Dewey, R.E.; Wilson, R.F.; Novitzky, W.P.; Goode, J.H.
Plant Cell 6, 1495-1507, 1994
A;Title: The AAPTI gene of soybean complements a cholinephosphotransferase-deficient mut
A;Reference number: 206169; MUID:95086383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Riwartinez, M.J.; Ruiz-Duenas, F.J.; Guillen, F.; Martinez, A.T.

Eur. J. Biochem. 237, 424-432, 1996
Affille: Purification and catalytic properties of two manganese peroxidase isoenzymes A; Reference number: S65434; MUID:96215438
A; Accession: S65435
                                                                                                                                                     C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: Ol-Nov-1996 #text_change 21-Jul-2000
C; Accession: 154351
R; Akli, S.; Chomel, J.C.; Lacorte, J.M.; Bachner, L.; Poenaru, A.; Poenaru, L. Hum. Mol. Genet. 2, 61-67, 1998
A; Title: Ten novel mutations in the HEXA gene in non-Jewish Tay-Sachs patients.
A; Reference number: 154351; MUID:93258352
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C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 29-Aug-1997
C;Accession: S65435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               manganese peroxidase (EC 1.11.1.13) MnP1 - Pleurotus eryngii (fragment)
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Pred. No. 1.6e+03;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 21;
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Pred. No. 1.5e+03;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-21 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GDB:120040; OMIM:272800
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A; Residues: 1-19 < MAR>
A; Experimental source:
C; Keywords: manganese; oxidoreductase
                                                                                                                                gene HEXA protein - human (fragment)
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C; Superfamily: beta-hexosaminidase
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Similarity 41.7%;
5; Conservative
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ilarity 53.8%;
Conservative
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Best Local Similarity
Matches 7; Conserv
|| || CCPLFN 13
                                                                                                                                                                                                                                                                                                                 A; Accession: I54351
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Best Local S.
Matches 5
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Ig H.chain V-D-J region (wild-type clone 306) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PHI598
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 11993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less m A;Reference number: PHI580; MUID:93301609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: A54534
R;Arita, M.; Honda, T.; Miwatani, T.; Takeda, T.; Takao, T.; Shimonishi, Y.
FEMS Microbiol. Lett. 79, 105-110, 1991
A;Title: Purification and characterization of a heat-stable enterotoxin of Vibrio mim
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 03-May-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
S65434
manganese peroxidase (EC 1.11.1.13) MnP2 - Pleurotus eryngii (fragment)
C;Species: Pleurotus eryngii
C;Species: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 29-Aug-1997
C;Accession: S65434
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2.4e+03;
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 14;
                                                                                                                                                                                                                                                                                 A;Residues: 1-14 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enterotoxin - Vibrio mimicus (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 25; DB 2;
Pred. No. 2e+03;
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Pred. No. 2
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A; Molecule type: protein
A; Mesidues: 1-17 <ARI>
C; Superfamily: heat-stable enterotoxin
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A,Accession: T06383 A,Status: Preliminary; translated from GB/EMBL/DDBJ

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A:Status: preliminary
A:Molecule type: protein
A:Molecule type: protein
B:Residues: 1-20 cFUJ-
B:Somers, E.; DasGupta, B.R.
J. Protein Chem. 10, 415-425, 1991
A:Title: Clostridium botulinum types A, B, Cl, and E produce proteins with or without
A:Reference number: A44644; MUID:92143938
                                                                                                                                                                                                                                                                                                                                                    R.Davison, M.D.; Rixon, F.J.; Davison, A.J.
J. Gen. Virol. 73, 2709-2713, 1992
A,Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of herp
A,Reference number: PQ0544; MUID:93019027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neuroboxin-associated protein type A Hn+ 17K chain - Clostridium botulinum (fragment)
N;Alternate names: HA-15 protein
C;Species: Clostridium botulinum
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 12-Jun-1998
C;Accession: S67990; C44644
R;Fujita, R.; Fujinaga, Y.; Inoue, K.; Nakajima, H.; Kumon, H.; Oguma, K.
R;Fujita, R.; Fujinaga, Y.; Inoue, K.; Nakajima, G.; Rumon, H.; Oguma, K.
A;Title: Molecular characterization of two forms of nontoxic-nonhemagglutinin compone
A;Reference number: S67998; MuID:96096783
A;Accession: S67990
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C;Species: Terebratella sanguinea
C;Date: 05-Jan.1996 #sequence_revision 05-Jan-1996 #text_change 20-Jun-2000
C;Accession: A56894
                                                                                                                                                                     capsid protein VP5 - human herpesvirus l (fragments)
C;Species: human herpesvirus l
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: PQ0544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 24; DB 2; Length 20;
Pred. No. 3.8e+03;
1; Mismatches 5; Indels
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Pred. No. 3.8e+03;
; Mismatches 1; Indels
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C;Keywords: hemagglutinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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66.7%;
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Best Local Similarity
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Best Local Similarity
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NGNYNI 14
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D48394
major Ed-globule membrane protein GP 55 - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 31-oct-1997
C;Accession: D48394
R;Mather, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig II-like sequences.
A;Reference number: A48394; MUID:93250576
A;Accession: D48394
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <AAT>
A;Residu
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S66222

Gefensin AMP2 - Dahlia merckii (fragment)
N'Alternate names: seed antifungal protein
C;Species: Dahlia merckii
C;Date: 19-7 #xequence_revision 29-Aug-1997 #text_change 17-Mar-1999
C;Accession: S66222
R;Osborn, R.W.; de Samblanx, G.W.; Thevissen, K.; Goderis, I.; Torrekens, S.; van Leuven FRBS Lett. 368, 257-262, 1995
A;Title: Isolation and characterisation of plant defensins from seeds of Asteraceae, Fab A;Reference number: S66218; MUID:95354848
A;Reference number: S66222
A;Moccession: S6622
A;Moccession
                                                                                              £
R;Martinez, M.J.; Ruiz-Duenas, F.J.; Guillen, F.; Martinez, A.T.

Eur. J. Biochem. 237, 424-432, 1996

A;Title: Purification and catalytic properties of two manganese peroxidase isoenzymes A;Reference number: S65434; MUID:96215438

A;Rocession: S65434

A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-19 <ARP>
A;Experimental source: CBS 613.91
C;Keywords: manganese; oxidoreductase
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Pred. No. 3.2e+03;
3; Mismatches 3;
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Best Local Similarity 35.3%;
Matches 6; Conservative
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Best Local Similarity 58.3
Matches 7; Conservative
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Matches 4; Conserv
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Best Local Similarity
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C; Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 15-Sep-2000
C; Accession: A01786; A23579
R; Sato, S.; Nakamura, H.; Ohizumi, Y.; Kobayashi, J.; Hirata, Y.
FEBS Lett. 155, 277-280, 1983
A; Title: The amino acid sequences of homologous hydroxyproline-containing myotoxins from A; Reference number: A91309; MUID:83210170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 1-22 <SAT>
R;Cruz, L.J.; Gray, W.R.; Olivera, B.M.; Zeikus, R.D.; Kerr, L.; Yoshikami, D.; Moczydld
J. Biol. Chem. 260, 9280-9288, 1985
A;Title: Conus geographus toxins that discriminate between neuronal and muscle sodium ch
A;Reference number: A23579; MUID:85261316
R;Cusack, M.; Curry, G.; Clegg, H.; Abbott, G.
Comp. Blochem. Physiol. B 102, 93-95, 1992
A;Title: An intracrystalline chromoprotein from red brachiopod shells: implications for A;Reference number: A56894; MUID:92405551
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A:Title: Solution structure of mu-conotoxin GIIIA analysed by 2D-NMR and distance geomet
A:Reference number: A58581; MUID:91122275
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R;Wakamatsu, K.; Kohda, D.; Hatanaka, H.; Lancelin, J.M.; Ishida, Y.; Oya, M.; Nakamura,
Biochemistry 31, 12577–12584, 1992
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C; Superfamily: mu-conotoxin
C; Keywords: amidated carboxyl end; hydroxyproline; myotoxin; sodium channel inhibitor;
F; 3-15, 4-20,10-21/Disulfide bonds: #status experimental
F; 5,7/Modified site: 4-hydroxyproline (Pro) #status experimental
F; 17/Modified site: 4-hydroxyproline (Pro) #status experimental
F; 22/Modified site: amidated carboxyl end (Ala) #status experimental
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R:Lancelin, J.M.; Kohda, D.; Tate, S.I.; Yanagawa, Y.; Abe, T.; Satake, M.; Inagabochemistry 30, 6908-6916, 1991
A; Title: Tertiary structure of conotoxin GIIIA in aqueous solution.
A; Reference number: A44659; MUID:91299744
A; Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR R; Ott, K.H.; Becker, S.; Gordon, R.D.; Rueterjans, H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mu-conotoxin GIIIA [validated] - cone shell (Conus geographus)
N.Alternate names: geographutoxin I (GTX I); myotoxin I
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Pred. No. 3.8e+03;
1; Mismatches 2; Indels
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                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <CUS>
A;Note: sequence extracted from NCBI backbone (NCBIP:114882)
C;Keywords: chromoprotein
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A;Residues: 1-22 <CRU>
R;Kohda, D:, Lancelin, J.M.; Inagaki, F.; Wakamatsu, K.
submitted to the Brookhaven Protein Data Bank, December 1992
A;Reference number: A51994; PDB:1TCG
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                                                                                                                            A;Contents: Leach, red brachiopod shells
A;Accession: A56894
                                                                                                                                                                                                                                                                                                                                                                                                                            19.5%;
62.5%;
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Matches 5; Conservative
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Gaps

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19.5%; Score 24; DB 1; Length 22; 100.0%; Pred. No. 4.1e+03; ive 0; Mismatches 0; Indels

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R;Sato, S.; Nakamura, H.; Ohizumi, Y.; Kobayashi, J.; Hirata, Y.
FEBS Lett. 155, 277-280, 1983
A;Title: The amino acid sequences of homologous hydroxyproline-containing myotoxins f A;Reference number: A91309; MUID:83210170
A;Accession: A01787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 1-22 <SAT>
R; Cruz, L.J.; Gray, W.R.; Olivera, B.M.; Zeikus, R.D.; Kerr, L.; Yoshikami, D.; Moczy
D. Biol. Chem. 260, 9280-9289, 1985
A; Title: Conus geographus toxins that discriminate between neuronal and muscle sodium
A; Reference number: A23579; MUID: 85261316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Afforesion: B23579
A,Molecule type: protein
A;Residues: 1-22 <CRU
A;Residues: 1-22 <CRU
A;Residues: 1-22 <CRU
B;Hill, J.M.; Alewood, P.F.; Craik, D.J.
Submitted to the Brookhaven Protein Data Bank, April 1996
A;Reference number: A65705; PDB:1GIB
A;Contents: annotation; Conformation by (1)H-NMR, residues 1-22
R;Hill, J.M.; Alewood, P.F.; Craik, D.J.
Biochemistry 35, 8824-8835, 1996
A;Title: Three-dimensional solution structure of mu-conotoxin GIIIB, a specific block
A;Reference number: A58590; MUID:96280640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Superfamily: mu-conotoxin
C:Keywords: amidated carboxyl end; hydroxyproline; myotoxin; sodium channel inhibitor
C:Keywords: amidated carboxyl end; #status experimental
C:3-15,4-20,10-21/Disulfide bonds: #status experimental
F:6,77/Modified site: 4-hydroxyproline (Pro) #status experimental
F:17/Modified site: 4-hydroxyproline (Pro) #status experimental
F:22/Modified site: amidated carboxyl end (Ala) #status experimental
                                    N.Alternate names: geographutoxin II (GTX II); myotoxin II C.Species: Conus geographus (geography cone) C.Species: Conus geographus (geography cone) C.Bate: 14 Nov-1983 #sequence_revision 14-Nov-1983 #text_change 15-Sep-2000 C.Accession: A01787; B23579
- cone shell (Conus geographus)
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     mu-conotoxin GIIIB [validated]
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Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

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penna
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conus ermin
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  magus
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-!- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE A LANTIBIOTICS.
InterPro; IRF001049; Gallidermin.
PF002052; Gallidermin.
PRINTS; PR00323; GalLidermin.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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8 B D-ABU (AMINOBUTARIC ACID).

MOD_RES
19 19 DHA (2,3-DIDEHYDROBUTRINE).

MOD_RES
19 19 DHA (2,3-DIDEHYDROBUTRINE).

THIOETH 8 11 ALA-S-ALA (LANTHIONINE).

THIOETH 19 21 ALA-S-ALA (LANTHIONINE).

THIOETH 19 22 DHA-S-ALA (ANTHIONINE).

SEQUENCE 22 AA; 2425 MW; 961C1480401F92CE CRC64;
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Q10996
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Pred. No. 8e+02;
3; Mismatches 4; Indels
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01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
LANTIBLOTIC MUTACIN B-NY266.
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CXAA_CONPE
CXAB_CONPE
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NU4M_TRIRU
CXA1_CONER
PPM2_LIMPO
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LCRP_PETMA
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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                                                                                                                                                                                             Sato S., Nakamura H., Ohizumi Y., Kobayashi J., Hirata Y.; The aminon acid sequences of homologous hydroxyproline-containing myotoxins from the marine snail Conus geographus venom."; FEBS Lett. 155:277-280(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Tertiary structure of conotoxin GIIIA in aqueous solution."; Biochemistry 30:6908-6916(1991).
-!- FUNCTION: MU-CONOTOXING BY BINDING TO THE VOLTAGE-ACTIVATED, SODIUM MUSCLE CONTRACTION BY BINDING TO THE VOLTAGE-ACTIVATED, SODIUM
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91122275; PubMed=1991506;
Ott K.-H., Becker S., Gordon R.D., Rueterjans H.;
Solution structure of mu-conotoxin GIIIA analysed by 2D-NMR and distance geometry calculations.";
FEBS Lett. 278:160-166(1991).
                                                                                        MEDILINE-85261316; PubMed-2410412;
Cruz L.J., Gray W.R., Olivera B.M., Zeikus R.D., Kerr L.,
Yoshikami D., Moczydlowski E.;
"Conus geographus toxins that discriminate between neuronal and
muscle sodium channels.";
21-JUL-1986 (Rel. 01, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
MU-CONOTOXIN GIIIA (MYOTOXIN I) (GEOGRAPHUTOXIN I) (GTX-I).
Conus geographus (Geography cone).
                                          Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBL_TaxID=6491;
                                                                                                                                                                                                                                                                     Hidaka Y., Sato K., Nakamura H., Kobayashi J., Ohizumi Y., Simonishi Y.;
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"Peptide toxins from venomous Conus snails.";
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HYDROXYLATION.
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MEDLINE-90249506; Pubmed-2338142;
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1TCK; 31-JAN-94
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A23579; A23579.
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-!- PUNCTION: MU-CONOTOXINS ACT ON MUSCLE MEMBRANES. THEY BLOCK MUSCLE CONTRACTION BY BINDING TO THE VOLTAGE-ACTIVATED SODIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sato S., Nakamura H., Ohizumi Y., Kobayashi J., Hirata Y.; The amino acid sequences of homologous hydroxyproline-containing myotoxins from the marine snail Conus geographus venom."; FEBS Lett. 155:277-280(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cruz L.J., Gray W.R., Olivera B.M., Zeikus R.D., Kerr L., Yoshikami D., Moczydlowski E.; "Conus geographus toxins that discriminate between neuronal and
                                                                                                                                                                                                                                                       P01524;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
MU-CONOTOXIN GIIIB (MYOTOXIN II) (GEOGRAPHUTOXIN II) (GTX-II).
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Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
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Sodium channel inhibitor; Hydroxylation; Amidation; Venom;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gray W.R., Olivera B.M., Cruz L.J., "Peptide toxins from venomous Conus Annu. Rev. Biochem. 57:665-700(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 260:9280-9288(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-83210170; PubMed-6852238;
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19.5%; ; 100.0%;
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B23579; B23579.
                      Similarity 3; Conserv
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C1. FUNCTION: C1Q ASSOCIATES WITH THE PROENZYMES C1R AND C1S TO YIELD C1, THE FIRST COMPONENT OF THE SERUM COMPLEMENT SYSTEM. THE CCLLAGEN-LIKE REGIONS OF C1Q INTERACT WITH THE CA(2+) -DEPENDENT CIR(2) C1S(2) PROENZYME COMPLEX, AND EFFCIENT ACTIVATION OF C1 TAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF C1Q WITH THE C2 FC REGIONS OF IGG OR IGM ANTIBODY PRESENT IN IMMUNE COMPLEXS.

C1- SUBUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEX OF C1Q, R AND S IN THE MOLAR RATION OF I.2.2. THE C1 SUBCOMPONENT IS COMPOSED OF THE A AND B CIS. THE C DIMERS OF THE A AND B CIAINS, AND THREE OF WHICH ARE DISULFIDE-LINKED LINKED DIMERS OF THE C CHAINS, AND THREE OF WHICH ARE DISULFIDE-LINKED C2 LINKED DIMERS OF THE C CHAINS, IN ADDITION TO THE MAJOR A:B AND C:C DIMER BANDS, RAT, UNLIKE HUMAN C1Q, CONTAINED MINOR DIMER SPECIES.

C1- SIMILARITY: CONTAINS A COLLAGENOUS DOMAIN.

FINGETE; PROSITE; PRO113; C1Q; PARTIAL.

ROSITE; PROSITE; PS01113; C1Q; PARTIAL.
                                                                                                                                                                                                                                                                                                                            INTERCHAIN (WITH CYS-4 IN B CHAIN).
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30-MAY-2000 (Rel. 39, Last sequence update)
20-MG-2001 (Rel. 40, Last annotation update)
20-MG-2001 (Rel. 40, Last annotation update)
EPSILON-CONOTOXIN TXIX.
Conus textile (Cloth-of-gold cone).
Eukaryota: Metazoa: Mollusca: Gastropoda; Caenogastropoda;
Neogastropoda: Conoidea: Conidae; Conus.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 22; DB 1; Length 15;
Pred. No. 1.6e+03;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                1B3D8000B7793965 CRC64;
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01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
23 KDA BASIC PROTEIN (FRAGMENT).
Bacillus stearothermophilus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.9%; Score 22; DB 1; Lei
21.4%; Pred. No. 2.3e+03;
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Submitted (OCT-1992) to the SWISS-PROT data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus/Staphylococcus group; Geobacillus.
NCBI_TaxID=1422;
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57.18;
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15 15
15 AA; 1488 MW;
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Best Local Similarity
3; Conserve
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Best Local Similarity
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P80166;
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23KD_BACST
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Wing M.G., Sellly D.J., Bridgman D.J., Harrison R.A.;
"Rapid isolation and biochemical characterization of rat Cl and Clq.";
MOI. Immunol. 30:433-440(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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-!- FUNCTION: MU-CONOTOXINS ACT ON MUSCLE MEMBRANES. THEY BLOCK MUSCLE CONTRACTION BY BINDING TO THE VOLTAGE-ACTIVATED SODIUM
                                                                                                                                                                                                                                                                                                                                                                                "Conus geographus toxins that discriminate between neuronal and muscle sodium channels.";
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                                                                                                                                                                                                                                 Gastropoda; Caenogastropoda;
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HSSP, P01524; 1GIB.
Sodium channel inhibitor; Hydroxylation; Amidation; Venom
                                                                                                                                                                                                                                                                                                                                           Cruz L.J., Gray W.R., Olivera B.M., Zeikus R.D., Kerr L.,
Yoshikami D., Moczydlowski E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 22;
1.1e+03;
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01-JUL-1993 (Rel. 26, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
COMPLEMENT CLQ SUBCOMPONENT, A CHAIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gray W.R., Olivera B.M., Cruz L.J.;
"Peptide toxins from venomous Conus snails.";
                                                                                                                               01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-AUG-1990 (Rel. 15, Last annotation update)
                                                                                                22 AA.
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BY SIMILARITY.
BY SIMILARITY.
HYDROXYLATION.
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HYDROXYLATION
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Neogastropoda; Conoidea; Conidae; Conus.
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                                                                                                                                                                                                            Conus geographus (Geography cone).
                                                                                                                                                                                                                                                                                                                        MEDLINE=85261316; PubMed=2410412;
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                                                                                                STANDARD;
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Best Local Similarity
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01-FEB-1995
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P01520;
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                              Rigby A.C., Lucas-Meunier E., Kalume D.E., Czerwiec E., Hambe B., Dahlqvist I., Fossier P., Baux G., Roepstorff P., Baleja J.D., Furie B., Stenflo J.P.;

"A conotoxin from Coust textile with unusual posttranslational modifications reduces presynaptic Ca2+ influx.";

Proc. Natl. Acad. Sci. U.S.A. 96:5758-573(1999).

-I- FUNCTION: CONOTOXIN WHICH ACTS AT PRESYNAPTIC MEMBRANES, BLOCKING THE CALCIUM CHANNELS.
                                                                                                                                             Presynaptic neurotoxin; Calcium channel inhibitor; Venom; Vitamin K; Gamma-carboxyglutamic acid; Glycoprotein; Hydroxylation; Bromination;
                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fasciola hepatica (Liver fluke).
Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 213:169-174(1995).
CARBOHYDRATE-LINKAGE SITE THR-10, AND STRUCTURE BY NMR.
                                                                                                                                                                                                                                                                                                                   0;
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Neodermata; Trematoda; Digenea; Echinostomida; Echinostomata;
Fascioloidea; Fasciolidae; Fasciola.
NCBI_TaxID=6192;
                                                                                                                       -i- PTM: O-GLYCAN CONSISTS OF THE DISACCHARIDE GAL-GALNAC. PDB; 1WCT; 08-JUN-99.
                                                                                                                                                                                                                                                                                            Score 21; DB 1; Length 13;
Pred. No. 2e+03;
2; Mismatches 0; Indels
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                                                                                                                                                                                                     GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
BROMINATION.
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386C9E1C74AFA378 CRC64;
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14 AA; 1581 MW; 9EOF0090CC8CODF1 CRC64;
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01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
NEWLY EXCYSTED JUVENILE PROTEIN 2 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                      14 AA.
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                    MEDLINE-99254114; PubMed-10318957;
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50.0%;
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Best Local Similarity 50.0°
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Best Local Similarity
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1 ECCE 4
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CXA2\_CONGE

RESULT

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PIR; A01783; NTKN2G.
HSSP; P01519; 1NOT.
Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rana margaratae (Chinese frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
NCBI_TaxID=121156;
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0
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Gray W.R., Olivera B.M., Cruz L.J.;
"Peptide toxins from venomous Conus snails.";
Annu. Rev. Blochem. 57:665-700(1988).
-!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, 'BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND 'BIND THEN THEN.
                                                                                                                                                                                                                                                                                                                                                                 DISULFIDE BONDS.

MEDLINE=84032400; PubMed=6630187;
Gray W.R., Rivier J.E., Galyean R., Cruz L.J., Olivera B.M.;
"Conotoxin MI. Disulfide bonding and conformational states.";
J. Biol. Chem. 258:12247-12251(1983).
                                                                                                                                                 Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
                                                                                                                                                                                                                                    MEDLINE=81191854; PubMed=7014556; Gray W.R., Luque A., Olivera B.M., Barrett J., Cruz L.J.; Peptide toxins from Conus geographus venom."; J. Biol. Chem. 256:4734-4740(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              skin of Chinese frog Rana margaratae.";
Sci. China, B, Chem. Life Sci. Earth Sci. 32:570-579(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEEE831C39297EBD CRC64;
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1; Mismatches 0
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                                                          (Rel. 01, Last sequence update)
(Rel. 09, Last annotation update)
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01-FEB-1995 (Rel. 31, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 AA
                                                                                                                                                                 Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=6491;
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PRT;
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                                                                                                                           Conus geographus (Geography cone)
                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequ
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66.78;
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Best Local Similarity 66.7
Matches 2; Conservative
STANDARD;
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ALPHA-CONOTOXIN GII.
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SYNTHESIS.
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Venom;
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FIBB_HORSE
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                             SAUMENTS.

SCI. China, B, Chem. Life Sci. Earth Sci. 33:170-177(1990).

SCI. China, B, Chem. Life Sci. Earth Sci. 33:170-177(1990).

-!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS, EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
                                                                                                                                                                                                                               Gaps
                Zon G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (1.2 ANGSTROMS) OF GI.
MEDLINE-96378624; PubMed-8784187;
Guddat L.W., Martin J.A., Shan L., Edmundson A.B., Gray W.R.;
"Three-dimensional structure of the alpha-conotoxin GI at 1.2-A
                                                                                                                                                                                                                               ;
            Lu Y.A., Peng J.L., Zhu Y.Q., Wu S.X., Tang Y.Q., Tian S.H., Z
"Synthesis and biological activity of a new frog skin peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-84032400; PubMed-6630187;
Gray W.R., Rivier J.E., Galyean R., Cruz L.J., Olivera B.M.;
"Conctoxin MI. Disulfide bonding and conformational states.";
J. Biol. Chem. 258:12247-12251(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                         Gastropoda; Caenogastropoda;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-89375269; PubMed-2775719;
Pardi A., Galdes A., Florance J., Maniconte D.;
"Solution structures of alpha-conotoxin Gl determined by
                                                                                                                                                                                                       Score 20; DB 1; Length 14; Pred. No. 3e+03;
                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ALPHA-CONOTOXIN GIA [CONTAINS: ALPHA-CONOTOXIN GI (G1)]
                                                                                                                                                                                                                             3; Indels
                                                                                                                 InterPro; IPR002040; Tachykinin.
PROSITE; PS00267; TACHYKININ; 1.
Tachykinin; Neuropeptide; Amidation; Amphibian skin.
                                                                                                                                                       AMIDATION.
D4593AE408C3673D CRC64;
                                                                                                          SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gray W.R., Olivera B.M., Cruz L.J.;
"Peptide toxins from venomous Conus snails.";
Annu. Rev. Biochem. 57:665-700(1988).
                                                                                                                                                                                                                                                                                                                                       15 AA
                                                                                                                                                                                                                               2; Mismatches
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Neogastropoda; Conoidea; Conidae; Conus
                                                                                                                                                                                                                                                                                                                                                                                                              Conus geographus (Geography cone).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE.
MEDLINE-81191854; PubMed-7014556;
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MEDLINE=90253600; PubMed=2340087;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUCTURE BY NMR OF GI. MEDLINE=98239743; PubMed=9571060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochemistry 28:5494-5501(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dimensional NMR spectroscopy.";
                                                                                                                                                                                                       16.3%;
44.4%;
                                                                                                                                                                   14 AA; 1617 MW;
                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
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P01519;
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SEQUENCE
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STRUCTURE BY NMR OF AN ANTITOXIC ANALOG OF GI.
MEDLINE=99438341; PubMed=10508392;
MOK K.H., Han K.H.;
"NMR solution conformation of an antitoxic analogue of alpha-conotoxin GI: identification of a common nicotinic acetylcholine receptor alpha(1)-subunit binding surface for small ligands and alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- MISCELLANDOUS: THE SEQUENCE SHOWN IS THAT OF CONOTOXIN GIA.
PIR; A01782; NTKRAG.
PDB; 1NOT; 07-DEC-96.
PDB; 1XGA; 16-FEB-99.
PDB; 1XGC; 23-MAR-99.
PDB; 10GC; 23-MAR-99.
PDB; 10GS; 06-OCT-99.
PDB; 10GS; 06-OCT-99.
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                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
Gehrmann J., Alewood P.F., Craik D.J.; "Structure determination of the three disulfide bond isomers of alpha-conotoxin GI: a model for the role of disulfide bonds in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
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2AE73EE90F8C2E19 CRC64;
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Pred. No. 3.2e+03;
1; Mismatches 0,
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01-JAN-1990 (Rel. 13, Last sequence update)
01-JAN-1990 (Rel. 13, Last annotation update)
FIBRINOPEPTIDE B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 AA
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"Studies on fibrinopeptides from mammals.";
Acta Chem. Scand. 19:1789-1791(1965).
                                             structural stability.";
J. Mol. Biol. 278:401-415(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.38;
66.78;
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tes 2; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15
                                                                                                                                                                                                                                            conotoxins.";
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P14471;
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ECC --
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-1- CATALYTIC ACTIVITY: N(5),N(10)-METHYLENETETRAHYDROMETHANOPTERIN +
REDUCED COENZYME F(420) = 5-METHYL-5,6,7,8-TETRAHYDROMETHANOPTERIN
(ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS. MISCELLANBOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                              01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
H(2)-FORMING NS, NIO-METHYLENETETRAHYDROWETHANOPTERIN DEHYDROGENASE (EC 1.5.99.11) (H2-DEPENDENT METHYLENE-H4MPT DEHYDROGENASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zirngibl C., van Dongen W., Schwoerer B., von Buenau R.,
Richter M., Klein A., Thauer R.K.;
"H2-forming methylenetertahydromethanopterin dehydrogenase, a nov
type of hydrogenase without iron-sulfur clusters in methanogenic
                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Buryarchaeota; Methanobacteriales; Methanobacteriaceae; Methanothermobacter.
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0
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                                                                                                                                                Score 20; DB 1; Length 19;
Pred. No. 4e+03;
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Pred. No. 4e+03;
                                                                                                                                                                        2; Indels
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                                                                                                                921A2B02D5F6891D CRC64;
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                                                       InterPro; IPR002181; Fibrinogen_C.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
Blood coagulation; Plasma; Sulfation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                           19 AA.
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                                                                                                                                                                        4; Mismatches
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-!- PATHWAY: INVOLVED IN METHANOGENESIS.
-!- SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oxidoreductase; Methanogenesis; Zinc.
                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                 16.3%;
33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.3%;
80.0%;
                                                                                                               19 AA; 2296 MW;
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                                                                                                                                                          Local Similarity 33.3
nes 3; Conservative
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                                                                                                                                                                                                                                                                           STANDARD;
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7 EEDGRIKVI 15
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12 RTDAA 16
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01-OCT-1993 (
20-AUG-2001 (
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ALAT_PIG
ID ALAT_PIG
AC P13191;
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SEQUENCE
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SEQUENCE
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Matches
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ALANINE AMINOTRANSFERASE (EC 2.6.1.2) (GLUTAMIC--PYRUVIC TRANSAMINASE) (GFT) (GLUTAMIC--ALANINE TRANSAMINASE) (FRAGMENT).
GPT OR GPT1 OR AAT1.
Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO CELLULASE FAMILY F (FAMILY 10 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                              BIOCHEMISTRY 18:3002-3007(1979).
-!- FUNCTION: PARTICIPATES IN CELLULAR NITROGEN METABOLISM AND ALSO IN LIVER GLUCONEOGENESIS STARTING WITH PRECURSORS TRANSPORTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą
                                                                                          Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBGNIT: HOMODIMER.
-!- SUBGELLULAR LOCATION: CYTOPLASMIC.
-!- MISCELLANBOUS: THERE ARE TWO ISOZYMES: A CYTOPLASMIC ONE AND MITOCHONDRIAL ONE.
                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: L-ALANINE + 2-OXOGLUTARATE = PYRUVATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adamsen A.K., Jacobsen S., Ahring B.K.;
Submitted (OCT-1996) to the SWISS-PROT data bank.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
LINKAGES IN XYLANS.
                                                                                                                                                                                                                                          Tanase S., Kojima H., Morino Y.; "Pyridoxal 5'-phosphate binding site of pig heart alanine aminotransferase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: TO OTHER SPECIES ALANINE AMINOTRANSFERASE PIR; A14344; A14344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1C2243A373EC4801 CRC64;
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                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferase; Aminotransferase; Pyridoxal phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENDO-1,4-BETA-XYLANASE A (EC 3.2.1.8) (XYLANÁSE A) (1,4-BETA-D-XYLAN XYLANOHYDROLASE A) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 20; DB 1; I
Pred. No. 4.2e+03;
4; Mismatches 4;
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Pred. No. 4.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYDROLASES).
InterPro; IPR001000; Glyco_hydro_10.
PROSITE; PS00591; GLYCOSYL_HYDROL_F10; PARTIAL.
Xylan_degradation; Hydrolase; Glycosidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Dictyoglomus group; Dictyoglomus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                            MEDLINE=79232426; PubMed=465450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PATHWAY: XYLAN DEGRADATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dictyoglomus sp. (strain B4A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.3%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 2/...
3; Conservative
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7 HSVSKGFMGEC 17
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Best Local Similarity
                                                                                                                                  NCBI_TaxID=9823
                                                                                                                                                                                                                                                                                                                                                                                                                                    L-GLUTAMATE
                                                                                                                                                                                SEQUENCE.
TISSUE-Heart;
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01-NOV-1997 (
01-NOV-1997 (
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P80718;
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SEQUENCE
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0;

sapien

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database :

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Q9qv05 rattus sp. Q9tws7 lamellibrac Q38571 bacteriopha Q83965 influenza a Q9r4t3 mycobacteri Q25087 herdmania m Q88229 mus musculu
                                 Q9twq6 tachypleus
Q36005 trypanosoma
Q9qv61 rattus sp.
Q35998 trypanosoma
                                                                                                                                                          099wb6 mus sp. sgp
036978 human papil
099n81 mus musculu
Q41580 triticum ae
                  solanum tub
theileria a
                                                                                                                                                                                   homo sapien
homo sapien
                                                                    Q29831 homo sapien
P78533 homo sapien
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escherichia
                                                                                                                                                                                                                      homo sapien
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Roberts D.L., Dalgleish R., Cohen G.M., MacFarlane M.; "The mammalian CED4 homologue, APAFI, exists as two distinct forms in
                                                                                                                                                 Q13726 homo
                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Q9tnp2
Q53326
Q9f581
                                                                                                                                                                                                                      Q9ucn1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30; DB 4; Length 18;
Pred. No. 4e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         human cells.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
EMBL, AJ133645; CAB65087.1;
NON_TER 1 1 1
NON_TER 18 18
SEQUENCE 18 AA; 2045 MW; 30D5FA30B885AEF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CONOTOXIN SCAFFOLD IX PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                           P78533
Q9QV05
Q9TWS7
Q38571
Q83965
Q9R4T3
Q25087
                091269
078379
09TWQ6
036005
090V61
035998
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Q9QWB6
                                                                                                                                                                  036978
099N81
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Q9F581
Q9UCN1
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                                                                    029831
                                                                                                                                                                                            Q9TNP2
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62.58;
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5; Conservative
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10 SRTEAADC 17
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SRSKVADC 13
Query Match
Best Local S
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90GN8
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Q9umr0 homo sapien
Q9b168 lingula ung
Q91165 ascaris suu
Q9tr06 bos taurus
Q9r581 vibrio chol
Q9r580 vibrio chol
Q9r579 vibrio chol
Q9r579 vibrio chol
Q9r579 vibrio chol
                                                                  (without alignments)
145.742 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              equus cabal
homo sapien
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bos taurus
                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                         February 21, 2002, 16:26:44; Search time 22.08 Seconds
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09r5n8
09uci4
09trg3
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       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                       473505 seqs, 146272329 residues
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                                                                                          US-08-753-851-1
123
1 CEKNGRYSISRTEAADCCKAFN 22
                                                                                                                                                                                                                                     Listing first 45 summaries
                                        OM protein - protein search, using sw model
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Q9NL65
Q9TR06
Q9R581
Q9R580
Q9R579
Q9S897
Q9S897
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Q9DE21
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Gapop 10.0 , Gapext 0.5
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Q9BP52
Q9N1W5
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Q9UCI4
Q9TRQ3
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sp_bacteria:*
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sp_virus:*
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Match Length DB
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sp_human:*
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Gaps

Score

Result Š Gaps

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Score 27; DB 7; Length 10; Pred. No. 1.2e+03;

22.0%; 50.0%;

1; Mismatches

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[1]
SEQUENCE FROM N.A.
SEQUENCE F., Tiercy J.M.;
Bettens F., Tiercy J.M.;
"Sequence of a new H.A-B44Null allele.";
Schaitted (NOV-1999). to the EMBL/GenBank/DDBJ databases.
EMBL; AJ251593; CAB95661.1; - 5AN9ADAD2C326362 CRC64;
                                                                                                                                          4; Conservative
                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                             11 RTEAADCC 18
                                                                                                                                                                                5 RPEPSSCC 12
                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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CQKRGR 18
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                                                                                            "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
Mol. Biol. Evol. 18:120-131(2001).
EMBL; AF215101; AAG60522.1;
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-20082971; PubMed-10613847;
Cactano A.K., Shlue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
Bowling A.T., Murray J.D.
"A comparative gene map of the horse (Equus caballus).";
Genome Res. 9:1239-1249(1999).
EMBL; AF134062; AAF31305.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 17, Last annotation update)
01-0TOCYTE ANTIGEN B.
H.A.B.
H.A.B.
H.A.B.
EUCCOYTE ANTIGEN B.
ELALYDEA: Metazoa (Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBL_TaxID=9796;
                                                                                                                                                                                           ;
0
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0
                                                  SEQUENCE FROM N.A.
MEDLINE-21105969; Pubmed=11158371;
Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
Fainzilber M.;
        Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=89451;
                                                                                                                                                                   Score 30; DB 5; Length 21; Pred. No. 4.6e+02; 1. Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 28; DB 6; Length 22;
Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 1
22 22
22 AA; 2643 MW; 2431653B0535E8EB CRC64;
                                                                                                                                        2F5672AB6B7171E9 CRC64
                                                                                                                                                                                                                                                                                                         01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
DOPAMINE RECEPTOR D2 (FRAGMENT).
                                                                                                                                                                                                                                                                                        22 AA
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                                                                                                                                                                     24.48;
66.78;
                                                                                                                                       21 AA; 2298 MW;
                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                               Equus caballus (Horse).
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                                                                                                                                                                     Query Match
Best Local Similarity
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 Conus arenatus.
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SEQUENCE
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NON_TER
SEQUENCE
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Q9MY73;
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09N1W5;
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MEDLINE-20528616; PubMed=11073974; Kobayashi M., Yu R.T., Yasuda K., Umesono K.; Kobayashi M., Yu R.T., Yasuda K., Umesono K.; "Cell-type-specific regulation of the retinoic acid receptor mediated by the orphan nuclear receptor TLX."; Mol. Cell. Biol. 20:8731-873(2000). EMBL; AF220160; AAG35365.1; ... SEQUENCE 19 AA; 2316 MW; 2CB3FB243FD48C28 CRC64;
                                                                                                                                                                    Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Akli S., Chomel J.C., Lacorte J.M., Bachner L., Poenaru A., Poenaru L.;
"Ten novel mutations in the HEXA gene in non-Jewish Tay-Sachs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.0%; Score 27; DB 13; Length 19; 66.7%; Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                        01-WAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
UORF4.
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Last sequence update)
Last annotation update)
19 AA
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PRT;
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Best Local Similarity 66.7
Matches 4; Conservative
PRELIMINARY;
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Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
Ascarididae; Ascaris.
NCBI_TaxID=6253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miura K., Miki H., Shimazaki K., Kawai N., Takenawa T.;
"Interaction of Ash/Grb-2 via its SH3 domains with neuron-specific
pl50 and p65.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea; Bovidae; Bovinae; Bos. NCBL_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9TR06;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
NEURON-SPECIFIC ASH/GRB-2 SH3 DOMAIN-BINDING PROTEIN (FRAGMENT).
Bos taurus (Bovine).
                                                                   Score 26; DB 5; Length 10, Pred. No. 1.7e+03;
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Pred. No. 1.6e+03;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Ascaris suum asabf-delta gene, exon 2.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB029815; BAA89496.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 316:639-645(1996).
16 AA; 1827 MW; E8B5540CDC9C828E CRC64;
                                      D41519D8611680C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8BADD0CD1EAB5861 CRC64;
                                                                                                                                                                                                                                                                                                         01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2000 (TrEMBLrel. 15, Last annotation update)
ASABF-DELTA (FRAGMENT).
                                                                                                                                                                                                                                                                            11 AA
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MEDLINE=96257761; PubMed=8687411;
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80.0%;
                                                                                       21.1%;
55.6%;
                                    1835 MW;
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                                                                   Ouery Match
Best Local Similarity 55...
5; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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18
18 AA;
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7 CEKRG 11
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Eukaryota, Metazoa; Brachlopoda; Linguliformea; Lingulata; Lingulida;
Linguloidea; Lingulidae; Lingula.
NCBL_TaxID=7574;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Usukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Pred. No. 1.2e+03;
2; Mismatches 2; Indels
                                                                                                               Score 27; DB 4; Length 21;
Pred. No. 1.4e+03;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Tillmann H., Eschrich K.;
"Structure of human FBD2 gene.";
Submitted (PRR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ238483; CAB53359.1;
HSSP; P00636; IFRP.
                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
FRUCTOSE-1,6-BISPHOSPHATASE (EC 3.1.3.11) (FRAGMENT)
FRP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 12 12
12 AA; 1382 MW; 4CEB259E57386403 CRC64;
                                                                     D4ACE2D1DA24D8EC CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ELONGATION FACTOR 1 ALPHA (FRAGMENT).
                                                                                                                                                                                                                                                                                                           12 AA.
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Hum. Mol. Genet. 2:61-67(1993).
EMBL; S61298; AAD13927.1; -.
HSSP; P06865; 1QBC.
NON TER
SEQUENCE 21 AA; 2494 MW; D41
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EMBL; AB056463; BAB33373.1; -.
                                                                                                                  22.0%;
41.7%;
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50.0%;
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Best Local Similarity 41./*,
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1 GTFFINKTEIED 12
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4 EKRGKYVV 11
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O86260;
01-NOV-1998 (TrEMBLrel. 08, Created)
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75.0%;
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50.0%;
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Best Local Similarity
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Best Local Similarity
Matches 3; Conserv
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4 DCCE 7
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Yoshino K., Miyachi M., Takao T., Bag P.K., Huang X., Nair G.B.,
Takeda T., Shimonishi Y.;
"Purification and sequence determination of heat-stable enterotoxin elaborated by a cholera toxin-producing strain of Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                         "Purification and sequence determination of heat-stable enterotoxin elaborated by a cholera toxin-producing strain of Vibrio cholerae
                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
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Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
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Yoshino K., Miyachi M., Takao T., Bag P.K., Huang X., Nair G.B.,
Takeda T., Shimonishi Y.;
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Pred. No. 2.5e+03;
1; Mismatches 0; Indels
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PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
SEQUENCE 17 AA; 1821 MW; 30FF036D018D601C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001489; Enterotoxin HS. PROSITE; PS00273; ENTEROTOXIN H STABLE; 1. SEQUENCE 18 AA; 1934 MW; 3080692D018D601C CRC64;
                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-ST-1, NAG-ST, VM-ST-HEAT-STABLE ENTEROTOXIN.
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Last annotation update)
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Pred. No. 2.4e+03;
1; Mismatches 0,
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01-MAY-2000 (TrEMBLrel. 13, Last sequence
01-UNV-2001 (TrEMBLrel. 17, Last annotation)
01-ST-2, VC-H-ST-HEAT-STABLE ENTEROTOXIN.
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NGRYSISRT 12
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                                                                                                                                                                                                                                                          Vibrio cholerae
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2 DCCE 5
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Q9R580;
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Q9R581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spernatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Sapindales; Rutaceae; Citrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                       MEDILINE-93314823; PubMed-8325391;
Yoshino K., Miyachi M., Takao T., Bag P.K., Huang X., Nair G.B.,
Takeda T., Shimonishi Y.;
"Purification and sequence determination of heat-stable enterotoxin
elaborated by a cholera toxin-producing strain of Vibrio cholerae
                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
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Pred. No. 3.18+03;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 25; DB 2; Length 19; Pred. No. 2.7e+03; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 FEBS Lett. 326:83-86(1993).
InterPro; IPR001489; Enterotoxin_HS.
PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
SEQUENCE 19 AA; 2048 MW; 308015F1A18D601C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chitin-binding proteins.";
Plant Physiol. 110:657-664(1996).
HSSP: P27275; IMMC.
PSEQUENCE. 22 AA; 2252 MW; 250CF86C0C32B748 CRC64;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
2N-BINDING PROTEIN (FRAGMENT).
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MEDLINE=96351190; PubMed=8742339;
                                                                                         01-ST-3-HEAT-STABLE ENTEROTOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Citrus sinensis (Sweet orange).
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DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DE TRXB PROTEIN (FRAGMENT).

GN 7RXB.

OS Riebsiella pneumoniae.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Riebsiella.

OC NCBL_TAXID=573;

RN [1]

RN Albrecht C. Kleiner D.;

RA Albrecht C. Kleiner D.;

RA Albrecht C. Kleiner D.;

RA Albrecht C. Sacural Similarity 80.08; Pred. No. 2.78+03;

RM 890C8715ECD2287A CRC64;

SQUENCE 13 AA: 1425 MW; 890C8715ECD2287A CRC64;

Best Local Similarity 80.0%; Pred. No. 2.78+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Search completed: February 21, 2002, 16:29:48 Job time: 184 sec

15 ADCCK 19 || || 9 ADACK 13

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Human proteoglycan MHC binding peptid Hepatitis GB virus Altered MHC determ Altered MHC determ Altered MHC determ KGF-2 deletion mut

KGF-2 antigenic re Human KGF-2 antige KGF-2 antigenic re

Human secreted pro Human gene 65 enco

Fragment of human

Tumour homing pept Mouse B16B15b mela

Murine melanoma ho Tumour homing pept

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Piq somatotropin t Immunogenic epitop

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Post-processing:

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Hanatoxin-like seq Hanatoxin-like seq Hanatoxin-like seq

Fragment of human

Binding agent homo T cell receptor be

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Amino acid sequenc

Hanatoxin-like seq Epitope comprising Peptide encoded by

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Use of CD44 protein and new peptide derivs - for developing prods for inflammation, immune-mediated tissue damage and tumour cell metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell adhesion molecule; CD44; antiinflammatory; rheumatoid; arthritis; tumor cell metastasis; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Telen MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patton KL,
                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
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AAR26097
AAW36061
AAY23788
                                                                                       AAY68195
AAY52849
                                                                                                                              AAY32892
AAB10306
                                                                                                                                                                       AAY87217
AAE06199
                                      AAY97107
AAG62723
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                  AAY99910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93WO-US10412.
92US-0973339
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Hale LP, Haynes BF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD44 peptide CD44-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-167121/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYDU-) UNIV DUKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-0CT-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9409811-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-MAY-1994
AAR53473;
                                                                                                                                                                                                                                                                                                                                                                                                            AAR53473
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                      Cattle, sheep GH p
Partial sequence o
Variant of residue
Pig GH peptide 35-
Epitope comprising
Tumour antigen ant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD44 peptide CD44-
CaMK peptide fragm
Partial sequence o
Residues 35-53 of
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                                                                             (without alignments)
68.385 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                  February 21, 2002, 16:26:09; Search time 23.83 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                             /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDS8/gcgdata/geneseqp/AA1981.DAT:*
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                                                                                                                                                                                                    210642
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                   hits satisfying chosen parameters:
                                                                                                                                                                               522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                              CEKNGRYSISRTEAADCCKAFN 22
                                                                                                                                                                                                                                                    Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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AAY57162
AAP80554
AAP805941
AAP80556
AAP80556
AAP80556
AAP80587
AAR49700
AAR49700
AAR49700
AAR49700

    protein search, using sw model

                                                                                                                                                           Gapop 10.0 , Gapext 0.5
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                                                                                                          US-08-753-851-1
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Match Length
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35.0
30.1
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Score

Result No. 123 37 37 36 36 36 35 35 35

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 $X \times C C C C C C \times S$ 

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The peptide has primary structural homology to a bovine growth hormone sequence. It can be used to raise antibodies which will potentiate the activity of the hormone in a vertebrate. The peptide can also be used to treat an (ab)normal vertebrate to boost growth, to having above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treat an (ab)normal vertebrate to boost growth, to bring abnormally low levels of growth up to the norm, to boost milk yield, or to boost or enhance other biological effects of growth hormone. Proportion of lean meat to fat may also be enhanced. The peptide may be linked to other antigens to produce a duel effect, eg all/part of somatostatin to create anti-somatostatin antibodies which would promote growth, or to all/part of a sex hormone molecule to provide simultaneous immunocastration.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Small peptide(s) contg. bovine growth hormone partial sequence - used for raising antibodies which will potentiate activity of hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Foot and mouth disease virus; bovine growth hormone; antibodies.
                                                                                                                                      Bovine growth hormone; peptide; partial sequence; antibody.
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Pred. No. 34;
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                                                                                                    Partial sequence of bovine growth hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Residues 35-53 of bovine growth hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA.
   AA.
                                                                                                                                                                                                                                                                                                                                              (COOP-) COOPERS ANIMAL HEALTH LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 12; 23pp; English.
 AAP80554 standard; protein; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide; 19
                                                                                                                                                                                                                                                                                                                                                                               James S, Aston R, Bomford R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.1%;
58.3%;
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                                                                    (first entry)
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Les 7; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in vertebrate.
                                                                                                                                                                                                                                                                         25-MAR-1988;
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                                                                   28-OCT-1990
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                                                                                                                                                                       Bos taurus.
                                                                                                                                                                                                         EP284406-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Si
Matches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention provides a peptide having an amino acid sequence KKXLKRQEAFDAY where X = Ala or Lys. The peptide is an excellent inhibitor for calmodulin-dependent phosphoenzyme II (CaMKII). Sequences AAX57160-161 are CaMKII inhibitor peptides and represent specific examples of the generic peptide given above. The present sequence represents a CaMK peptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - calmodulin-dependent phosphoenzyme
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                              The peptide can be used for treating inflammation and immune-mediated tissue damage such as occurs in the course of autoimmune diseases, e.g. rheumatoid arthritis. It can also be used for determining metastatic potential or to treat or prevent tumor cell metastasis. This peptide corresponds to AA 37-57 of the CD44
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Calmodulin-dependent phosphoenzyme II; CaMKII; inhibitor.
                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                     Score 123; DB 15;
Pred. No. 1.7e-12;
Mismatches 0;
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Pred. No. 4.7;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CaMK peptide fragment (residues 281-302)
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                                                                                                                                                                                                                                                                                                                                                                                            AAY57162 standard; peptide; 22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 2; 5pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A specific peptide inhibitor for
Claim 4; Page 14; 83pp; English
                                                                                                                                                                                                                                       ;;
0
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Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 8; Conserv
                                                                                                                                                    22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 AA;
                                                                                                                  protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP11152298-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-NOV-1997;
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                                                                                                                                                      Sequence
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AAY57162 RESULT

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Gaps

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Length 19; Indels

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RESULT AAP80554

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us-08-753-851-1.rag

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or more peptide fragments of GH, especially those of sequence AAR49699-719 and R455776-77, and/or peptide fragments of GRF.
                                                                                                                                                                                                                                                                                                                                                                           (COOP-) COOPERS ANIMAL HEALTH LTD.
                                                                                                                                                                      AAP80556 standard; protein; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 12; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               S, Aston R, Bomford R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.3%;
58.3%;
                                                           30.1%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                        87GB-0007398.
                                                                                                                                                                                                                                                                                                                                    88EP-0302656
                                                                                                                                                                                                               (first entry)
                                                 Query Match
Best Local Similarity 58.3°
المحافظ 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 58.3.
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rysignagaafc 19
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                                                                                                  6 RYSISRTEAADC 17
                                                                                                                    8 rysigntgvafc 19
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1988-272829/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA:
                               AA;
                               19
                                                                                                                                                                                                                                                                                                                                    25-MAR-1988;
                                                                                                                                                                                                                                                                                                                                                       27-MAR-1987;
                                                                                                                                                                                                               28-OCT-1990
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                                                                                                                                                                                                                                                                                             EP284406-A.
                                                                                                                                                                                                                                                                          Bos taurus
                                                                                                                                                                                          AAP80556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                James
                                                                                                                                                                                                                                                                                                                                                                                                                                      Small
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                                                                                                                                                              AAP80556
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                                                                                                                                                                              The peptide is residues 35-53 of bovine growth hormone. It can be used with peptides from foot and mouth disease virus in a vaccine to prevent FMDV infection, or to potentiate hormone activity, eg to improve growth
                                                                                                                    New peptide contg. T-helper cell epitope of foot and mouth virus - and opt. B-cell epitope, useful in vaccines and for potentiating hormone
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       {\tt GH} secretion in ruminants is induced by anti-somatostatin immunization and/or by potentiating immunomodulation of {\tt GRF} using 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Growth hormone; GH; somatotropin; growth hormone releasing factor; GRF; somatoliberin; somatostatin; ruminant; anabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Improving growth and carcass quality in pigs and ruminants - by stimulating secretion of endogenous growth hormone, partic. by vaccination with e.g. somatostatin
                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                               Length 19
                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                               Score 37; DB 10;
Pred. No. 34;
                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRF; somatoliberin; somatostatin; rum
feed-additive; immunization; vaccine.
                                                (COOP-) COOPERS ANIMAL HEALTH LTD. (WELL ) THE WELLCOME FOUNDATION LTD.
                                                                               Francis MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 29; 48pp; French.
                                                                                                                                                                                                                                                                                                                                                                          AAR49699 standard; peptide; 19 AA.
                                                                                                                                                            Claim 9; page 25; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Cattle, sheep GH peptide 35-53.
                                                                                                                                                                                                                                                               30.1%;
58.3%;
89WO-GB00311
                  88EP-0302656.
88GB-0021076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93WO-FR00793
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                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INMR ) RHONE MERIEUX SA.
                                                                                                                                                                                                                                                                                 7; Conservative
                                                                              James S, Rowlands DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus; Ovis aries
                                                                                                                                                                                                                                                                                                                  6 RYSISRTEAADC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roulet C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1994-082840/10.
                                                                                                 WPI; 1989-309504/42
                                                                                                                                                                                                              rate or milk prodn.
                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 7; Conser
                                                                                                                                                                                                                                 19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-AUG-1993;
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23-MAR-1989;
                  25-MAR-1988;
08-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                30-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9404187-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dufour R,
                                                                                                                                        activity.
                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                              AAR49699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The peptide has primary structural homology to a bovine growth hormone sequence. It can be used to raise antibodies which will potentiate the activity of the hormone in a vertebrate. The peptide can also be used to treat an (ab)normal vertebrate to boost growth, to bring abnormally low levels of growth up to the norm, to boost milk yield, or to boost or enhance other biological effects of growth hormone. Proportion of lean meat to fat may also be enhanced. The peptide may be linked to other antigens to produce a duel effect, ag all/part of somatostatin to create antisomatostatin antibodies which would promote growth, or to all/part of a sex hormone molecule to provide simultaneous immunocastration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                all peptide(s) contg. bovine growth hormone partial sequence - used r raising antibodies which will potentiate activity of hormone vertebrate.
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                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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   Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Length 19;
                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
Score 37; DB 15;
Pred. No. 34;
L; Mismatches 4
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Pred. No. 49;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Partial sequence of bovine growth hormone.
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Jones EV,
            92FR-0010159.
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                                                                                                                                                                                                                                                                                                                                       (first entry)
                            (INMR ) RHONE MERIEUX SA.
                                                                                                                                                                                                                        Conservative
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8 rysiqnagaafc 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clark MT,
                                                                                                                                                                                                                                        6 RYSISRTEAADC 17
                                             Roulet C;
                                                              WPI; 1994-082840/10.
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                                                                                                                                                                                                             Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PFIZ ) PFIZER INC.
                                                                                                                                                                              19 AA;
            20-AUG-1992;
                                                                                                                                                                                                                                                                                                                                      17-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JAN-1995;
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27-JAN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            epitope(s)
antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alila HW,
Sathe GM;
                                             Dufour R,
                                                                                                                                                                                                                                                                                                                                                                                        antibody.
                                                                                                                                                                                                                                                                                                                     AAW35265;
                                                                                                                                                                              Sequence
                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                            AAW35265
                                                                                                                                                                                                                                                                                    RESULT
     δy
                                                                                                                                                                                                                                                         Dp
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                                                                                                                                                                                                                                                                                                         The peptide is a variant which is antiqenically equiv. to residues 35-53 of bovine growth hormone. It can be used with peptides from foot and mouth disease virus in a vaccine to prevent FMDV infection, or to potentiate hormone activity, eg to improve growth rate or milk prodn.
                                                                                                                                                                                                                                                        New peptide contg. T-helper cell epitope of foot and mouth virus - and opt. B-cell epitope, useful in vaccines and for potentiating hormone
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Growth hormone; GH; somatotropin; growth hormone releasing factor; GRF; somatoliberin; somatostatin; ruminant; anabolism; feed-additive; immunization; vaccine.
                                                                              Foot and mouth disease virus; bovine growth hormone; antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                               Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                             Variant of residues 35-53 of bovine growth hormone.
                                                                                                                                                                                                                                                                                                                                                                             29.3%; Score 36; DB 10;
58.3%; Pred. No. 49;
iive 1; Mismatches 4;
                                                                                                                                                                                            (COOP-) COOPERS ANIMAL HEALTH LTD. (WELL ) THE WELLCOME FOUNDATION LTD.
                                                                                                                                                                                                                       Francis MJ;
         AAP90943 standard; peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA.
                                                                                                                                                                                                                                                                                         Claim 9; page 25; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR49700 standard; peptide; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 93WO-FR00793.
                                                                                                                                                                  88EP-0302656.
                                                                                                                                                   89WO-GB00311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUL-1994 (first entry)
                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                               7; Conservative
                                                                                                                                                                                                                      James S, Rowlands DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pig GH peptide 35-53.
                                                                                                                                                                                                                                                                                                                                                                                                                 6 RYSISRTEAADC 17
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8 rysignagaafc 19
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                                                                                                                                                                                                                                                                                                                                                      19 AA;
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                                            02-MAR-1990
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08-SEP-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa,
                                                                                                                                                                                                                                                                         activity.
                           AAP90943;
                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR49700;
                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                Bovidae
                                                                                                                                                                                                                                                                                                                                                                                               Matches
AAP90943
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                          Dp
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA for composite peptide comprising at least 2 somatotropin epitope(s) - useful as immunogen to elicit somatotropin stabilising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is an epitope comprising porcine somatotropin (pST) 1-190 residues 33-53. An expression vector containing a DNA molecule encoding a composite peptide, which comprises at least 2
Improving growth and carcass quality in pigs and ruminants - by stimulating secretion of endogenous growth hormone, partic. by vaccination with e.g. somatostatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Epitope comprising porcine somatotropin 1-190 residues 33-53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.3%; Score 36; DB 15; Length 19; 58.3%; Pred. No. 49; 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Epitope; pig; porcine; somatotropin; somatotrophin;
recombinant production; composite peptide; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O'Brien SP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miller TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Columns 29-30; 32pp; English.
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                                                                                                                                                                   Disclosure; Page 29; 48pp; French.
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19 AA;

Sequence

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The invention relates to a method for identifying a binding molecule having selective affinity for a ligand comprising: (a) selectively immobilising a diverse population of binding molecules to a solid support; (b) simultaneously contacting the diverse population immobilised on the solid support with 2 or more ligands; and (c) determining at least one binding molecule which selectively binds to one or more of the ligands. The method allows for the rapid and efficient methods for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identification of binding molecules which exhibit selective affinity for one or more ligands of interest. They are used particularly for identifying tumour-specific binding polypeptides which can be used as targeting agents for cancer therapy that minimises impact on non-tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumour antigen, antibody, CDR; complementarity determining region; binding molecule identification; tumour-specific binding polypeptide; cancer therapy; heavy chain.
                                                                                                                                                                                                                                    Gaps
non-contiguous ST epitopic amino acid sequences, e.g. the present sequence, and is free of receptor binding domain sequences, can be used to transform a host cell. The transformed cell can be used for the recombinant production of the composite peptide, which can be used as an immunogen to stimulate the production of anti-pST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying binding molecules for ligands, particularly tumour antitions - by selectively immobilising a population of binding molecules to a solid support and screening for binding to two or more ligands
                                                                                    antibodies (Ab) in pigs. Such Ab may increase the half life of co-administered pST in circulation.
                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                 DB 18; Length 21;
                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumour antigen antibody heavy chain CDR3 clone TA50.
                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                              29.3%; Score 36; 58.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                          AAY05067 standard; peptide; 19 AA.
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                                                                                                                                                                                                              Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Watkins JD,
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9 rysiqnaqaafc 20
                                                                                                                                                                                                                                                                 6 RYSISRTEAADC 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IXSY-) IXSYS INC.
                                                                                                                                           21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAX28244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-AUG-1997;
04-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huse WD,
                                                                                                                                                                                                                                                                                                                                                                                                                             AAY05067;
                                                                                                                                            Sequence
                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissues
                                                                                                                                                                                                                                                                                                                                                                          AAY05067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     viral infection; rheumatoid arthritis; AIDS; meningococcal bacteria; immunoglobulin; human connective tissue; cartilage; link protein; proteoglycan tandem repeat; PTR; Deisseria gonorrhoeae; MHC; major histocompatibility complex; class II; self epitope; autoantigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IgA protease precursor; IPP; bacterial polyprotein; autoimmune;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            substances interfering with bacterial poly:protein function
Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Medicaments for treating auto-immune or viral diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34; DB 17;
Pred. No. 77;
3; Mismatches 5;
   20;
DB 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cartilage link protein derivative H1.
                                                               Mismatches
Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                         AAR96887 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 32; Page 86; 117pp; German.
28.5%;
46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.68; 42.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95WO-EP03726.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94DE-4433708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                           3 KNGRYSISRTEAA 15
                                                                                                                                                                                           3 ktsrytlrrseas 15
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-188456/19.
                              Best_Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9609395-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                        AAR96887;
   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beck SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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DNA for composite peptide comprising at least 2 somatotropin epitope(s) – useful as immunogen to elicit somatotropin stabilising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is an epitope comprising porcine somatotropin (pST) 1-191 residues 35-53. An expression vector containing a DNA molecule encoding a composite peptide, which comprises at least 2 non-contiguous ST epitopic amino acid sequences, e.g. the present sequence, and is free of receptor binding domain sequences, can be used to transform a host cell. The transformed cell can be used for the recombinant production of the composite peptide, which can be used as an immunogen to stimulate the production of anti-pST antibodies (Ab) in pigs. Such Ab may increase the half life of co-administered pST in circulation.
                                       Epitope comprising porcine somatotropin 1-191 residues 35-53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide encoded by Snut 2425ES DNA used in HIV DNA vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.6%; Score 34; DB 18; Length 19; 58.3%; Pred. No. 1e+02;
                                                                                Epitope; pig; porcine; somatotropin; somatotrophin; recombinant production; composite peptide; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                          O'Brien SP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIV; human immunodeficiency virus; vaccine; AIDS; snut;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5;
                                                                                                                                                                                                                                                                                                                                                                                                                          Jones EV, Miller TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Columns 31-32; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY99910 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            silent nucleotide substitution.
                                                                                                                                                                                                                                                                                 95US-0388267.
                                                                                                                                                                                                                                                                                                                           92US-0901704
                                                                                                                                                                                                                                                                                                                                                95US-0388267
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17-FEB-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          Clark MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 RYSISRTEAADC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-558137/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                   (PFIZ ) PFIZER INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200029561-A2.
                                                                                                                                                                                                                                                                                                                     19-JUN-1992;
                                                                                                                                                                                                                                                                                   27-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                27-JAN-1995;
                                                                                                                                                                                                  US5686268-A.
                                                                                                                                                                                                                                            11-NOV-1997.
                                                                                                                                                               Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                          Alila HW,
Sathe GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibodies
                                                                                                                      antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG62702-22 represent hanatoxin-like sequences (HTLS) found in the semaphorin domain of mammalian secreted semaphorins. Hanatoxin is a tarantula toxin that selectively blocks some voltege-gated potassium and calcium channels. The HTLS is responsible for the dorsal root ganglion repulsion and growth come collapse activities associated with semaphorins. Polypeptides containing HTLS can be used to modulate the activity of calcium channels. The peptides can also be used as an antigen to generate antibodies that can then be used to modulate the activity of calcium channels by inactivating naturally occurring channel ligands. The peptides or antibodies can be used as an activity of calcium channels by inactivating naturally occurring channel ligands. The peptides or antibodies can be used as drugs to treat any condition or disease that is characterized by abnormal calcium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptide sequences that encompass the hanatoxin-like sequences of semaphorins, useful as a drugs to treat any condition or disease that is characterized by abnormal calcium channel function -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                           voltage-gated calcium channel; hanatoxin-like sequence; HTLS; semaphorin; dorsal root ganglion repulsion; growth cone collapse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
0
                                                                                                                                                                                                                                                                                                                       Hanatoxin; tarantula; toxin; voltage-gated potassium channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34; DB 22; Length 17;
Pred. No. 88;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                 Hanatoxin-like sequence from type 3 semaphorin hSema3C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW35266 standard; peptide; 19 AA.
                                                                                                                                                         AAG62706 standard; peptide; 17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 10; 29pp; English.
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66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-NOV-2000; 2000WO-US41943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0164056
                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 66.,
6; Conservative
                18
                                         ||||::: || |
| grynlnfheaggac 14
                  GRYSISRTEAADCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ||||| |
| tacadccla 9
                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200138491-A2
                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                          17-SEP-2001
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31-MAY-2001

Behar O,

AAG62706;

AAG627

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Gaps

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Indels

25-MAY-2000

AAW352667

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RESULT 13

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AAW35266

function. Sequence

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Search completed: February 21, 2002, 16:26:41
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              10-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Job time: 32 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                        The present invention relates to a nucleotide construct with optimised codons for use as a human immunodeficiency virus (HIV) DNA vaccine. The construct uses codons from highly expressed mammalian proteins to code for each derivative of an early, primary HIV envelope gene. The first stage in the production of the construct was the cloning of an HIV envelope gene. A nucleotide sequence encoding this gene was then created using codons from highly expressed mammalian genes. The present sequence is the peptide encoded by one of the snuts (AAA49060-A49079) that were created by redesigning the nucleotide construct so that restriction enzyme sites surrounded functional regions of the sequence. The snuts were then assembled into pieces (AAA49080-A49092). Each derivative of the envelope gene (AAA49097) was then built using the pieces. The HIV DNA vaccine may be used as a prophylactic vaccine and as a charactering the pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                   Producing nucleotide sequence construct with optimized codons for human immunodeficiency virus (HIV) genetic vaccine involves obtaining a first nucleotide sequence from a HIV patient, redesigning and assembling it with snuts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conotoxin; chronic pain; neuropathic pain; acetylcholine; receptor; antagonist; analgesic; drug; peptide; tau; cone snail; Conus; venom; migraine; treatment; therapy.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Lys, N-methyl-Lys, N,N-dimethyl-Lys or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 21; Length 13;
Pred. No. 94;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "Glu or gamma-carboxy-Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Glu or gamma-carboxy-Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N, N, N-trimethyl-Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY97089 standard; peptide; 20 AA.
                                                                                                                                                                                                                                  Example 3; 107; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.8%;
50.0%;
            27-MAR-2000; 2000WO-DK00144
                                    99DK-0000427
99US-0128558
                                                                           (STAT-) STATENS SERUM INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 26.8
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tau conotoxin sequence.
                                                                                                                              WPI; 2000-387778/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 SRTEAADCCK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :| :| ||||
3 arassapcck 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 AA;
                                                                                                                                         N-PSDB; AAA49079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conus marmoreus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200046371-A1
                                   29-MAR-1999;
09-APR-1999;
                                                                                                     Fomsgaard A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Novel analgesic short peptides from predatory cone snails for treating acute, chronic and neuropathic pain and migraines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                           Steele D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Several peptides have been characterised from Conus venoms. These include the alpha and mu conotoxins which target nicotinic acetylcholine receptors and muscle sodium channels respectively. Chronic or intractable pain as well as neuropathic pain is currently treated with a range of analgesic compounds. It is thought that the tau-conotoxins described could have applications as analgesic drugs and could be used for treating such acute, chronic and neuropathic pain as well as migraines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The venom of predatory cone snails comprises relatively small peptides which are targetted to various neuromuscular receptors and may be equivalent in their pharmacological diversity to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plants or secondary metabolites of microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 20;
                                                                                                                                                                                                           Shetty R, Olivera BM, Hooper D, Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 21;
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 28; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.8%;
62.5%;
04-FEB-2000; 2000WO-US03021.
                                                          99US-0118642
                                                                                                                     (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 26.8
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                (COGN-) COGNETIX INC
                                                                                                                                                                                                                                                                                              WPI; 2000-543489/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 AA;
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                                                          04-FEB-1999;
                                                                                                                                                                                                        Walker C,
Jones RM;
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Sequence Sequence Sequence Sequence

Sequence 45, P. Sequence 27, A. Sequence 27, A. Sequence 27, A. Seguence 27, A

Sequence

Sequence Sequence Sequence

Appli

Sequence Sequence S

Sequence

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SOFTWARES PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/143,311B
FILING DATE: 29-0CT-1993
CLASSIETCATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,339
FILING DATE: 30-0CT-1992
CLASSIETCATION: 436
APPLICATION NUMBER: 07/69,730
        US-08-651-136C-102
US-08-651-136C-103
US-08-651-136C-104
US-08-651-136C-108
US-08-651-136C-79
US-09-230-222-3
                                                                        US-08-208-264A-45
US-08-467-023-27
                                                                                              US-09-230-222-28
US-08-129-456A-26
                                                                                                                   US-08-360-821B-23
US-08-853-910-8
                                                                                                                                         US-08-432-871C-98
                                                                                                                                                  US-08-553-257A-17
                                                                                                                                                                                                                                                                                                    APPLICANT: HAYNES, BARTON F.
APPLICANT: HALE, LAURA P.
APPLICANT: PATTON, KAREN L.
APPLICANT: TELEN, MARILYN J.
APPLICANT: LIAO, HUA-XIN
TITLE OF INVENTION: AN ADHESION MOLECULE
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
                                                                                                                                                                        US-09-164-186-2
US-09-164-186-11
                                                                                                                                                               US-09-171-410-3
                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                              CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1579-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 07/669,730 FILING DATE: 15-MAR-1991 CLASSIFICATION: 436 ATTORNEY,AGENT INFORMATION: NAME: WILSON, MARY J.
                                                                                                                                                                                                                                                                     Sequence 1, Application US/08143311B Patent No. 5863540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 1579
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: peptide US-08-143-311B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
 US-08-143-311B-1
(without alignments)
39.701 Million cell updates/sec
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Patent No. 5210180
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Appli
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                                                                      February 21, 2002, 16:26:14; Search time 12.47 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3,
Sequence 5,
Sequence 5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 1,
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Sequence
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                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/3/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-388-267C-5
US-08-484-905-27
US-08-481-985-27
US-08-09-199-802-135
US-09-033-085A-26
US-09-033-085A-26
US-09-139-802-135
US-09-031-802-135
US-08-05-136-48
US-08-05-136-48
US-08-488-212A-31
US-08-468-203-31
US-08-468-203-31
US-08-468-203-31
US-08-468-203-31
US-08-468-203-31
US-08-408-111-31
US-08-408-011-31
US-08-408-014
US-08-276-776-14
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US-09-329-350-8
US-09-189-060B-57
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                                                                                                                                                                                             212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                        CEKNGRYSISRTEAADCCKAFN 22
                                                                                                                                                                                                                                                                                            Listing first 45 summaries
                                                    - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5210180-5
                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                 Issued_Patents_AA:*
                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                   US-08-753-851-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0 Maximum DB seq length: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                   Title:
Perfect score:
                                                                                                                                                               Scoring table:
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                                                                                                                                                                                             Searched:
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                                                                        Run on:
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APPLICANT: ROWLANDS, Stephen
APPLICANT: ROWLANDS, David J.
APPLICANT: FRANCIS, Michael J.
TITLE OF INVENTION: PEPTIDES
NUMBER OF SEQUENCES: 1
CORRESPONDER ADDRESS:
ADDRESSEE: DONALD BROWN; DIKE, BRONSTEIN, ROBERTS &
                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB 2;
Pred. No. 24;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 20845
REFERENCE/DOCKET NUMBER: 40366-PCT
FELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEFAX: 200291 STRE UR
INFORMATION FOR SEG ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/571615
FILING DATE: 09-NOV-1990
APPLICATION NUMBER: GB 8821076.0
FILING DATE: 08-SEP-1988
ATTORNEY AGENT INFORMATION:
NAME: BROWN, DONALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CLARK, MICHAEL T.
APPLICANT: ALILA, HECTOR W.
APPLICANT: MILLER, THOTHY J.
TITLE OF INVENTION: FUSION PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/07/921,447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08388267C Patent No. 568628 GENERAL INFORMATION: APPLICANT: JONES,, ELAINE V. APPLICANT: SATHE,, GANESH M.
Sequence 5, Application US/07921447 Patent No. 5864008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.3%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLARK,, MICHAEL T
                                                                                                                                                                                                             130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O'BRIEN, SHAWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 amino acids
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Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                    STATE: Massachusetts
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                               CUSHMAN
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RYSIQNAQAAFC 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 RYSISRTEAADC 17
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                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY.

MOLECULE TYPE: pe
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                                                                                                                                                                                                                                                                                          02109
                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-388-267C-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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                                                     ;
                   Length 22;
                                                         Indels
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                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: JAMES, Stephen
APPLICANT: ROWIANDS, David J.
APPLICANT: FRANCIS, Michael J.
TITLE OF INVENTION: PEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: DONALD BROWN; DIKE, BRONSTEIN, ROBERTS ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/921,447
     100.0%; Score 123; DB 2; 100.0%; Pred. No. 3.2e-12; Vienatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 2;
Pred. No. 17;
1; Mismatches
                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/571615
FILING DATE: 09-NOV-1990
APPLICATION NUMBER: GB 8821076.0
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                             Sequence 3, Application US/07921447 Patent No. 5864008
                                                                                          1 CEKNGRYSISRTEAADCCKAFN 22
                                                                                                                  1 CEKNGRYSISRTEAADCCKAFN 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: BROWN, DONALD
REGISTRATION NUMBER: 20845
REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
TELECHHONE: (617) 523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.1%;
58.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
       Ouery Match
Best Local Similarity 100.0
Matches 22, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 19 amino acids
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Best Local Similarity 58.3
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ANTI-SENSE:
US-07-921-447-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: M. COUNTRY:
                                                                                                                                                                                           RESULT 2
US-07-921-447-3
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Length 19; 4.; Indels

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APPLICANT: Mottez, Estelle
APPLICANT: Mottez, Jean-Pierre
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourlisky, Philippe
TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
TITLE OF INVENTION: Determinant
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.6%; Score 34; DB 1; Length 19; 58.3%; Pred. No. 47; 5. Indels ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= ""THIS PEPTIDE REPRESENTS RESIDUES 35-53 OF PST1-191""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: PC-DOS-/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 1300 I Street, N.W., Suite 700 Washington
                                                                                          APPLICATION NUMBER: US/08/388, 267C FILING DATE: 27-JAN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/484,905
                                                                                                                                                                                                                  PC9042A
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27, Application US/08484905
Patent No. 5976551
GENERAL INFORMATION:
                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: KOLLER, ALAN L.
REGISTRATION NUMBER: 37,371
REFERENCE/DOCKET NUMBER: PC9(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-573-2118
TELEPHONE: 212-808-883
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUNE-1995
                                                                                                                                                                                                                                                                                                                                 LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          internal
                                                                                                                                                                                                                                                                                                                                                                                                                peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1..19
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 RYSISRTEAADC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 RYSIQNANAAFC 19
                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: D.C.
ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linea MOLECULE TYPE: pe HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 0'
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE: 1 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-388-267C-6
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OF PST1-190""
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                                                                                                                                                                                                        SOFTAMES PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,267C
FILING DATE: 27-JAN 1995
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: ROLLER, ALAN L.
REGISTRATION NUMBER: 37,371
REFERENCE/DOCKET NUMBER: 97,371
REFERENCE/DOCKET NUMBER: 37,371
RELEPHONE: 212-573-2118
TELEPHONE: 212-608-8893
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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Patent No. 5686268
GENERAL INFORMATION:
APPLICANT: JONES,, ELAINE V.
APPLICANT: O'BRIEN, SHAWN
APPLICANT: CLARK,, MICHAEL T.
APPLICANT: ALILA,, HECTOR W.
APPLICANT: ALLICA, TIMOTHY J.
TITLE OF INVENTION: FUSION PROTEINS
COMMUNER OF SEQUENCES: 24
                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                  ADDRESSEE: PFIZER INC.
STREET: 235 EAST 42ND STREET
CITY: NEW YORK
STATE: NY
COUNTRY: U.S.A.
ZIP: 10017-5755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: PFIZER INC.
235 EAST 42ND STREET
                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 58.37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
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ADDRESSEE: PFIZER IN
STREET: 235 EAST 42N
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 RYSISRTEAADC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 10017-5755
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Gaps

us-08-753-851-1.rai

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APPLICANT: Ojcius, David
APPLICANT: Casrouge, Armanda
TITLE OF INVENTION: Altered Major Histocompatibility Complex
NUMBER OF SEQUENCES: 127
                                                                                                                                                                                                                       Score 32; DB 3; Length 16; Pred. No. 78;
                                                                                                                                                                                                                                                                      2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/370,476 FILING DATE:
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REGISTRATION NUMBER: 25,146
                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
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PRIOR APPLICATION DATA:
APPLICATION UNDRER: US 08/117,575
FILING DATE: 07-5EP-193
APPLICATION NUMBER: US 08/072,787
FILING DATE: 06-UN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
PRIOR APPLICATION NUMBER: US 07/92,473
FILING DATE: 15-NOV-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mottez, Estelle
Abastado, Jean-Pierre
Kourilsky, Phillipe
Lone, Yu-Chun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27, Application US/08370476 Patent No. 6153408
                                                                                                                                                                                                                     Query Match 26.0
Best Local Similarity 41.7
Matches 5; Conservative
    TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                       16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202-408-4400
                                                                                         ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-481-985B-27
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4 ENGKETLQRTDA 15
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ADDRESSEE:
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APPLICANT:
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APPLICANT: Abastado, Jean-Pierre
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourlisky, Phillipe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION:
NUMBER OF SEGUENCES: 148
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/481,985B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                 CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNBER: US 07/792,473
FILING DATE: UNOV-1991
CLASSIFICATION: 530
ATTORNEY,AGENT INFORMATION:
NAME: POTLER, Jane E. R. REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 03495.0106-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Meyers, Kenneth J.
NAME: Meyers, Kenneth J.
NEGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0106-04000
TELECOMPUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32; DB
Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27, Application US/08481985B Patent No. 6011146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                 TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 41.7%
Best Local Similarity 5.7%
                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: peptide US-08-484-905-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 KNGRYSISRTEA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 ENGKETLQRTDA 15
                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
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ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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TITLE OF INVENTION: PEPTIDES IMMUNOLOGICALLY RELATED TO PROTEINS OF A VIRAL AGENT AND THEIR BIOLOGICAL APPLICATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ruoslahti, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
TITLE OF INVENTION: Same
                                                                                                                                                                                                                                                                                 Gaps
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US-09-139-802-132
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94;
                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                               4; Mismatches
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CURRENT FILING DATE: 1998-08-25
EARLIER APPLICATION NUMBER: 08/926,914
EARLIER APPLICATION NUMBER: 08/710,067
EARLIER FILING DATE: 1997-09-10
MUMBER: OB/710,067
NUMBER: OF SEQ ID NOS: 226
SOFTWARE: PATENTIN Ver: 2.0
SEQ ID NO 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
                                                                                                                                                                                                                                        Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COSIC, IRENA
BIQUARD, JEAN-MICHEL
HEARN, MILTON TW
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 132, Application US/09139802
; Patent No. 6180084
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 48, Application US/08290736C Patent No. 6294174 GENERAL INFORMATION: APPLICANT: KRSMANOVIC, VELIBOR
                                                                                                                        not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.2%;
                                                                                                                                                                                                                                        26.0%;
43.8%;
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TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                          not relevant
                                                                                                                                                                                                                                                                               7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                        TOPOLOGY: not relevan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: P-LJ 3203
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Best Local Similarity
                                                                                                 TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                            Best Local Similarity
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2 CCRQFN 7
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US-09-139-802-132
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                                                           Score 32; DB 4; Length 16;
Pred. No. 78;
5; Mismatches 2; Indels
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STREET: 1100 NEW YORK AVE, NW, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, version #1.30 CURRENT APPLICATION DATA:

PPLICATION NUMBER: US/09/023,082A FILING DATE: 13-FEB-1998 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: GENTZ, REINER L.
TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1488.0360008/EKS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01790
FILING DATE: 14-FEB-1995
PRIOR APPLICATION NUMBER: US 08/461,195
FILING DATE: 05-JUN-1995
FILING DATE: 05-JUN-1995
FILING DATE: 13-AUG-1996
FILING DATE: 13-AUG-1996
FILING DATE: 13-AUG-1996
FILING DATE: 13-AUG-1996
FILING DATE: 28-FEB-1997
FILING DATE: 28-FEB-1997
FILING DATE: 28-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/910,875
FILING DATE: 13-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,561
FILING DATE: 13-AUG-1997
ATTORNEYAGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/862,432 FILING DATE: 23-MAY-1997
                                                                                                                                                                                                                                                                           Sequence 26, Application US/09023082A Patent No. 6077692 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COLEMAN, TIMOTHY A. GRUBER, JOACHIM R. DILLON, PATRICK J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36,688
                                                                                                                                                                                                                                                                                                                                    RUBEN, STEVEN M.
JIMENEZ, PABLO
DUAN, D. ROXANNE
RAMPY, MARK A.
MENNRICK, DONNA
ZHANG, JUN
NI, JIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOORE, PAUL A.
                                                                                                   5; Conservative
                                                                                                                                                               4 ENGKETLQRTDA 15
                                                                                                                                        3 KNGRYSISRTEA 14
                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                        RESULT 9
US-09-023-082A-26
  US-08-370-476-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                 Matches
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GENERAL INFORMATION:
APPLICANT: Huber, Brian
APPLICANT: Richards, Cynthia
APPLICANT: Richards, Cynthia
TITLE OF INVENTION: Molecular Constructs Comprising a Carcinoembryonic Antigen (
TITLE OF INVENTION: Transcriptional Regulatory Region
FILE REFERENCE: PB1087US4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Consensus sequence G2 from transcriptional dictionary of Locke; OTHER INFORMATION: nd Buzard (1990). US-08-481-968A-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1.21

OTHER INFORMATION: /note= "Partial amino acid sequence OTHER INFORMATION: of the growth inhibitory factor" US-07-696-051B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31; DB 1; Length 21;
Pred. No. 1.5e+02;
3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 30; DB 4; Length 8; Pred. No. 1.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/08/481,968A CURRENT FILING DATE: 1998-06-07 NUMBER OF SEQ ID NOS: 36
                                          FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 410164/1990
FILING DATE: 13-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 410165/1990
FILING DATE: 13-DEC-1990
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 119620/1990
FILING DATE: 09-MAY-1990
                                                                                                                                                                                                                   NAME: Blerman, Jordan B.
REGISTRATION NUMBER: 18,629
REFERENCE/DOCKET NUMBER: TSU-16
TELECOMMUNICATION INFORMATION:
TELEPAN: (212)889-6426
TELERAX: (212)889-6426
IFELEX: PATENLAW (via ITT)
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-481-968A-33; Sequence 33, Application US/08481968A; Patent No. 6300490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.2%; 29.4%;
                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 21 amino acids
TYPE: AMINO ACID
TYPE: AMINO ACID
TYPE: Peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Consensus sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
TISSUE TYPE: Cerebral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 KNGRYSISRTEAADCCK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 KGGEAAEAEAEKCSCCQ 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Peptide LOCATION: 1..21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: 1
SEQ ID NO 33
LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δy
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APPLICANT: Miyatake, Tadashi
APPLICANT: Uchida, Yoko
APPLICANT: Ihara, Yasuo
ITILE OF INVENTION: GROWTH-INHIBITORY FACTOR AND CDING
TITLE OF INVENTION: FOR GROWTH-INHIBITORY FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Jordan B. Bierman, BIERMAN AND MUSERLIAN 757 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
AURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O7/696,051B
FILING DATE: 19910506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 31; DB 4; Pred. No. 1.4e+02;
                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,736C
FILING DATE: 16-No. 6294174-1994
CLASSIFICATION OATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 19-FEB-1993
APPLICATION NUMBER: FR92/01883
FILING DATE: 19-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
NAME: SADOFF, B.J.
PREGISTATION NUMBER: 366633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 1721-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-290-736C-48
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
TELEFAX: 7038164100
                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/07696051B Patent No. 5214031 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 48: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 25.2%;
Best Local Similarity 46.2%;
Matches 6; Conservative
                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                      CITY: ARLINGTON
                                     STATE: VA
COUNTRY: USA
ZIP: 22201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10017
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Jordan B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 NNEYRNSRTESSN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 NGRYSISRTEAAD 16
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New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-696-051B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
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NUMBER OF SEQUENCES: 57
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    Gaps
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    Indels
                                                                                                                                                                         Sequent No. 5665355
Setent No. 5665355
GENERAL INFORMATION:
APPLICANT: Primi, Daniele
TITLE OF INVENTION: Diagnosis and Treatment of
TITLE OF INVENTION: ADDS Onset
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas E. Popovich, Thomas
ADDRESSEE: Popovich & Associates
STREET: 80 South 8th Street
CITY: Minneapolis
STATE: Minneapolis
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 31, Application US/08320306
Sequence 31, Application US/08320306
GENERAL INFORMATION:
APPLICANT: Primi, Daniele
TITLE OF INVENTION: Diagnosis and Treatment of
TITLE OF INVENTION: AIDS Onset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB MEDIUM TYPE: Storage
COMPUTER: IBM Compatible Compaq Prolinea
COMPUTER: 4/66
OPERATING SYSTEM: MS-DOS Version 5
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,212A
FILING DATE: 07-Jun-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/973,485
FILLING DATE: NO. 566535ember 9, 1992
FILLING DATE: NO. 566535ember 9, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. Popovich
REGISTRATION NUMBER: 30699
REFERENCE/DOCKET NUMBER: 3678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 334-8994
INFORMATION FOR SEQ ID NO: 31: SEQUENCE CHARACTERISTICS:
    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chemical Synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 50.0
Matches 5; Conservative
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; IMMEDIATE SURCE: Chemius-08-488-212A-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 YSISRTEAAD 16
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                                         14 AADCCKA 20
                                                                                1 AANCCAA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                US-08-488-212A-31
  Matches
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                                                                                                                                                                            COMPOTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB MEDIUM TYPE: Storage
COMPUTER: IBM Compatible Compag Prolinea COMPUTER: 4/66
OPERATING SYSTEM: MS-DOS Version 5
SOFTWARE: Microsoft Word for Windows CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/973,485
FITUING DATE: NO. 5891623ember 9, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. Popovich
REGISTRATION NUMBER: 36099
REFERENCE/DOCKET NUMBER: 3678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 334-8991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: February 21, 2002, 16:27:00 Job time: 46 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemical Synthesis
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/320,306
FILING DATE: 06-OCT-1994
CLASSIFICATION: 435
CORRESPONDENCE ADDRESS:
ADDRESSE: Thomas E. Popovich,
ADDRESSE: Popovich & Associate
STREET: 80 South 8th Street
CITY: Minneapolis
STATE: Minnesota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (612) 334-8991
TELEFAX: (612) 334-8994
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                    COUNTRY: USA
ZIP: 55402-2111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 YSISRTEAAD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 YSVSRSKTED 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) DESCRIPTION: pe
; IMMEDIATE SOURCE:
US-08-320-306-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 21, 2002, 16:29:24; search time 12.81 Seconds (without alignments) 136.769 Million cell updates/sec Run on:

US-08-753-851-2

135 1 CNTSQYDTYCFNASAPPEEDCTS 23 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

4466 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 23

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:\* pir2:\* pir3:\* pir4:\* PIR\_68:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result		8 0.00			Paris Contract	CONTRACTOR	
	Score	Match	Length	DB.	GI .		Description
П	28	20.7	18	7	S39845		2-aminobenzoate-Co
7		20.0	19	7	C48363		2-hydroxyglutaryl-
3		20.0	21	7	S47207		T-cell receptor J-
4	56	19.3	12	~	PT0228		Iq heavy chain CDR
Ŋ	56	19.3	13	7	A28953		alpha-conotoxin SI
9	56	19.3	16	~	A39109	C	hypothetical prote
7	2	19.3	16	~	PH1317	•	Ig heavy chain DJ
œ	25.5	18.9	20	~	209802	_	hypothetical prote
6	52	18.5	12	7	PH1458	_	T-cell receptor be
10	25	18.5	15	7	B45474		thrombospondin 2 -
11	25	18.5	16	7	A60839		neurokinin A homol
12	25	18.5	16	N	PH0763		T-cell receptor be
13	25	18.5	16	N	PH0759		T-cell receptor be
14		18.5	17	~	A42920		fatty acid ethyl e
15		18.5	18	7	B24867		scyliorhinin II -
16	25	18.5	20	7	877989		cytochrome-c oxida
17		18.5	20	~	S17992		cytochrome-c oxida
18	N	18.5	22	~	C39800		calcium-activated
19	24.5		23	7	B42382		replication initia
20	24	17.8	10	7	PC2171		triacylglycerol li
21	24	•	12	7	S26544		T-cell receptor be
22	24		13	-	NTKNAS		alpha-conotoxin SI
23	24	•	18	7	A56798		dermatan sulfate p
24	24	•	19	~	A44379		alpha-conotoxin SI
25	24	•	19	7	A61377		endometrial secret
56	24	•	20	~	JT0410		bombyxin-IV chain
27	24	17.8	20	7	B60977		
28	24	17.8	20	7	_		hypothetical prote
29	24	17.8	22	7	PH1359		•—

alpha-conotoxin Ep collagen alpha 1(I	tocopherol-binding	preabsorbing antig	C1-inhibitor - hum	light harvesting c	mannose-specific 1	45/47K antigen - M	protein-tyrosine k	Ig heavy chain CDR	H+-transporting AT	nucleolin - bovine	crystallin - Pacif	T-cell receptor be	convulsant peptide
A59042 I65270	S29272	. A46463	I54284	PT0037	C39509	A49237	S24780	PT0286	868393	S02808	E60894	C49404	A59048
0 0	<b>(7</b> (	N (N	7	7	7	7	7	7	7	~	7	7	7
16	8 5	13	14	15	16	17	18	18	19	19	20	20	23
17.4	17.0	17.0	17.0	17.0	17.0	17.0	17.0	17.0	17.0	17.0	17.0	17.0	17.0
23.5	23	23	23	23	23	23	23	23	23	23	23	23	23
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## ALIGNMENTS

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C.Species: Pseudomonas sp.
C.Species: Pseudomonas sp.
C.Species: Pseudomonas sp.
C.Species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
C.Accession: S39845
R.Altenschmidt, U.; Fuchs, G.
Eur. J. Biochem. 205, 721-727, 1992
A.Title: Novel aerobic 2-aminobenzoate metabolism. Purification and characterization from a denitrifying Pseudomonas sp.
A.Reference number: S22402; MUID:92241310
A.Accession: S39845
2-aminobenzoate-CoA ligase, anaerobic - Pseudomonas sp. (strain KB740) (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 8.8e+02;
2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                        A;Accession: S39845
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10,'X',12-14,'X',16-18 <ALT>
                                                                                                                                                                                                                                                                                                                                                                                               20.7%;
35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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3 TSQYDTYCFNASAPPEE 19 δ

1 TSHVDTFARRXLPPXEQ 17 qq

2.hydroxyglutaryl-CoA dehydratase gamma chain - Fusobacterium nucleatum (fragment)
2.hydroxyglutaryl-CoA dehydratase gamma chain - Fusobacterium nucleatum
C;Species: Fusobacterium nucleatum
C;Date: 19-Nov-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Mar-1995
C;Accession: C48363
B;Klees, A.G.; Linder, D.; Buckel, W.
Arch. Microbiol. 158, 254-301, 1992
A;Title: 2-Hydroxyglutaryl-CoA dehydratase from Fusobacterium nucleatum (subsp. nucle
A;Reference number: A48363; MUID:9303807
A;Accession: C48363
A;Accession: C48363
A;Accession: C48363
A;Accession: C48363
A;Residues: preliminary
A;Molecule type: protein
A;Residues: 1-19 < KLES
A;Residues: 1-19 < KLES
A;Residues: 1-19 < KLES
A;Residues: 1-19 < KLES
A;Rote: sequence extracted from NCBI backbone (NCBIP:118485)

Gaps ; 0 20.0%; Score 27; DB 2; Length 19; 40.0%; Pred. No. 1.3e+03; ive 2; Mismatches 4; Indels 4; Conservative Query Match Best Local Similarity Matches 4; Conserv

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2 NTSQYDTYCF 11 | :|| : | 2 NIXEYDDFIF 11 ōλ

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Gaps

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hypothetical protein 1 - hepatitis C virus
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Species: 18-0ct-1991 #sequence_revision 18-0ct-1991 #text_change 18-Jun-1993
C;Accession: A39109
R;Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Teka Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
A;Title: Characterization of the terminal regions of hepatitis C viral RNA: identific A;Reference number: A39109; MUID:91156678
A;Accession: A39109
A;Stetus: preliminary
A;Molecule type: mRNA
A;Residues: 1-16 cHAN>
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A;Title: Predominance of fetal type DJH joining in young children with B precursor ly A;Reference number: PH1302; MUID:93094761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein 1 estrogen receptor 5'-region - chicken (Species: Gallus Ghicken) (C.) Species: Gallus (chicken) (C.) Species: Gallus (chicken) (C.) Species: Gallus (chicken) (C.) Accession: S08605 (C.) Accession: S08605 (C.) Accession: S08605 (C.) Accession: S08605 (C.) Accession: Somethy (C.) Accession: S08605 (C.) Accession: S086
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PH1317
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            Length 13;
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Pred. No. 1.5e+03;
2; Mismatches 7; Indels
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                                                                                      6; Indels
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        Score 26; DB 2;
Pred. No. 1.2e+03;
                                                                                      Mismatches
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A; Residues: 1-16 <WAS>
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
19.3%;
Best Local Similarity 35.7%;
Matches 5; Conservative
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                                                                                          Conservative
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Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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A; Residues: 1-13 <2AF>
A; Residues: 1-13 <2AF>
A; Note: this sequence was confirmed by chemical synthesis
C; Comment: This paralytic toxin from a fish-hunting cone snail inhibits the acetylcholin C; Superfamily: alpha-conotoxin
C; Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurot F; 2-7, 3-13, Oslutiide bonds: #status experimental
F; 2-7, 3-13, Modifica site: amidated carboxyl end (Cys) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ig heavy chain CDR3 region (clone 1-112) - human (fragment)
C; Species: Homo sapiens (man)
C; Scacession: PT0228
R; Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A; Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A; Reference number: PT0222; MUID:91108337
A; Accession: PT0228
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C;Species: Conus striatus (striated cone)
C;Species: 30-Jun-1989 #sequence_revision 25-Apr-1997 #text_change 23-May-1997
C;Accession: A28953
R;Zafaralla, G.C.; Ramilo, C.; Gray, W.R.; Karlstrom, R.; Olivera, B.M.; Cruz, Biochemistry 27, 7102-7105, 1988
A;Title: Phylogenetic specificity of cholinergic ligands: alpha-conotoxin SI. A;Reference number: A28953; MUID:89062448
                                                                      T-cell receptor J-alpha wnVIII.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Bate: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 05-Nov-1999
C;Accession: S47207
R;Plaza, A.; Kono, D.H.; Theofilopoulos, A.N.
submitted to the EMBL Data Library, February 1993
A;Reference number: S40133
A;Reference number: S40133
A;Recession: S47207
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-21 <-PLA>
A;Residues: 1-21 <-PLA>
A;Cross-references: EMBL:X71032; NID:9506610; PIDN:CAA50349.1; PID:9510318
C;Keywords: T-cell receptor
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A; Residues: 1-12 < YAM>
A; Experimental source: B lymphocyte
C; Keywords: heterotetramer; immunoglobulin
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Best Local Similarity 62.5
Matches 5; Conservative
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Matches 7; Conservative
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R;Conlon, J.M.; Thim, L.
Gen. Comp. Endocrinol. 71, 383-388, 1988
A;Title: Isolation of the tachykinin, Des[Ser(1)Pro(2)] scyliorhinin II from the inte
A;Reference number: A60839; MUID:89053024
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J. Exp. Med. 174, 1371-1383, 1991
A,Title: T cell receptor genes in a series of class I major histocompatibility compleallelic exclusion and antigen-specific repertoire.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: T cell receptor genes in a series of class I major histocompatibility comple allelic exclusion and antigen-specific repertoire.

A; Reference number: PH0746; MUID:92078846

A; Accession: PH0763
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                                                                                                                                                                                                                                                   neurokinin A homolog - marbled electric ray
N;Alternate names: des-Ser(1),Pro(2) scyliorhinin II
C;Species: Torpedo marmorata (marbled electric ray)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: A60839
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C;Accession: PH0759
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
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R; Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
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A;Cross-references: EMBL:X60857; NID:g50933; PIDN:CAA43247.1; PID:g50934
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 1-16 (CON>
C;Reywords: amidated carboxyl end; neuropeptide; tachykinin
F;16/Modified site: amidated carboxyl end (Met) #status experimental
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Pred. No. 2.1e+03;
1; Mismatches 5; Indels
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                               Indels
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Pred. No. 2.1e+03;
  Pred. No. 1.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                               Mismatches
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                         2;
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40.0%;
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66.7%;
57.1%;
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                               Conservative
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
                                                                                2 NTSQYDT 8
                                                                                                                  | :|:||
3 NQAQFDT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A60839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 ASAPPE 18
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PH0759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treal receptor beta chain (clone 332/1K) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Stecession: PH1458; S26543
R; Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Kc
J. Exp. Med. 177, 811-820, 1993
A; Title: T cell receptor selection by and recognition of two class I major histocompatib
A; Reference number: PH1430; MUID:93171821
A; Reference number: PH1430; MUID:93171821
A; Molecule type: mRNA
A; Residues: 1-12 cASA
A; Experimental source: cytclytic T-lymphocyte, clone 332/1K
R; Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wić
J; Exp. Med. 176, 439-447, 1992
A; Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A; Reference number: S26512; MUID:92364546
A; Residues: 1-12 cAA2
A; Casarova: preliminary
A; Molecule type: mRNA
A; Residues: 1-12 cAA2
A; Casarova: 1-12 cAA2
A; Cross-references: EMBL: K67993
A; Experimental source: cytolytic T-lymphocyte, clone Cw3/C44
C; Superfamily: immunoglobulin homology
C; Keywords: receptor; T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hrombospondin 2 - bovine (fragment)

Ithrombospondin 2 - bovine (fragment)

NyAlternate names: corticotropin-induced secreted protein (CISP); thrombospondin homolog (Species: Bos primigenius taurus (cattle)

C; Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997

R; Peblerin, S: Lafeuillade, B; Scherrer, N.; Gagnon, J.; Shi, D.L.; Chambaz, E.M.; Fei J. Biol. Chem. 268, 4304-4310, 1993

A; Title: Corticotropin-induced secreted protein, an ACTH-induced protein secreted by adr. A; Reference number: A45474

A; Reference number: A45474

A; Molecule type: protein

A; Residues: 1-15 < Peb.

A; Experimental source: adrenocortical cells

A; Note: sequence extracted from NCBI backbone (NCBIP:125842)
                                                   PIDN:CAA27431.1; PID:963379 for residue 5 as Gly and TTC for residue
                                                                                                                                                                                                                                                   ij
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Pred. No. 1.6e+03;
1: Mismatches 5; Indels
                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                       Score 25.5; DB 2;
Pred. No. 2.2e+03;
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                                                                                                                                                                                                                                                1; Mismatches
                                                A;Cross-references: EMBL:X03805; NID:963378; A;Note: the authors translated the codon TTT C;Superfamily: unassigned leader peptides
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Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity
Matches 5; Conserv
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A; Molecule type: mRNA
A; Residues: 1-20 <KRU>
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õ g Query Match

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Job time: 109 sec
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C;Species: Homo sapiens (man)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C;Accession: A42920
R;Bora, P.S.; Wu, X.; Spilburg, C.A.; Lange, L.G.
A;Biol. Chen. 267, 131217-13221, 1992
A;Title: Purification and characterization of fatty acid ethyl ester synthase-II from hu
A;Reference number: A42920; MUID:92317032
A;Accession: A42920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)
C;Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 08-Dec-1995
C;Accession: B24867
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                                                A;Molecule type: mRNA
A;Residues: 1-16 <CAS>
A;Cross-references: EMBL:X60854; NID:q53878; PIDN:CAA43244.1; PID:q53879
A;Experimental source: Tlymphocyte
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Riconton, J.M.; Deacon, C.F.; O'Toole, L.; Thim, L.
FEBS Lett. 200, 111-116, 1986
A;Title: Scyliorhinin I and II: two novel tachykinins from dogfish gut.
A;Reference number: A91359; MUID:86192829
A;Rocession: B24867
A;Rodecule type: protein
A;Redecule type: protein
A;Redecule type: protein
A;Redecule type: protein
A;Redecule type: protein
CONN
C;Reywords: 1-18 <CONN
C;Reywords: amidated carboxyl end; neuropeptide
F;18/Modified site: amidated carboxyl end (Met) #status experimental
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                                                                                                                                                                                                                                    Score 25; DB 2; Length 16;
Pred. No. 2.1e+03;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.5%; Score 25; DB 2; Length 17; 57.1%; Pred. No. 2.2e+03; Live 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: nucleic acid
A; Residues: 1-17 <BOR>
A; Experimental source: myocardium
A; Note: sequence extracted from NCBI backbone (NCBIP:107742)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fatty acid ethyl ester synthase-II - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: February 21, 2002, 16:31:13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       scyliorhinin II - smaller spotted catshark
A;Reference number: PH0746; MUID:92078846
A;Accession: PH0759
                                                                                                                                                                                                                                       18.5%;
66.7%;
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Best Local Similarity 57.19
Matches 4; Conservative
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Best Local Similarity 66.7
Matches 4; Conservative
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Best Local Similarity 40.0
Matches 4; Conservative
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3 PPDPDTT 9
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2 ASSPPQ 7
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ALIGNMENTS

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Title:

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Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
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NCBI_TaxID=1309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochemistry 27:7102-7105(1988).
-!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS INHIBIT THEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ^{1}\mathrm{Phylogenetic} specificity of cholinergic ligands: alpha-conotoxin ^{1}\mathrm{T}
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-89062448; PubMed-3196703;
Zafaralla G.C., Ramilo C., Gray W.R., Karlstroem R., Olivera B.M.
                                                                                                                                                                                                                                                                                                                     ALPHA-CONOTOXIN SI (S1).

Conus striatus (Striated cone).

Conus striatus (Striated cone).

Coules traca; Metazoa; Mollusca; Gastropoda; Caenogastropoda;

Neogastropoda; Conoidea; Conidae; Conus.
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Pred. No. 3.3e+02;
2; Mismatches 6; Indels
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DEE90F8EF2457EBD CRC64;
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01-NoV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
LANTIBLOTIC MUTACIN B-NY266.
                                                                                                                                                                                                                                                                                   01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
           PSAF_MAIZE
GYRA_STRSH
TRYP_PROAT
CXN_CONGE
CXYT_BUFRE
OXYT_EISFO
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ilarity 33.3%;
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Streptococcus mutans.
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HSSP; P01519; 1NOT.
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CCNPACGPKYSC 13
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Best Local Similarity
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                                                            100059 seqs, 36664827 residues
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UC06_MAIZE
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Gapop 10.0 , Gapext 0.5
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22 AA

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Gaps

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Length 22;

Score 26; DB 1; 1 Pred. No. 5.6e+02;

19.3%; ilarity 54.5%; Conservative

1; Mismatches

2849C330172CC5C2 CRC64;

2291 MW;

22 AA;

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Transport; Sugar transport; Transmembrane; Inner membrane.
TRANSMEM 13 >22 POTENTIAL.
NON_TER 22 22
 Stygene; SG10423; setB.
                                                                                                                                        13 ASAPPEEDCTS 23
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Matches 6; Conserv
                                      NON_TER
SEQUENCE
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SEQUENCE
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COXM_THUOB
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TKN2_SCYCA
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Geerse R.H., Izzo F., Postma P.W.;

"The PEP: fructose phosphotransferase system in Salmonella
typhimurium: FPr combines enzyme IIFru and pseudo-HPr activities.";

Mol. Gen. Genet. 216.517-555(1989).

-!- FUNCTION: INVOLVED IN THE EFFLUX OF SUGARS. THE PHYSIOLOGICAL ROLE
MAY BE THE DETOXIFICATION OF NON-METABOLIZABLE SUGAR ANALOGS. CAN
                                             Gaps
                                                                                                                                   -i- MASS SPECTROMETRY: MW-2270.29; MW_ERR-0.21; METHOD=ELECTROSPRAY.
-i- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE A LANTIBIOTICS.
InterPro: IFR001049; Gallidermin.
Pfam, PF02052; Gallidermin.
PRINTS; PR00323; GALLIDERMIN.
Antibiotic; Bacteriocin; Lantibiotic; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSPORT LACTOSE AND GLUCOSE (BY SIMILARITY).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                        Mota-Meira M., Lacroix C., Lapointe G., Lavoie M.C.; "Purification and structure of mutacin B-Ny266: a new lantibiotic
                                                                                                                                                                                                             DHA (2.3-DIDEHYDROALANINE).
D-ABU (AMINOBUTYRIC ACID).
DHB (2.3-DIDEHYDROBUTYRINE).
DHA (2.3-DIDEHYDROALANINE).
ALA-S-ALA (LANTHIONINE).
ABU-S-ALA (BETA-METHYLLANTHIONINE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Pred. No. 5.6e+02;
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DHA-S-ALA (AVI).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SUGAR EFFLUX TRANSPORTER B (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
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           MEDLINE-97379322; PubMed-9237644;
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illarity 37.5%;
Conservative
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ID SETB_SALTY
AC P33027;
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                                                                                                                                                                                                                                                                                                                                     MEDLINE-86192829; PubMed-2422058;
Conlon J. M., Deacon C.F., O'Toole L., Thim L.;
"Scyliorhinin I and II: two novel tachykinins from dogfish gut.";
FEBS Lett. 200:111-116(1986).
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Pred. No. 6.4e+02;
1; Mismatches 5; Indels
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FCCA3FB01E2F3907 CRC64;
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PIR; B24867; B24867.
                                                                                                                               01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
SCYLIORHININ II (RECTIN).
                                                                                              18 AA.
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Pfam; PF022021; Tachykinin. 1.
PROSITE; PS00267; TACHYKININ. 1.
Tachykinin; Neuropeptide; Amidation.
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40.0%;
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                                                                                          STANDARD;
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7 AAAPKSFDLTS 17
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Best Local Similarity
Matches 4; Conserv
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01-AUG-1988
30-MAY-2000
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P08609;
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STANDARD;
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                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A40312; NTKNAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MaizeDB; 123951; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                         ||| | : |
NTSHQDFHLF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 AA;
 NTSQYDTYCF 11
                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Coleoptile;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INHIBIT THEM
                                                                                                                                                                                                                                                   Zea mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CXAA_CONST
P28878; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptors."
                                                                                                                        UC19_MAIZE
                                                                                                                                                                                                                                (FRAGMENT)
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SEQUENCE
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                                                                                                                                          P80625
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CXAA_CONST
                                                                                       RESULT 7
UC19_MAIZE
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                         Thunnus obesus (Bigeye tuna).

Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;

Scombridae; Thunnus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thunuus obesus (Bigeye tuna).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
Scombridae; Thunnus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CYTOCHROME C OXIDASE POLYPEPTIDE VIIB-HEART (EC 1.9.3.1) (FRAGMENT).
01-NOV-1997 (Rel. 35, Last annotation update)
CYTOCHROME C OXIDASE POLYPEPTIDE VIIB-LIVER (EC 1.9.3.1) (FRAGMENT).
                                                                                                                                                                                                                                                                            ur. J. Blochem. 248:99-103(1997).
I- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eur. J. Biochem. 248:99-103(1997).
-!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
                                                                                                                                                                                                                                               "The subunit structure of cytochrome-c oxidase from tuna heart and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The subunit structure of cytochrome-c oxidase from tuna heart and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                          Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F., Kadenbach B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
Kadenbach B.;
                                                                                                                                                                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O 4 FERRICYTOCHROME C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O 4 FERRICYTOCHROME C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.5%; Score 25; DB 1; Length 20; 50.0%; Pred. No. 7.2e+02; ive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2303 MW; 0A33BD34006E5AA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                           2213 MW; 03B902A70F3E41A6 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 25; DB 1; 1
Pred. No. 7.2e+02;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 AA.
                                                                                                                                                                                                                                                                                                                                   MITOCHONDRIAL ELECTRON TRANSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                          MEDLINE=97454291; PubMed=9310366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97454291; PubMed=9310366;
                                                                                                                                                                                                                                                                                                                                                                                        Oxidoreductase; Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oxidoreductase; Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.5%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
5; Conserve
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 NTSQYDTYCF 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8241;
                                                                                                                    NCBI_TaxID=8241;
                                                                                                                                                                           TISSUE=Liver;
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P80980:
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SEQUENCE
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Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C., Pernollet J.-C., Zivy M., de Vienne D.; "The maize two dimensional gel protein database: towards an integrated
                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                  genome analysis program.";
Theor. Appl. Genet. 93:997-1005(1996).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5.6, ITS WW IS: 18.4 KDA.
Maize-2DPAGE; P80625; COLEOPTILE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Alpha-conotoxins, small peptide probes of nicotinic acetylcholine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
                                     01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 406)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ٠.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91369955; PubMed=1892838; Myers R.A., Zafarella G.C., Gray W.R., Abbot J., Cruz L.J., Olivera B.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBL_TaxID=6493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15
1672 MW; 1CF69D4DA8737F9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 24.5; DB 1;
Pred. No. 6.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 AA.
15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochemistry 30:9370-9377(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALPHA-CONOTOXIN SIA (SIA).
Conus striatus (Striated cone).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-1992 (Rel. 24, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.18;
37.58;
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16
1792 MW;
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50.0%;
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66.7%;
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                           PDB; 1A0M; 13-JAN-99
                                                                                                                     3
15
16
16 AA;
                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                               1 CNTSQYDTYC 10
                                                                                                                                                                                                                                           || : | ||
CNMNNPD-YC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
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SQYDGF 10
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P80612;
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                                                                                                                                                                                                                                                                                                      UH05_RAT
P56573;
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SEQUENCE
                                                                                                                                           MOD_RES
SEQUENCE
                                                                                                                       DISULFID
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                                                                                                                                  MOD_RES
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UC06_MAIZE
                                                                                                                                                                                                                                                                                   RESULT 11
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   AC DT DT DT DT DT DE DE DE DE OC OC OC
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                                                                                                                                                                                                                                                                                                                            Ramilo C., Zafaralla G.C., Nadasdi L., Hammerland L.G., Yoshikami D., Gray W.R., Kristipati R., Ramachandran J., Miljanich G., Olivera B.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                           "Novel alpha- and omega-conotoxins from Conus striatus venom.";
Biochemistry 31:9919-9926(1992).
-!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
INHIBIT THEM.
                                                                                                                                                                                                                                                                                                                                                                                                        INTELLATION.

PIR, A44379, A44379.

POSTSYNAPTIC neurotoxin; Acetylcholine receptor inhibitor; Venom.

DISULFID 2 18 POTENTIAL.

DISULFID 3 8 BY SIMILARITY.

DISULFID 4 14 BY SIMILARITY.

FERMINE 19 AA; 1797 MW; A158B024273EF4CF CRC64;
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MEDLINE=98376423: PubMed=9708977;
Hu S.H., Loughnan M., Miller R., Weeks C.M., Blessing R.H.,
Alewood P.E., Lewis R.J., Martin J.L.;
"The 1.1-A regolution crystal structure of [Tyr15]EpI, a novel
                                                                                                                                                                                01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
ALPHA-CONOTOXIN SII (S2).
Conus striatus (Striated cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
NOBI_TaxID=6493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conus episcopatus (Bishop's cone).
Usukaryota; Metazoa; Moliusca; Gastropoda; Caenogastropoda; Conoidae; Conidae; Conus.
NCBL_TaxID=88764;
                                                      Score 24; DB 1; Length 13;
Pred. No. 6.4e+02;
2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 24; DB 1; Length 19;
Pred. No. 9.6e+02;
1; Mismatches 7; Indels
            AMIDATION.
DEF1931982457EBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ALPHA-CONOTOXIN EPI.
                                                                                                                                                                          19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 AA.
                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                       TISSUE=Venom;
MEDLINE=93003172; PubMed=1390774;
                                                      17.8%;
30.8%;
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                      1461 MW;
                                                     Query Match 17.8
Best Local Similarity 30.8
Matches 4; Conservative
                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                             SEQUENCE, AND SYNTHESIS.
                                                                                                              1 YCCHPACGKNFDC 13
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                                                                                                9 YCFNASAPPEEDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 4; Conserv
 3
13
13 AA;
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                                                                                                                                                                         CXA2_CONST
P28879;
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P56638;
DISULFID
MOD_RES
SEQUENCE
                                                                                                                                                   RESULT 9
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SEQUENCE.
STRAINWLE.
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STRAINWLE.
LI X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
Jungblut P.R.,
Submitted (SEP-1998) to the SWISS-PROT data bank.
-- MISCELLANBOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
-- MISCELLANBOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
-- PROTEIN IS: 8.3, ITS MW IS: 30 KDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                 Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation; Venom; Sulfation; 3D-structure.
DISULFID 2 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
alpha-conotoxin from Conus episcopatus, solved by direct methods.";
Biochemistry 37:11425-11433 (1998)
-i- FUNCTION: ALPHA-CONOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC
ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-2 AND ALPHA-
3/BETA-4 SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF HEART TISSUE (SPOT P5) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 1131)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                            AMIDATION.
C63385F376C99B4C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 23.5; DB 1;
Pred. No. 9.5e+02;
; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 23; DB 1; i
Pred. No. 6.9e+02;
1; Mismatches 1;
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01-0CT-1996 (Rel. 34, Last sequ
15-JUL-1999 (Rel. 38, Last anno
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proto-oncogene; Tyrosine-protein kinase; Phosphorylation; Transferase; ATP-binding; Myristate; Palmitate; Lipoprotein.
                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                     PROTO-ONCOGENE TYROSINE-PROTEIN KINASE LCK (EC 2.7.1.112) (P56-LCK)
                                                                                                                                                                                                                                                                                                                                                                   OVEREXPRESSION, LEADING TO THE DEVELOPMENT OF THYMIC LYMPHOMA.
-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metažoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Mygalomorphae; Theraphosidae; Acanthoscurria.
NCBL_TaxID=115339;
                                                                                                                                                                                                                                                                                                                                                   -!- DISEASE: PROVIRAL INSERTION UPSTREAM OF THE LCK GENE CAUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 23; DB 1; Length 17;
Pred. No. 1.2e+03;
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PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001245; Tyr_kin.
PROSITE; PS00107; PROTEIN_KINASE_ATP; PARTIAL.
PROSITE; PS00109; PROTEIN_KINASE_TYR; PARTIAL.
PROSITE; PS50011; PROTEIN_KINASE_DOM; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GOMESIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROBABLE
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Matches 4; Conser
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                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                       NCBI_TaxID=10116;
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5 SSNPEDD 11
                                                                                                                                                            STRAIN-FISCHER;
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                  (FRAGMENT).
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P82358;
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NON_TER
SEQUENCE
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GOME_ACAGO
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                                                             Toucet P., Ricardi F., Morin C., Damerval C., Huet J.-C.,

Pernollet J.-C., Zivy M., de Vienne D.;

"The maize two dimensibional gel protein database: towards an integrated genome analysis program.";

Theor. Appl. Genet. 93:997-1005(1996).

-! MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN 1S: 6.8, ITS MW IS: 71.0 KDA.

Maize-2DPAGE: P806612; COLEOPTILE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Romain F., Laqueyrerie A., Militzer P., Pescher P., Chavarot P.,
Lagranderie M., Auregan G., Gheorghiu, M., Marchal G.A.;
"Identification of a Mycobacterium bovis BGG 45/47 kilodatton antigen
complex, an immunodominant terget for antibody response after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunization with living bacteria.";
Infect. Immun. 61:742-750(1993).
-!- SUBCELLULAR LOCATION: SECRETED.
-!- SIMILARITY: TO M.LEPRAE NL43, AND M.TUBERCULOSIS MPT32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 23; DB 1; Length 17; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                               17.0%; Score 23; DB 1; Length 15; 80.0%; Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                   0; Indels
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15 AA; 1390 MW; 7005E22830F23D61 CRC64;
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A45K_MYCBO
ID A45K_MYCBO STANDARD; PRT; 17 AA.
AC P80069.
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DF 45/47 KDA ANTIGEN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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29, Last seques 39, Last anno
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80.0%;
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(Rel.
(Rel.
                                                  TISSUE=Coleoptile
NCBI_TaxID=4577;
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Q01621;
01-JUN-1994 (
01-JUN-1994 (
30-MAY-2000 (
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2 AAAPP 6
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Matches

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Gaps

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1; Indels

RESULT 14

LCK\_RAT ID LCK AC Q01: DT 01-DT 30-

Matches

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RX MEDLINE=20517902; PubMed=10942757;

RA Silva P.I. Jr., Daffre S., Bulet P.;

RT "Isolation and characterization of gomesin, an 18-residue cysteine-
RT rich defense peptide from the spider Acanthoscurria gomesiana
hemocytes with sequence similarities to horseshoe crab antimicrobial
RT peptides of the tachyplesin family";

RI Jaiol. Chem. 275.33464-3347(2000).

CC -1- FUNCTION: ACTIVE AGAINST SEVERAL GRAM-DOSITIVE BACTERIA SUCH AS
CC BACTIVE BACTERIA SUCH AS E.COLI, K.PNEUMONIAE, P.AERUGINOSA AND
CC SALMONELLA SPP, FILAMENTOUS FUNDS INCRASSA, T.VIRIDAE
CC LAMAZONENSIS SA WELL. IT SHOWS HEMOLYTIC ACTIVITY.

C. I. AMAZONENSIS SA WELL. IT SHOWS HEMOLYTIC ACTIVITY.

C. I. AMAZONENSIS SA WELL. IT SHOWS HEMOLYTIC ACTIVITY.

C. I. MASS SPECTROMETRY: MW=2270.4; METHOD=MALDI.

KW AMIGHION: Antibiotic; Fungicide; Hemolysis.

FT MOD_RES 18 18 AMIDATION.

FT DISULFID 2 15

FT DISULFID 6 11

SQ SEQUENCE 18 AA; 2293 MW; 25ED499784908913 CRC64;

DUEST MATCHES 4; CONSERVATIVE 1; MISMATCHES 5; Indels 0; Gaps 0;

MATCHES 4; CONSERVATIVE 1; MISMATCHES 5; Indels 0; Gaps 0;
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Search completed: February 21, 2002, 16:33:57 Job time: 182 sec

1 CNTSQYDTYC 10 | : ||| 6 CYKQRCVTYC 15

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hordeum vul

homo sapien didelphis m macropus eu choloepus h chaetophrac tamandua te myrmecophag erinaceus c talpa altai condylura c sorex arane echinops te trichechus procavia ca loxodonta a orycteropus cynocephalu

09byk5 Q9bfc3 Q9bfc2 euphractus

09bfc1 09bfc0 09bfb9 09bfb7 09bfb7 09bfb5 09bfb2 09bfb1 09bfb1 09bfb1 09bfb1 09bfb1

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Q9bfa5 Q9bfa4 29bfa3

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Total number

Searched:

Minimum DB Maximum DB

Database

Perfect score:

Title:

Sequence:

OM protein

Run on:

Scoring table:

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Q9r963 helicobacte
Q53399 bacillus th
Q9udd6 homo sapien
Q9s915 triticum tu
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HYPOTHETICAL 2.6 KDA PROTEIN (FRAGMENT).
Pseudomonas stutzeri (Pseudomonas perfectomarina).
Bacteria, Proteobacteria; gamma subdivision; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34.5; DB 12; Length 22; Pred. No. 99; 0; Mismatches 2; Indels
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Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
NCBI_TaxID=11886;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
P19GAG AND P2GAG PROTEINS (FRAGMENT).
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              Q9R963
Q53399
Q9UDD6
Q9S915
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Q9BFC3
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Q9BFB7
Q9BFB6
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Q9BFB3
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09BFB1
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Q9BFB9
                                                                                                         Q9BFC2
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Submitted (MAR-1996) to the E
EMBL: M77660; AAA91044.1; -.
NON_TER
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Best Local Similarity 47.1.

Best Local 8; Conservative
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SEQUENCE
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Q85481;
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Q9x7j5 pseudomonas
Q9r5u3 pseudomonas
Q95202 drosophila
Q9qv27 rattus sp.
Q6qv27 rattus sp.
Q6qy8 cricetulus:
Q9qy8 cricetulus:
                                                                                                   February 21, 2002, 16:30:39 ; Search time 22.06 Seconds (without alignments) 152.505 Million cell updates/sec
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091329 human immun
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Q987J3
Q985U3
Q985U3
Q9QV2
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Q9GV8
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P82110
Q9UMI8
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Q14890
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sp_unclassified:*
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Forsberg E., Ek B., Engstrom A., Johansson S.;
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Best Local Similarity
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MEDLINE-91358127; PubMed-1885526;
Altenschmidt U., Oswald B., Fuchs G.;
"Purification and characterization of benzoate-coenzyme A ligase and 2-aminobenzoate-coenzyme A ligases from a denitrifying Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-91358327; PubMed-1885526; Altenschmidt U., Oswald B., Fuchs G.; "Purification and characterization of benzoate-coenzyme A ligase and 2-aminobenzoate-coenzyme A ligases from a denitrifying Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                              STRAIN=ZOBELL, ATCC14405;
MEDLINE=99226217; PubMed=10209742;
Vollack K.U., Hartig E., Korner H., Zumft W.G.;
"Multiple transcription factors of the FNR family in denitrifying Pseudomonas stutzeri: characterization of four fnr-like genes, requlatory responses and cognate metabolic processes.";
Mol. Microbiol. 31:1681-1694(1999).
EMBL: AJ131715; CAB40904.1: -
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Pseudomonas (fluorescent pseudomonads).
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae.
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae.
NCBL_TaxID=286;
                                                                                                                                                                          Length 23;
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J. Bacteriol. 173:5494-5501(1991).
SEQUENCE 22 AA; 2526 MW; 5D37FA76363F8792 CRC64;
                                                                                                                                         EF68EA0F803A5EBD CRC64;
                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                          Score 34; DB 2; I
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7e+02;
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Pred. No. 1.7e+03
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illarity 33.3%;
Conservative
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Best Local Similarity 33.3
Matches 7; Conservative
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                                                                                                                    Hypothetical protein.
                                                                                                                                                              Query Match
Best Local Similarity
'... 5; Conserv?
                    SEQUENCE FROM N.A.
NCBI_TaxID=316;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila heteroneura (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=32382;
                                                                                                                                                                    Gaps
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Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                      Length 18
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sp.";
J. Bacteriol. 173:5494-5501(1991).
SEQUENCE 18 AA; 2061 MW; C43F8799692771EF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BICOID PROTEIN (FRAGMENT).
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Last annotation update)
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Pred. No.
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100.0%; Fr
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35.3%;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
INTEGRIN BETA 1 CHAIN.
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Mammalia; Eutheria;
NCBI_TaxID=10118;
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Peters J., Takahashi S., Tada M., Miyake Y.;
"mGK 6-derived true tissue kallikrein is synthesized, processed, and
targeted through a regulated secretory pathway in mouse pituitary AtT
20 cells.";
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                     Klees A.G., Linder D., Buckel W.;
"2-Hydroxyglutaryl-CoA dehydratase from Fusobacterium nucleatum (subsp. nucleatum): an iron-sulfur flavoprotein.";
Arch. Microbiol. 158:294-301(1992).
SEQUENCE 19 AA; 2255 WW; IE3C577D5B00802D CRC64;
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    Indels
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QUENCE 19 AA; 2296 MW; 250436479C0E6626 CRC64;
                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
2-HYDROXYGLUTARYL-COA DEHYDRATASE GAMMA-SUBUNIT.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
TRUE TISSUE KALLIKREIN (EC 3.4.21.35) (FRAGMENT)
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Bacteria; Fusobacterium
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                                                               AAAPPAE 15
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Q9QVB8
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ID 09
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
40S RIBOSOMAL PROTEIN S27A (FRAGMENT).
LUMDbitus rubellus (Humus earthworm).
Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
Lumbricina; Lumbricidae, Lumbricus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HISTONE HI (FRAGNENT).
Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
"Purification and characterization of integrin alpha 9 beta 1."; Exp. Cell Res. 213:183-190(1994). SEQUENCE 20 AA; 2335 MW; 50220366111FB2D8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 20;
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                                                                                Length 20;
                                                                                                             4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sturzenbaum S.R., Kille P., Morgan J.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases
EMBL, AJ223199; CAA11174.1; -
InterPro, 1PR002906; Ribosomal_S27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 AA; 2388 MW; 7685DE00FB23B91B CRC64;
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AA; 1479 MW; 75EB488737288C8A CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                              Score 28; DB 11;
Pred. No. 9.6e+02;
1; Mismatches 4;
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Pred. No. 1.1e+03;
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Pred. No. 1.1e+03;
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                                                                              20.7%;
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58.3%;
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71.4%;
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Matches 7; Conservative
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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NON_TER 1
SEQUENCE 20 AA;
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Query Match

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SEQUENCE.

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Query Match
Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
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SEQUENCE.
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                                                                                               SEQUENCE FROM N.A.
STRAIN-PATIENT SI FROM FRANCE;
MEDLINE-98285741; pubmed-9621043;
Belec L., Si Mohamed A., Muller-Trutwin M.C., Gilquin J., Gutmann L.,
Safar M., Barre-Sinoussi F., Kazatchkine M.D.;
"Genetically related human immunodeficiency virus type 1 in three
adults of a family with no identified risk factor for intrafamilial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Belec L., Si Mohamed A., Mueller-Trutwin M.C., Gilquin J., Gutmann L., Safar M., Barrate-Sinoussi F., Kazatchkine M.D., "Genetically related human immunodeficiency virus type 1 in three adults of a family with no identified risk factor for intrafamilial
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Pred. No. 1.3e+03;
3; Mismatches 1; Indels
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08, Last sequence update)
17, Last annotation update)
                                                      Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Last annotation update)
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Pred. No. 1.3e+03;
3; Mismatches 1;
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                                  ENVELOPE GLYCOPROTEIN (FRAGMENT).
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MEDLINE=98285741; PubMed=9621043;
                                                                                                                                                                                      J. Virol. 72:5831-5839(1998).
EMBL. U87220; AAC32280.1; -.
Interpro; IPRO0777; GP120.
Pfam; PF00516; GP120; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Virol. 72:5831-5839(1998).
EMBL, 1087216; AAC32976.1; -.
InterPro: IPRO0077; GP120.
Pfam; PF00516; GP120; 1.
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01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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Best Local Similarity
Matches 6; Conserv
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Matches 6; Conserv
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SECUENCE
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                                                                                                                                                                                                                                                                                                         MEDLINE-95100972; PubMed-7802674; Sallberg M., Sherefa K., Zhang Z.X.; Sallberg M., Sherefa K., Zhang Z.X.; "The antigen/antibody specificity exchanger: a new peptide based tool for re-directing antibodies of other specificities to recognize the V3
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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May L.T., Shaw J.E., Khanna A.K., Zabriskie J.B., Sehgal P.B.;
"Marked cell-type-specific differences in glycosylation of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synechococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).
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                                                                                                                                                                                                                                                                                                                                                                                                                        domain of HIV-1 gpl20.";
Blochem. Biophys. Res. Commun. 205:1386-1390(1994).
SEQUENCE 22 AA; 2704 MW; 36E8F13D871579CE CRC64;
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                                              01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
INTERLEUKIN-6=23-25 KDA.
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                                                                                                                                   A/ASE PROTEIN (FRAGMENT).
Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 26.5; DB 12;
Pred. No. 1.8e+03;
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22 AA
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36.8%;
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SEQUENCE 13 AA; 1281 MW;
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OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.

OX NCBI_TaxID=32049;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=PR6009;
RX MEDLINE=90314661; PubMed=2114862;
RX MEDLINE=90314661; PubMed=2114862;
RX MEDLINE=90314661; PubMed=2114862;
RX MEDLINE=90314661; PubMed=2114862;
RY Scructure and mutation of a gene encoding a Mr 33,000 phycocyanin-RT associated linker polypeptide.";
RY SSCUENCE Associated linker polypeptide.";
RY Arch. Microbiol. 153:541-549(1990).
DR EMBL; X81868; CAA57456.1; -...
DR EMBL; X81868; CAA57456.1; -...
DR HSSP; PO7122; ICPC.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1601 MW; 9BD40C7EF60CDA5A CRC64;
Best Local Similarity 45.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
CV 3 TSOYTYCFNA 13
FT 1 | 1 | 1 | 1 |
DD 2 TNNYIDYAINA 12
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Search completed: February 21, 2002, 16:33:41 Job time: 182 sec

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Hepatitis C virus Hepatitis C virus

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Peptide derived fr
HCV antigen, NS3 1
Cow's milk beta-la
Hepatitis C virus
P185 binding and e
P185 binding and e
P185 binding and e
P185 binding and e
Peptide encoded by
P185 binding and e
Cytochemical assay
Cytochemical assay
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GPIb alpha peptide
GPIb-alpha-derived
Canine immunoglobi
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Human antithrombin
c-raf-related pept
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AAB17050
AAB70303
AAR13137
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AAW24104
AAR38579
AAW14605
                  AAW42772
AAB82056
                                      AAB21106
AAJ03719
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AAW16772
AAB57304
AAW16692
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AAW16755
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AAB29280
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AAJ00888
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AAJ02943
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93WO-US10412
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Hale LP, Haynes BF,
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Homo sapiens
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AAR53474;
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RESULT
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Cytochemical assay
Human SNP associat
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CD44 peptide CD44-
TK-SH2 association
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                                                            February 21, 2002, 16:27:39; Search time 23.62 Seconds (without alignments) 72.129 Million cell updates/sec
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                              hits satisfying chosen parameters:
                                                                                                                                                                             522463 seqs, 74073290 residues
                                                                                                                          CNTSQYDTYCFNASAPPEEDCTS 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
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Maximum Match 100% .
Listing first 45 summaries
                                               protein - protein search, using sw model
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AAR52889
AAR52890
AAB29282
AAG98102
AAB48871
AAY85630
AAY98406
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AAR53486
AAR52917
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Gapop 10.0 , Gapext 0.5
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113
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117
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Match
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Score

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Database :

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Scoring table:

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Claim 4; Page 14; 83pp; English.

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inhibit tyrosine kinase association with regulatory proteins, used for treating, e.g., hyper-proliferative, viral, allergic inflammatory, auto-immune and cardiovascular diseases
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                                                                                                                                                                                    Tyrosine kinase; SH2 domains; inhibition of association; abl; Epidermal Growth Factor Receptor; phosphotyrosine residue; control proliferative disease; control cancer; TK; EGFR; Src-homology domains.
                                                                                                                                                                                                                                                                                                                                                  /note= "phosphotyrosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McNamara DJ,
                                                                                                                                                     TK-SH2 association inhibitory peptide.
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                                                    AAR52917 standard; peptide; 13 AA.
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58.3%;
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2 ycynpshnpeee 13
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Best Local Similarity
Matches 7; Conser
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Modified-site
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The peptide can be used for treating inflammation and immunemediated tissue damage such as occurs in the course of autoimmune diseases, e.g. rheumatoid arthritis. It can also be used for determining metastatic potential or to treat or prevent tumor cell metastasis. This peptide corresponds to AA 110-131 of the CD44 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The peptide can be used for treating inflammation and immune-mediated tissue damage such as occurs in the course of autoimmune diseases, e.g. rheumatoid arthritis. It can also be used for determining metastatic potential or to treat or prevent tumor cell metastasis. This peptide corresponds to AA 107-117 of the CD44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of CD44 protein and new peptide derivs - for developing prods for inflammation, immune-mediated tissue damage and tumour cell
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0
                                                                                                                                                                     Length 23;
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                                                                                                                                                                   100.0%; Score 135; DB 15;
100.0%; Pred. No. 1.9e-11;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                      AAR53486 standard; peptide; 11 AA.
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Best Local Similarity 100.
Matches 23; Conservative
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Matches 8; Conservative
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                                                                                                                     23 AA;
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RESULT

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                                                 from specific signal transduction pathways. The peptide inhibition is probably the result of competition between the phosphorylated peptide and the phosphorylated receptor for the same binding site on the SH2 domains. The inventors claim the peptides can be used for the control of several proliferative diseases, eg. cancer.
The peptide inhibits the association of a tyrosine kinase with its cellular substrates and effectively uncouples the tyrosine kinase
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ed. No. 17;
Mismatches 3; Indels
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Pred. No.
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ID AAR5:
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Synthetic

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The peptide inhibits the association of a tyrosine kinase with its cellular substrates and effectively uncouples the tyrosine kinase from specific signal transduction pathways. The peptide inhibition is probably the result of competition between the phosphorylated peptide and the phosphorylated receptor for the same binding site on the SH2 domains. The inventors claim the peptides can be used for the control of several proliferative diseases,eg. cancer.
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inhibit tyrosine kinase association with regulatory proteins,
used for treating, e.g., hyper-proliferative, viral, allergic
inflammatory, auto-immune and cardiovascular diseases
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Pred. No. 32;
1; Mismatches 3;
control cancer; TK; EGFR; Src-homology domains
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/note= "phosphotyrosine"
                                                                                                                       /note= "phosphotyrosine"
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                                                                   Location/Qualifiers
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                                                                                                      /label= other
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2 ycynpshnpee 12
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                                                                   Key
Modified-site
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptide(s) with a tyrosine auto-phosphorylation site -
inhibit tyrosine kinase association with regulatory proteins,
used for treating, e.g., hyper-proliferative, viral, allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 13;
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                                                                              Tyrosine kinase; SH2 domains; inhibition of association; abl; Epidermal Growth Factor Receptor; phosphotyrosine residue; control proliferative disease; control cancer; TK; EGFR; Src-homology domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used for treating, e.g., hyper-proliferative, viral, a inflammatory, auto-immune and cardiovascular diseases
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Pred. No.
                                             TK-SH2 association inhibitory peptide.
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63.6%;
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93US-0122028
            07-NOV-1994 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 30.4
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maclean D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-135508/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thieme-sefler,
                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                     22-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                        25-SEP-1992;
15-SEP-1993;
                                                                                                                                                                                                                                                                                                WO9407913-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dobrusin EM,
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Seguence

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AAR52889 RESULT

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test platform. The present sequence was used in assays to demonstrate the
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                                                                                                                                                 quality of cytochemical assays such as immunohistochemical stains. These assays can be used in cancer diagnosis, and in the diagnosis of viral infections. The quality control device comprises a matrix with a top surface having a quality control reagent moiety and the bottom surface having an adhesive to enable the adherence of the device to a planar
 in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to nucleic acids (AAH79386-AAH80036) encoding polymorphic variants of proteins (AAG98010-AAG98238) related to angiopojetin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate (APP)-dependent RNA helicase, major histocompatibility complex (MHC)
                                                                                                                                The present invention is related to a device useful for measuring the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphic nucleic acids encoding e.g. anglopoietin, dehydrogenase, adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate kinase, useful for diagnosing and treating, e.g. cancer, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
             sample, comprises matrix with top surface having a quality control reagent moiety and a bottom adhesive surface for adhering device to
 Quality control device for cytochemical assays measuring analytes
                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 21; Length 18; Pred. No. 60; 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human SNP associated peptide SEQ ID NO. 744.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 454; 484pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG98102 standard; Peptide; 14 AA.
                                                                                           6; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                           29.6%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-DEC-2000; 2000WO-US35346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diseases and infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16
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                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                       AA;
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                                                                                           Claim 20; Fig
                                                                                                                                                                                                                                                                                                     18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2001
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                                                      platform
                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                device
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                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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AAG98102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    The peptide inhibits the association of a tyrosine kinase with its cellular substrates and effectively uncouples the tyrosine kinase from specific signal transduction pathways. The peptide inhibition is probably the result of competition between the phosphorylated peptide and the phosphorylated receptor for the same binding site on the SH2 domains. The inventors claim the peptides can be used for the control of several proliferative diseases, eg. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nical assay; quality control; immunohistochemical stain; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                    New peptide(s) with a tyrosine auto-phosphorylation site -
inhibit tyrosine kinase association with regulatory proteins,
used for treating, e.g., hyper-proliferative, viral, allergic
inflammatory, auto-immune and cardiovascular diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytochemical assay quality control 1D5 peptide SEQ ID NO: 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 15; Length 13; 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ramanathan H;
                                                                                                                                                                                                                           McNamara DJ, Soltiel AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 1
Pred. No. 32;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB29282 standard; Peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                 Table 1; Page 11; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.4%;
                                                                                       93WO-US08996
                                                                                                                            92US-0951241
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                                                                                                                                                                                      (WARN ) WARNER LAMBERT CO
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Best Local Similarity bo...
7; Conservative
                                                                                                                                                                                                                           Maclean D,
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                                                                                                                                                                                                                                                                                 WPI; 1994-135508/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 YCFNASAPPEE 19
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2 ycynpshnpee 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 AA;
                                                                                                                                                                                                                           Dobrusin EM, M
Thieme-sefler,
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                                                                                         2-SEP-1993;
                                                                                                                              25-SEP-1992;
                                                                                                                                                 L5-SEP-1993;
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               WO9407913-A
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                                                      14-APR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB29282:
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class I histocompatibility antigen and/or phosphoglycerate kinase. These nucleic acid single nucleotide polymorphisms (SNPs) and the encoded proteins have potential immunosuppressive, immunostimulatory, antisclerotic, antidiabetic, antiinflammatory, cytostatic, antisclerotic, and antimicrobial activity and may be useful in gene/protein therapy, vaccines, modulation of the expression and activity of proteins related to anglopoietin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase, major histocompatibility complex (MHC) Class I histocompatibility antigen and/or phosphoglycerate Kinase. Disorders that may be prevented, diagnosed and/or treated by the above methods include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus crythenatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukemia), diseases of the nervous system, an infection of pathogenic organisms. They may also be used to alter phenotypic traits such as longevity, appearance,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Non-naturally occurring protein with insulin activity useful for treating type 1 and type 2 diabetes, comprising amino acid substitutions as compared to native human insulin and having enhanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                           28.1%; Score 38; DB 22; Length 14; 100.0%; Pred. No. 86; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human insulin; insulin activity protein; IA protein;
diabetes mellitus; type 1; type 2; stability;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mutant human insulin (IA protein) trz_06 A chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB48871 standard; peptide; 21 AA.
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                                                                                                                                                                                                                                                                                                                                 strength, speed and endurance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAY-2000; 2000WO-US13764
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Matches 7; Conservative
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altered ability to oligomerise) compared to wild-type mature human insulin (AAB48848, AB48849) but which are still capable of binding to an insulin receptor. The insulin mutants of the invention have less than 98% sequence identity to wild-type human insulin, but have a 3D structure which substantially corresponds to that of wild-type human insulin. The invention also relates to recombinant nucleic acids encoding the insulin mutants, expression vectors and host cells comprising mutant insulin mutants, expression vectors and host cells comprising mutant can da pharmaceutical composition comprising an insulin mutant of the invention. The mature human insulin mutants are useful for treating these insulin mutants are used in gene therapy techniques for treating these conditions. The insulin mutants are more stable compared to wild-type mature human insulin, or have an improved ability to form insulin have improved stability.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to a method for the production of a subunit peptide originating from a polymer protein with disulphide bonds within and between subunits. The method comprises denaturing the protein or its subunit using a protein denaturing agent in a solution, removing the agent in the presence of a polyoxyalkyl polyether which reacts with a thiol group and unwinds the subunit, and separating the polyoxyalkyl polyether-bound subunit peptide. The method can be used for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Producing physiologically-active subunit peptides originating in polymer proteins by denaturation and specific separation, with lower antigenicity but improved solubility and stability, e.g. blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Subunit peptide production; snake venom; rattlesnake; thrombolytic; von Willebrand's factor; blood platelet-inhibitory activity.
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                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 22; Length 11. Pred. No. 1.7e+02; 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Snake venom derived protein fragment #3.
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                                                                                                                                                                                                                                                                                                                                                                                          27.4%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fukuchi N, Kageyama S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-664985/64.
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Best Local Similarity
Matches 5; Consery
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                                                                                                                                                                                                                                                                                                                                    21 AA;
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                                                                                                                                                                                                                                                                                                                                        Sequence
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physiologically-active subunit peptides for polymer proteins e.g. snake venom-originated dimer peptide with blood platelet-inhibitory activity on von Willebrand's factor. The peptides produced have platelet-binding inhibitory, and thrombolytic activity. The present sequence represents a fragment of a rattleenake protein used in an example illustrating the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kinase alpha D region comprising 5-30 amino acids, which modulates kinase alpha D region comprising 5-30 amino acids, which modulates the activity of the protein kinase. AAY98286 to AAY98455 represent peptides derived from protein kinase alpha D regions, which are used in the exemplification of the present invention. The peptides have cytostatic, anti-diabetic, ancectic, antiinflammatory, dermatological, cardiant, immunosuppressive, immunomodulator, osteopathic, vasotropic and antiarteriosclerotic activities, and are protein kinase modulators. The peptides can be used as test peptides to identify protein kinase The peptides can a subject, and in a method of detecting a ligand that binds to the alpha D region of a protein kinase. They may be used to protein kinase. They may be used to protein kinase. They may be used to protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alpha D peptide; Alpha D region; protein kinase; modulation; activity; cytostatic; anti-diabetic; anorectic; antiinflammatory; dermatological; immunosuppressive; immunomodulator; osteopathic; cardiant; vasotropic; antiarteriosclerotic; protein kinase modulator; cancer; proliferation; restenosis; atherosclerosis; skin disorder; diabetes; obesity; central nervous system disorder; inflammatory disorder; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide derivatives of protein kinase alpha D regions which selectively modulate the activity of protein kinases {\ \ }
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         he peptides are useful in the treatment of diseases caused by over-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune disease; immune disorder; cardiovascular disease.
                                                                                                                                                                                               Score 35; DB 21; Length 17;
Pred. No. 2.6e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alpha D peptide derived from FGFR-3 SEQ ID NO:121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHILDRENS MEDICAL CENT. YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      AAY98406 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 23; Fig 3; 148pp; English.
                                                                                                                                                                                                 25.9%;
62.5%;
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                                                                                                                                                                                                                       Best_Local Similarity 62.5
Matches 5; Conservative
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                                                                                                                                            17 AA;
                                                                                                                                                                                                                                                                                                                     9 ssydrycy 16
                                                                                                                                                                                                                                                                                  4 SQYDTYCF 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                            Sequence
                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121. These are derived from HCV HLA-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The
                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence is an epitope used in the disclosure of the invention.
or under-activity of a protein kinase, e.g. cancer, diseases caused by proliferation of smooth muscle (e.g. restenosis and atherosclerosis), skin disorders, diabetes, obesity, diseases of the central nervous system, inflammatory disorders, autoimmune diseases and other immune disorders, osteoporosis and cardiovascular diseases.
                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention describes a composition comprising a prepared
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                                                                                                                      Length 13;
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                                                                                                                                                2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S, Livingston BD,
Grey HM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 22;
Pred. No. 3.1e+02;
3; Mismatches 1;
                                                                                                                     Score 34; DB 21;
Pred. No. 2.7e+02;
                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 182; 214pp; English.
                                                                                                                                                                                                                                                                 AAJ03726 standard; Peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus epitope #3717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Southwood
Kubo RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.2%;
55.6%;
                                                                                                                     25.2%;
66.7%;
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                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EPIM-) EPIMMUNE INC.
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Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-308046/32
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Best Local Similarity
Matches 5; Conserv
                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus.
                                                                                                                                                                        11 FNASAPPEE 19
                                                                                                                                                                                                3 fdtskppee 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 YDTYCFNAS 14
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Baker DM,
                                                                                                                                                                                                                                                                                                                                                                                   antiviral
                                                                                                                                                                                                                                                                                         AAJ03726;
                                                                                Sequence
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                                                                                                                                                                                                                                        RESULT 12
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                                                                                                                                                Matches
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ID AAJ0
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antiviral.

AAJ03739;

Sette A, Baker DM,

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The present peptide is derived from a Sp17 protein. Sp17 peptides contain antigenic epitopes in mice, rabbits, non-human primates and humans. They induce antibodies which recognies sperm, and inhibit fertilisation. The peptides can be used in immunocontraceptive methods as a fimunocontraceptive vaccine to reduce the fertility of animals, particularly in females. The presence of the antigenic peptides can be detected to diagnose autoimmune fertility in both male and female
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (a) an antigen; (b) an immunostimulating substance consisting of neuroactive compounds, hormones, compounds having growth hormone activity or their mixtures; and (c) a polycationic polymer. The present sequence is an antigenic peptide derived from Hepatitis c virus, which was used in the present invention. The composition is useful in manufacturing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antigen; immunostimulant; vaccine; pharmaceutical composition; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a pharmaceutical composition comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New pharmaceutical composition comprising an antigen, an immunostimulating substance and a polycationic polymer, useful
                                                                                                                                                                                                                                                                                                                                                                ; DB 18; Le.,
                                                                                   Sperm protein Sp17 antigenic peptide(s) - used as immuno:contraceptive to reduce fertility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Melling J;
                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB82056 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; Page 16; 20pp; English.
                                                                                                                                   Claim 1; Page 83; 160pp; English.
                Widgren EE;
                                                                                                                                                                                                                                                                                                                                                                               25.2%;
35.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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8 ynnhafeeqeppek
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                                                WPI; 1997-526394/48
                 O'Rand MG,
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                               21 AA;
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                 Lea I,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121. These are derived from HCV HLA-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention.
                                                                                                                  Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sp17; sperm autoantigen; antigen; antigenic epitope; fertility; immunocontraception; immunocontraceptive vaccine; autoimmune fertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A new composition useful as a vaccines against hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 15;
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                                                                                                                                                                                                                                                                                                                                                                             Southwood S, Livingston BD, Kubo RT, Grey HM;
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Pred. No. 3.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 183; 214pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW42772 standard; Peptide; 21 AA.
                                                                                  Hepatitis C virus epitope #3730.
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55.6%;
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                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                           (EPIM-) EPIMMUNE INC
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Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-308046/32
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Best Local Similarity
Matches 5; Conserv
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6 ydtrcfdst 14
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                                                02-JUL-2001
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Sequence

Synthetic.

AAW42772;

RESULT 14 AAW42772

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Gaps

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Length 21;

XX SQ Sequence 20 AA;

Query Match
24.4%; Score 33; DB 22; Length 20;
Best Local Similarity 60.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 4; Indels ò

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8 TYCFNASAPP 17 | | | | | ||| 8 tvcaraqapp 17 QQ

Search completed: February 21, 2002, 16:30:34 Job time: 175 sec

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LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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MOLECULE TYPE:
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RESULT
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40.980 Million cell updates/sec
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Sequence 2
Sequence 8
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/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-143-311B-14
US-08-143-318A-104
US-08-433-318A-105
US-08-433-318A-167
US-08-433-318A-167
US-08-922-048-104
US-08-922-048-107
US-08-922-048-107
US-08-922-048-167
US-08-922-048-168
PCT-US96-06270-105
PCT-US96-06270-168
US-08-433-318A-88
US-08-433-318A-88
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US-08-922-048-152
PCT-US96-06270-88
PCT-US96-06270-89
PCT-US96-06270-151
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US-08-433-318A-152
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US-08-922-048-89
                                                                                                                                                                                                                212252 seqs, 22503292 residues
                                                                                                                                            135
1 CNTSQYDTYCFNASAPPEEDCTS 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                 February 21, 2002, 16:28:59
                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100% .
Listing first 45 summaries
                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                              US-08-753-851-2
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length: 23
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Maximum DB seq
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APPLICATION NUMBER: US/08/143,311B
FILING DATE: 29-0CT-1993
CLASSIFICATION 36
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,339
FILING DATE: 30-0CT-1992
CLASSIFICATION: 436
APPLICATION NUMBER: 07/669,730
FILING DATE: 15-MAR-1991
CLASSIFICATION: 436
APPLICATION: 436
APPLICATION: 436
CLASSIFICATION: 436
APPLICATION: 436
US-08-866-545-16
US-08-179-481-99
US-08-520-977A-8
US-08-462-018-9
US-08-823-245-9
US-08-853-910-8
US-08-853-910-8
US-08-853-910-8
US-08-853-910-8
US-08-853-910-8
US-08-853-910-8
US-08-853-913-8
US-08-853-913-8
US-08-853-918-135
US-08-433-118A-135
US-08-433-118A-135
US-08-922-048-135
US-08-922-048-137
US-08-922-048-137
US-08-922-048-137
US-08-922-048-137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1579-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08143311B Patent No. 5863540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REPERENCE/DOCKET NUMBER: 157
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HAYNES, BARTON F.
APPLICANT: HALE, LAURA P.
APPLICANT: PATTON, KAREN L.
APPLICANT: TELEN, MARILYN J.
APPLICANT: LIAO, HUA-XIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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Length 22;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 5663144ris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33.5; DB 1;
Pred. No. 1.3e+02;
                                                                                         APPLICANT: CARRAWAY, KERMIT L.
APPLICANT: CAROTHERS CARRAWAY, CORALIE A.
APPLICANT: FRGIEN, NEVIS L.
TITLE OF INVENTION: ONCOGENE PRODUCT LIGAND
WINBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                   ADDRESSEE: CUSHMAN, DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-433-318A-104
Sequence 104, Application US/08433318A
Sequence 104, Application US/08433318A
Sensent No. 5663144
GENERAL INFORMATION:
APPLICANT: Greene Mark I.
APPLICANT: Greene COMPOUNS THAT ITLE OF INVENTION: METHODS OF USIN.
Sequence 108, Application US/08179481 Patent No. 5624816 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 108:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.8%;
                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 YCYNHGHCDISGPP--DC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 YCFN----ASAPPEEDC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 22 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: peptide US-08-179-481-108
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COMPUTER READABLE FORM:
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CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
''^a 8; Conserve
                                                                                                                                                                                                                                                                                                                                                    CITY: WASHINGTON STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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0
                                Length 23;
                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                            Query Match 100.0%; Score 135; DB 2; Best Local Similarity 100.0%; Pred. No. 1.9e-12; Matches 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: AN ADHESION MOLECULE NUMBER OF SEQUENCES: 28 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/143,311B
FILING DATE: 29-OCT-1993
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,339
FILING DATE: 30-0CT-1992
CLASSIFICATION: 436
APPLICATION 1014BER: 07/669,730
FILING DATE: 15-MAR-1991
CLASSIFICATION: 436
ATONNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/08143311B Patent No. 5863540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
COMPUTUT TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                      1 CNTSQYDTYCFNASAPPEEDCTS 23
                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: HAYNES, BARTON F.
APPLICANT: PAILE, LARRA P.
APPLICANT: PAITON, KAREN L.
APPLICANT: TELEN, MARILYN J.
APPLICANT: LIAO, HUA-XIN
                                                                                                                                                         1 CNTSQYDTYCFNASAPPEEDCTS 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4100
TELEFAX: 703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISCS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 11 amino acids
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 29
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 NTSOYDTY 11
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                                                                                                                                                                                                                                                                                                                                          US-08-143-311B-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-143-311B-14
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Score 32; DB 1; Length 14;
Pred. No. 1.3e+02;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 167, Application US/08433318A

Patent No. 5663144

GENERAL INPORMATION:
APPLICAMY:
TITLE OF INVENTION: COMPOUNDS THAT BIND TO p185 AND
TITLE OF INVENTION: METHODS OF USING THE SAME
NUMBER OF SEQUENCES:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-2106
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WORDPERPECT 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 03-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                           23.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 167
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 46.2
Matches 6; Conservative
        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                           Query Match 23.7
Best Local Similarity 46.2
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: peptide US-08-433-318A-167
                                               TYPE: amino acid
TYPELOGGY: unknown
MOLECULE TYPE: peptide
US-08-433-318A-105
                                                                                                                                                                                                                                                           5 QYDTYCFNASAPP 17
                                                                                                                                                                                                                                                                                                  4 QWDWYCY----PP 12
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4 QWDWYCY----PP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Mark DeLuca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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US-08-433-318A-168
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US-08-433-318A-167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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Patent No. 5663144
GENERAL INFORMATION:
APPLICANT: Greene, Mark I.
TITLE OF INVENTION: COMPOUNDS THAT BIND TO p185 AND TITLE OF INVENTION: METHODS OF USING THE SAME NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 5663144ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.7%; Score 32; DB 1; I
46.2%; Pred. No. 1.3e+02;
tive . 2; Mismatches 1;
MEDIUM TYPE: DISKETTE, 3.5 INCH
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows
SOFTWARE: WORDPERFECT 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,318A
FILING DATE: 03-MAY-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mark Deluca
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-2106
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ...аек: US/08/433,318A
03-MAY-1995
)N: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATILITY, 3.5 INCOMPUTER: IBM PC COMPATILITY, 3.5 INCOMPATION SYSTEM: WINDOWS SOFTWARE: WORDERFECT 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,
FILING DATE: 03-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Mark Deluca
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 105:
                                                                                                                                                                                                                                                                                                               : LLEFRAX: (215) 568-3100
: TELEFAX: (215) 568-3439
: INFORMATION FOR SEQ ID NO: 104: SEQUENCE CHARACTERISTICS: LENGTH: 14
TYPP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 23.77
Best Local Similarity 46.2
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
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4 QWDWYCY----PP 12
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Gaps
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Pred. No. 1.3e+02;
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Patent No. 5919764

GENERAL INFORMATION:
APPLICANT: GENERAL INFORMATION:
TITLE OF INVENTION: COMPOUNDS THAT BIND TO p185 AND TITLE OF INVENTION: METHODS OF USING THE SAME NUMBER OF SEQUENCES: 184

CORRESPONDENCES. 184

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 5919764ris

STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                      PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/433,318
FILING DATE: 03-MAY-1995
ATTORNEY, AGENT INFORMATION:
NAME: MARK DELUCA
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-2106
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARRACTERISTICS:
LENGTH: 14

"VPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/922,048
FILING DATE:
CLASSIFFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/433,318
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
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ZIP: 19103
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH
TYPE: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-2106
TELECOMMUNICATION INFORMATION:
                                                    US/08/922,048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 105
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: Windows SOFTWARE: WORDPERFECT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 23.7%;
Best Local Similarity 46.2%;
Matches 6; Conservative
           WORDPERFECT 6
        SOFTWARE: WORDPERFECT CURRENT APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-922-048-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 QWDWYCY----PP 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 104, Application US/08922048

Patent No. 5919764

GENERAL INFORMATION:
TITLE OF INVENTION: COMPOUNDS THAT BIND TO p185 AND TITLE OF INVENTION: METHODS OF USING THE SAME NUMBER OF SEQUENCES: 184

CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No 5919764ris
STREET: One Liberty Place - 46th Floor
Sequence 168, Application US/0843318A
Fatert No. 5663144
GENERAL INFORMATION:
TITLE OF INVENTION: COMPOUNDS THAT BIND TO p185 AND TITLE OF INVENTION: METHODS OF USING THE SAME NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 66631441s:
ADDRESSEE: NO. 66631441s:
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: Windows
SOFTWARE: WORDERFECT 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/433,318A
FILING DATE: 03-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Mark DeLuca
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-2106
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WEDIUM TYPE: DISKETTE, 3.5 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INPORMATION FOR SEO ID NO: 168
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: ATTORNEY/AGENT · INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 46.2
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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4 QWDWYCY---PP 12
                                                                                                                                                                                                                                         Philadelphia
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ZIP: 19103
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US-08-922-048-104
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                                                                                                                                                                                                                                           CITY: P
STATE:
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STATE:
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APPLICANT: Greene, Mark I.
TITLE OF INVENTION: COMPOU
TITLE OF INVENTION: METHOD
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                   ZIP: 19103
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                                                                                                                                                                     COUNTRY:
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46.2%; Pred. No. 1.3e+02;
Live 2; Mismatches 1; Indels
                                                                                  Length 14;
                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                     COMPOUNDS THAT BIND TO p185 AND METHODS OF USING THE SAME
                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 184

CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 5919764ris
STREET: One Liberty Place - 46th Floor CITY: Philadelphia
STATE: PA
COUNTRY: USA
                                                                                Score 32; DB 2;
Pred. No. 1.3e+02;
                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-2106
TELECOMONNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 167:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 19103
COMPUTER READABLE FORM:
MEDUUM TYPE: DISKETTE, 3.5 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: WINGOWS
SOFTWARE: WORDPRFECT 6
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/433,318
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/922,048
                                                                                                                                                                                                                                                              Sequence 167, Application US/08922048 Patent No. 5919764 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-08-922-048-168
Sequence 168, Application US/08922048
; Patent No. 5919764
; GENERAL INFORMATION:
                                                                                  23.78;
                                                                                                                                                                                                                                                                                                                  APPLICANT: Greene, Mark I.
TITLE OF INVENTION: COMPOU
                                                                   Query Match
Best Local Similarity 46.2%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 46.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide US-08-922-048-167
               ; MOLECULE TYPE: peptide US-08-922-048-105
                                                                                                                                                  5 QYDTYCFNASAPP 17
                                                                                                                                                                     |:| ||:: ||
4 QWDWYCY----PP 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Mark DeLuca
 unknown
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                                                                                                                                                                                                                                                  US-08-922-048-167
 TOPOLOGY:
                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                 qq
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1; Indels
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46.2%; Pred. No. 1.3e+02;
Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Woodcock Washburn Kurtz Mackiewicz & Norris
One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Greene, Mark I.
APPLICANT: Zhang, Xin
TITLE OF INVENTION: COMPOUNDS THAT BIND TO p185 AND
TITLE OF INVENTION: METHODS OF USING THE SAME
COMPOUNDS THAT BIND TO p185 AND METHODS OF USING THE SAME
                                                                                                                                                                                                                  ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: No. 5919764ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-2106
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 168:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/433,318
FILING DATE: 03-MAY-1995
ATTORNEY AGENT INFORMATION:
NAME: MAIK DELUCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US96-06270-104; Sequence 104, Application PC/TUS9606270; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: WORDPERFECT 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/922,048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INC
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: ISM PC COMPATIBLE
COMPATIBLE
COMPATIBLE
COMPUTER: ISM PC COMPATIBLE

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: DISKETTE, 3.5
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 23.7
Best Local Similarity 46.2
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-922-048-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
             Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 14;
                                                                                                                                                                                                                        Sequence 167, Application PC/TUS9606270
Sequence 167, Application PC/TUS9606270
GENERAL INFORMATION:
APPLICANT: Greene, Mark I.
APPLICANT: Zhang, Xin
TITLE OF INVENTION: COMPOUNDS THAT BIND TO p185 AND
TITLE OF INVENTION: METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
      Score 32; DB 5; I
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.7%; Score 32; DB 5; 46.2%; Pred. No. 1.3e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
PCT-US96-06270-168
; Sequence 168, Application PC/TUS9606270
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
APPLICANT: Zhang, Xin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/433,318
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Mark Deluca
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 167:
      23.7%;
ilarity 46.2%;
Conservative 2
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                                                                                              5 QYDTYCFNASAPP 17
                                                                                                                       |:| ||: ||
4 QWDWYCY----PP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 QYDTYCFNASAPP 17
           Query Match
Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32; DB 5; Length 14; Pred. No. 1.3e+02; i Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 105, Application PC/TUS9606270
GENERAL INFORMATION:
APPLICANT: Greene, Mark I.
APPLICANT: Zhang, Xin
TITLE OF INVENTION: COMPOUNDS THAT BIND TO p185 AND
TITLE OF INVENTION: METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOOGCOCK WAShburn Kurtz Mackiewicz & NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06270
                                                                                                            NAME: MARK DeLuca
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-2748
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFTCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/433,318
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mark DeLuca
REGISTRATION NUMBER: 33,229
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/433,318
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: UDN-2748
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 105:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 23.7
Best Local Similarity 46.2
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown

MQLECULE TYPE: peptide
PCT-US96-06270-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 QYDTYCFNASAPP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1:1 ||: ||
4 QWDWYCY----PP 12
                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US96-06270-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 19103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: PA
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STREET: One Liberty Place - 46th Floor
CTTY: Philadelphia
STATE: PA
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH
COMPUTER: IBB PC Compatible
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06270
FILING DATE:
CLASSIPICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/433,318
FILING DATE: 03-MAY-1995
ATTOMNEY AGENT INFORMATION:
FELECOMMUNICATION NUMBER: 33,229
REFERENCE/DOCKET NUMBE
```

Search completed: February 21, 2002, 16:30:53 Job time: 114 sec

Query Match
23.7%; Score 32; DB 5; Length 14;
Best Local Similarity 46.2%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels

5 QYDTYCFNASAPP 17 |:| ||: 4 QWDWYCY----PP 12

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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OM protein - protein search, using sw model

Run on:

February 21, 2002, 16:33:15 ; Search time 12.69 Seconds
(without alignments)
192.087 Million cell updates/sec

Title: Perfect score: Sequence:

US-08-753-851-3 179 1 CRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSS 32

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

6754 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 32

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR\_68:\* Database

pir1:\*
pir2:\*
pir3:\*
pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		ATPase-beta chain	X-Pro aminopeptida	aspartate transcar	T-cell receptor da	or	omega-gliadin - ei	pyrrhocoricin - Py	tical pro	pollen allergen Fe		pollen allergen Fe	$\rightarrow$		pollen allergen Ag		犘	trichocyst protein	hyaluronate recept	endometrial secret	mannose-specific 1	RNA-binding protei	annexin V - rat (f	2-phosphinomethylm	hypothetical prote	hypothetical prote	protein-tyrosine k	gene NF1 protein -	hrom
SUMMARIES	ID	149732	T01689	PC2307	S51176	S35924	A41299	A03356	S44465	A84412	C37396	G61491	D37396	I50533	F37396	E37396	G37396	B56817	B60698	A41683	A61377	A39509	S28837	D53507	PS0106	T01701	B34962	478	4	C25629
	88	7	7	7	7	~	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	~	~	~	N	4	7	7	7
	Query Match Length		25	30	27	29	19	28	20	30	17	20	20	22	26	26	26	29	29	29	19	24	25	26	28	31	32	18	24	25
	ch		9.	9.	0.	0.	4.	4.		٠.										8.					•	٠	7			
æ	Query	22	15	15	15	57	18	18	17	17	17	16	16	ĭ	16	16	ĭ	76	16	Ť	ĭ	ĭ	ĭ	76	16	16	16		ï	
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	Result No.		7	ю	4	5	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

ribosomal protein	pseudogermin - whe	calmodulin, vasoac	tubulin alpha chai	glycoprotein, 11.7	hypothetical prote	L protein - rabies	ribosomal protein	major immunophilin	trp operon leader	trp operon leader	chemoattractant pr	calsequestrin, car	protein phosphatas	major outer membra	cytochrome-c oxida
S32387	S27248	C44101	A54519	S13899	S52357	PQ0369	S51055	C49480	LFECW	B85761	A36279	A39040	A32917	S28434	S77983
7	7	7	7	7	7	7	7	7	1	7	7	7	7	7	7
20	15	15	20	22	22	25	26	32	14	14	15	18	18	20	50
15.4	15.1	15.1	15.1	15.1	15.1	15.1	15.1	15.1	14.5	14.5	14.5	14.5	14.5	14.5	14.5
27.5	27	. 27	27	27	27	27	27	27	26	26	26	26	26	26	26
30	31	32	33	34	35	36	37	38	39	40	41	. 42	43	44	45

## ALIGNMENTS

NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 14K chain - potato mitochondrion (fragme NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 14K chain. NADH-ubiquinone oxidoreductase C; Shecies: mitochondrion Solanum tuberosum (potato)
C; Date: 12-May-1994 #sequence\_revision 12-May-1994 #text\_change 07-May-1999
C; Accession: 149732
R; Herz, u.; Schroeder, W.; Liddell, A.; Leaver, C.J.; Brennicke, A.; Grohmann, L. J. Biol. Chem. 269, 2263-2269, 1994
A; Title: Purification of the NADH:ubiquinone oxidoreductase (complex I) of the respir A; Accession: 149732
A; Accession: 149732
A; Accession: 149732
A; Mulb: 94124587
A; Accession: 149732
A; Mulcule type: protein
A; Residues: 1-29 cHER>
C; Genetics:
A; Genome: mitochondrion
C; Keywords: electron transfer; hydrogen ion transport; mitochondrial inner membrane;

Gaps ö 22.3%; Score 40; DB 2; Length 29; 46.7%; Pred. No. 45; 5; Indels ive 3; Mismatches 5; Indels Query Match 22.3 Best Local Similarity 46.7 Matches 7; Conservative

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17 PEDIYPSNPTDDDVS 31 ολ

|:| |:| ||: 13 PDDFDPNNPYKKDVA 27 Db

ATPase-beta chain - maize chloroplast (fragment)
C;Species: chloroplast Zea mays (maize)
C;Species: 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change 29-Oct-1999
C;Accession: T01689
B;Bradley, D.; Gatenby, A.A.
EMBO J. 4, 3641-3648, 1985
A;Title: Mutational analysis of the maize chloroplast ATPase-beta subunit gene promot

A:Cross-references: EMBL:X03396; NID:g12404; PIDN:CAA27131.1; PID:g12405 C;Genetics: system.
A.Reference number: Z14396; MUID:86136006
A.Refession: T01689
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A:Residues: 1-25 < GRA>- ..................... NTD.612404; PIDN:Cl

A; Genome: chloroplast C; Keywords: chloroplast

Score 35; DB 2; Length 25; Pred. No. 1.9e+02;

19.6%; 38.9%; Query Match Best Local Similarity ö

Gaps

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Indels

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submitted to the EMBL Data Library, May 1993
A;Description: An alternative splicing between VgammaJgamma2.3 and Cgamma2 gene segme
A;Reference number: S32764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Species: Homo sapiens (man)
C; Date: 28-May.1992 #sequence_revision 28-May-1992 #text_change 23-Jul-1999
C; Accession: A41299
E; Accession: A41299
E; Wege, H.; Straus, A.; Ott, M.; Bannwarth, W.; Lanchbury, J.; Panayi, G
Proc. Natl. Acad. Sci. U.S.A. 88, 8534-8538, 1991
A; Title: The T-cell-receptor repertoire in the synovial fluid of a patient with rheum A; Accession: A41299; MUID:92020887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   omega gliadin - einkorn wheat (fragment)
C;Species: Triticum monococcum (einkorn wheat)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 18-Jun-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Cross-references: GB:S57433; NID:g236318; PIDN:AAB19956.1; PID:g236319 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T-cell receptor alpha chain precursor V region (17.2) · human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Shewry, P.R.; Autran, J.C.; Nimmo, C.C.; Lew, E.J.L.; Kasarda, D.D. Nature 286, 520-522, 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 28;
                                                                                                                                                                                                                                                   Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33; DB 2; Ler
Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 2;
Pred. No. 4e+02;
3; Mismatches
                                                                                                                                                                                                                                                      Score 34; DB 2;
Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                  1; Mismatches
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40.0%;
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53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.48;
58.38;
                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-29 <MATA
A;Cross-references: EMBL:222684
C;Keywords: T-cell receptor
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A;Accession: A03356
                                                                                                                                                                                                                                                                                                                                              4 GTRYVQKGEYRTN 16
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A; Residues: 1-28 <SHE>
C; Superfamily: gliadin
                                                                                                                                                                                                                                                                                                                                                                                        12 GTTLVVTGKYRKN
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Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
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Best Local Similarity
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A; Residues: 1-19 <UEM>
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                                                                     A; Accession: S35924
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R;Denslow, N.D.; Ryan, J.W.; Nguyen, H.P.
Biochem. Blophys. Res. Commun. 205, 1790-1795, 1994
A;Title: Guinea pig membrane-bound aminopeptidase P is a member of the proline peptidase A;Reference number: PC2307; MUID:95110325
A;Accession: PC2307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Molecule type: protein
A.Residues: 1-26 <DE2>
A.Experimental source: kidney
C.Comment: This enzyme is a membrane bound protein.
C.Comment: This enzyme hydrolyzes imido bonds.
C.Comment: This emzyme acts as an aminoacylproline hydrolase and is a member of the prol
C.Superfamily: pig X-Pro aminopeptidase
C.Superfamily: pig X-Pro aminoacylpeptide hydrolase; membrane protein
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C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 25-Apr-1997
C;Accession: S51176
R;Hemmens, B; Carrey, E.A.
Eur. J. Blochem. 225, 845-853, 1994
A;Title: Proteolytic cleavage of the multienzyme polypeptide CAD to release the mammalia A;Reference number: S51176; MUID:95045561
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Bate: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 23-Mar-2001
C;Accession: S35924
R;Mathioudakis, G; Platsoucas, C.D.
                                                                                                                                                                                                     X-Pro aminopeptidase (EC 3.4.11.9) L13K - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 25-Feb-1995 #sequence_revision 26-May-1995 #text_change 17-Nov-2000
  Gaps
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Pred. No. 2.3e+02;
3; Mismatches 6; Indels
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    Mismatches
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Similarity 40.0%;
6; Conservative
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Best Local Similarity 44.**,
8; Conservative
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RTNPTTSRPGDPLESTCS 19
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                                            14 RTNPEDIYPSNPTDDDVS 31
  Conservative
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10 YYQDGEFGIRIEDVF 24
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A; Residues: 1-30 <DEN>
A; Experimental source: lung
A; Accession: PC2310
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Best Local Similarity
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A; Molecule type: protein
A; Residues: 1-27 <HEM>
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7;
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  Matches
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A; Title: Isolation and characterization of a major cross-reactive grass group I aller A; Reference number: A37396; MUID:89364850
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A, Title: Microsequence analysis of winged bean seed proteins electroblotted from two-
A, Reference number: A61491; MUID:89351606
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C;Species: Festuca elatior (reed fescue)
C;Acte: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 09-Jun-2000
C;Accession: D37396
R;Esch, R.E.; Klapper, D.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Blectrophorus electricus (electric eel)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 29-Sep-1999
C;Accession: 150531 # Sequence_revision 13-Sep-1996 #text_change 29-Sep-1999
B;Munjaal, R.P.; Dedman, J.R.; Means, A.R.
Ann. N. Y. Acad. Sci. 356, 110-118, 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Psophocarpus tetragonolobus (winged bean)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 17-Mar-2000
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                                                                            Length 17;
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Pred. No. 7e+02;
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A;Molecule type: protein
A;Residues: 1-20 <HIR>
C;Superfamily: plant Kunitz-type proteinase inhibitor
C;Keywords: glycoprotein; seed
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                                                                            Score 31; DB 2
Pred. No. 4.2e4
4; Mismatches
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Pred. No.
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31.2%;
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Best Local Similarity 31.2
Final 5; Conservative
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Best Local Similarity 45.5'
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| YTTEGGTKSEAEDVIP 16
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| YTTEGGTKSEVEDVIP 16
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A; Residues: 1-20 <ESC>
C; Superfamily: expansin
C; Keywords: pollen
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9 DGNKLVNRGYY 19
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A; Status: preliminary
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R; Hirano, H.
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A84412
hypothetical protein Vng2626h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: A84412
R;NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reierence number: A84160; MUID:20504483
A;Reierence number: A84160; MUID:20504483
A;Accession: A84412
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-30 <STO>
A;Cross-references: GB:AE004437; NID:910582006; PIDN:AAG20661.1; GSPDB:GN00138
C;Genetics:
A;Genetics:
S44465

Pyrrhocoricin - Pyrrhocoris apterus
C;Species: D-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C;Accession: S44465
R;Cociancich, S; Dupont, A.; Hegy, G.; Lanot, R.; Holder, F.; Hetru, C.; Hoffmann, J.A.
Biochem. J. 300, 567-575, 1994
A;Title: Novel inducible antibacterial peptides from a hemipteran insect, the sap-suckin
A;Reference number: S44463; MUID:94271176
A;Molecule type: protein
A;Residues: 1-20 <CCC>
C;Function:
A;Residues: 1-20 <CCC>
C;Function:
A;Bescription: antibacterial protein
A;Note: active against Gram-negative bacteria
C;Reywords: antibacterial; hemolymph; immune response
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(237396
pollen allergen Fes e I type A - reed fescue (fragment)
(5.Species: Festuca elatior (reed fescue)
(5.Species: Festuca elatior (reed fescue)
(5.Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 25-Oct-1996
(5.Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 25-Oct-1996
(5.Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 25-Oct-1996
(7.Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 25-Oct-1996
(7.Date: 28-Apr-1996
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45.0%; Pred. No. 4.4e+02;
tive 0; Mismatches 8;
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Search completed: February 21, 2002, 16:35:06 Job time: 111 sec
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C;Species: Poa pratensis (Kentucky bluegrass)
C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 09-Jun-2000
C;Cession: F731396
C;Cession: F731396
C;Cession: E57346
C;Cession: E77396
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C;Species: Agrostis alba (bent grass)
C;Species: Agrostis alba (bent grass)
C;Species: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 09-Jun-2000
C;Accession: E37396
R;Esch, R.E.; Klapper, D.G.
Mol. Immunol. 26, 557-561, 1989
Mol
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A;Molecule type: mRNA
A;Residues: 1-22 <MUN>
A;Cross-references: GB:M25058; NID:g213127; PIDN:AAA62797.1; PID:g213128
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: EF hand
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Pred. No. 9.4e+02;
3; Mismatches 8; Indels
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A,Title: Isolation of the structural gene for calmodulin. A,Reference number: ISO533; MUID:81205530 A,Accession: ISO533
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us-08-753-851-3.rpr

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 21, 2002, 16:34:50; Search time 10.07 Seconds (without alignments) 116.512 Million cell updates/sec Run on:

US-08-753-851-3 179 1 CRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSS 32

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

1983

Minimum DB seq length: 0 Maximum DB seq length: 32

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		Description	P80267 solanum tub	P81079 desulfuromo	P80707 amycolatops		P37362 pyrrhocoris			_		~	6	P80411 palomena pr		-	P03053 escherichia		P08497 bacillus su	P80556 anabaena sp		P13179 chandipura		P80611 zea mays (m	P42992 bufo regula	P29207 rana ridibu	rana c	felis	P81071 felis silve		σ.	6 phyll	_	036 uperolei	P14469 felis silve
SUMMAKIES		QI	NUO1_SOLTU	CY35_DESAC	FEDG_AMYME	GDO_TRIMO	PYRR_PYRAP	PSAF_SYNP6	MK2B_PALPR	LCK_RAT	COX6_NEUCR	MK1_PALPR	MK2A_PALPR	MK3_PALPR	ECDB_LYMDI	HORC_HORSP	LPW_ECOLI	COXB_THUOB	LPA2_BACSU	PHAC_ANASP	ANT3_MESAU	RRPL_CHAV	NUO3_SOLTU	UC05_MAIZE	NEUV_BUFRE	TKNA_RANRI	TKND_RANCA	FIBA_FELCA	TRYP_FELCA	UPA2_HUMAN	FARI_CALVO	TP13_PHYRO	UN02_PINPS	- 1	FIBB_FELCA
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P56738 treponema p P29322 homo sapien	P12239 synechococc P82542 squalus aca	P52390 streptomyce P41124 photorhabdu		P80622 zea mays (m P80501 solanum tub		P24744 solanum tub
CFPA_TREPH EPA8_HUMAN	PSBF_SYNVU PLMS_SQUAC	EFTU_STRLU MALK_PHOLU	RECX_METCL CXA2_CONAL	UC16_MAIZE MMPX_SOLTU	COXF_ONCMY	PK12_SOLTU
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23	23	23	23	22 22 23	22	22
34 35	36	8 6 8 8	40 41	42	44	45

### ALIGNMENTS

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Shewry P.R., Autran J.-C., Nimmo C.C., Lew B.J.-L., Kasarda D.D.;
"N-terminal amino acid sequence homology of storage protein components
from barley and a diploid wheat.";
Nature 286:520-522(1980).
PIR; A03356; A03356.
Seed storage protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Hemolymph;
MEDLINE-94271176; PubMed=8002963;
Cociancich S., Dupont A., Hegy G., Lanot R., Holder F., Hetru C.,
Hoffmann J.A., Bulet P.;
"Novel inducible antibacterial peptides from a hemipteran insect, the sap-sucking bug Pyrrhocoris apterus.";
Biochem. J. 300:567-575(1994).
                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
Triticeae, Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pyrrhocoris apterus (Sap sucking bug).
Bukaryota, Metazoa, Arthropoda, Trachheata; Hexapoda, Insecta,
Pterygota, Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
Heteroptera; Panheteroptera; Pentatomomorpha; Lygaeoidea;
                                                                                                                                                                                                                                                                                                                                                                                        Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                             Triticum monococcum (Einkorn wheat) (Small spelt).
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Pred. No. 1.8e+02;
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                                                                (Rel. 01, Last sequence update) (Rel. 23, Last annotation update)
                28 AA.
                  PRT;
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                                                 Created)
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40.0%;
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28 AA; 3343 MW;
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NCBI_TaxID=37000;
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                STANDARD;
                                                                                                OMEGA-GLIADIN (FRAGMENT)
                                              21-JUL-1986 (Rel. 01,
21-JUL-1986 (Rel. 01,
01-AUG-1992 (Rel. 23,
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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              GDO_TRIMO
P02865;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-NCIB 11946;
MEDLINE-96140591; PubMed-8554333;
Kim S.W., Luykx D.M.A.M., de Vries S., Duine J.A.;
"A second molybdoprotein aldehyde dehydrogenase from Amycolatopsis methanolica NCIB 11946.";
Arch. Blochem. Blophys. 325:1-7(1996).
                                                                          Bruschi M., Woudstra M., Guigliarelli B., Asso M., Lojou E., Petillot Y., Abergel C.;
"Biochemical and spectroscopic characterization of two new cytochromes isolated from Desulfuromonas acetoxidans.";
Biochemistry 36:10601-10608(1997).
-i- FUNCTION: PARTICIPATES IN SULFATE RESPIRATION COUPLED WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
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                                                                                                                                                                          PHOSPHORYLATION BY TRANSFERRING ELECTRONS FROM THE ENZYME DEHYDROGENASE TO FERREDOXIN. THE REDOX POTENTIALS OF THIS CYTOCHROME ARE -140 MV, -210 MV AND -240 MV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEDG_AMYME STANDARD; PRT; 24 AA.
P80707;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
FORMATE ESTER DEHYDROGENASE, GAMMA CHAIN (EC 1.2.99.-) (FEDH)
                                                                                                                                                                                                                                                                                 InterPro; IPR000345; Cyt_heme_bind.
PROSITE; PS00190; CYTOCHROME_C; PARTIAL.
Electron transport; Sulfate respiration; Heme; Periplasmic.
NON_TER 30 30
                                                                                                                                                                                                                                                                                                                                                                                                   Score 34; DB 1; Length 30; Pred. No. 1.4e+02; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.4%; Score 33; DB 1; Length 24; 53.8%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Firmicutes, Actinobacteria, Actinobacteridae, Actinomycetales, Pseudonocardineae,
                                                                                                                                                                                                                                                                                                                                                     30 AA; 3018 MW; B0D52603DD5069B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24
2746 MW; A93A8EA007D0FC6B CRC64;
                                                                                                                                                                                                                       -!- SUBUNIT: MONOMER.
-!- SUBUNIT: MONOMER.
-!- PTM: BINDS 4 HEMES.
-!- SIMILARITY: TO OTHER C3-TYPE CYTOCHROMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                             MEDLINE=97419123; PubMed=9271490;
                                                                                                                                                                                                                                                                                                                                                                                                       19.0%;
                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 47.17
The Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 RDGTRYVQKGEYRTNPE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amycolatopsis methanolica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 RDGTIAATKGKAKTLAE 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 DGTSYTDEVEPRT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 DGTRYVQKGEYRT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oxidoreductase.
              NCBI_TaxID=891;
Desulfuromonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amycolatopsis
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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SEOUENCE
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FEDG\_AMYME

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SEQUENCE

Query Match

Matches

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Gaps ; 0

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"The inducible antibacterial peptides of the hemipteran insect
Palomena prasina. Identification of a unique family of proline-rich
peptides and of a novel insect defensin.";
J. Insect Physiol. 42:81-89(1996).
-i- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;;
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01-JUL-1993 (Rel. 26, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PHOTOSYSTEM I REACTION CENTRE SUBUNIT III (PSI-F) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
Heteroptera; Panheteroptera; Pentatomomorpha; Pentatomoidea;
                             Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oymecmococcus sp. (strain PCC 6301) (Anacystis nidulans).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=1139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.8%; Score 30; DB 1; Length 29; 25.0%; Pred. No. 4.7e+02;
                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 AA; 3040 MW; 535DDC7A63B18711 CRC64;
                                                                              8;
                             1;
                        Score 31.5; DB 1
Pred. No. 2e+02;
); Mismatches
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01-NoV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
METALMIKOWIN IIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 AA.
                                                                                                                                                                                                                                                                                                                     29 AA
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                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91355213; PubMed=1653017;
                        17.6%;
                                                                                                                               VQKGEY --- RTNPEDIYPSN 24
                                                                                                                                                                                   1 VDKGSYLPRPTPPRPIYNRN 20
Ouery Match
Best Local Similarity 45.0.
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                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESPRFIQRAEAAATPQ 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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NCBI_TaxID=55431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Palomena prasina
                                                                                                                                                                                                                                               PSAF_SYNP6
ID PSAF_SYNP6
AC P31083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACTERIA
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SEQUENCE
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MK2B_PALPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001245; Tyr_kin.
PROSTIE: PS00107; PROTEIN KINASE_ATP; PARTIAL.
PROSTIE; PS00109; PROTEIN_KINASE_TYR; PARTIAL.
PROSITE; PS30011; PROTEIN_KINASE_TOM; PARTIAL.
PROSITE; PS30011; PROTEIN_KINASE_DOM; PARTIAL.
Proto-oncogene; Tyrosine-protein kinase; Phosphorylation; Transferase;
ATP-binding; Myristate, Palmitate; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1994 (Rel. 29, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE LCK (EC 2.7.1.112) (P56-LCK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: BOUND TO THE CYTOPLASMIC DOMAIN OF EITHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- DISEASE: PROVIRAL INSERTION UPSTREAM OF THE LCK GENE CAUSES OVERSYPRESSION, LEADING TO THE DEVELOPMENT OF THYMIC LYMPHOMA.
-!- SIMILARIY: TO OTHER PROPEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
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                                                                               Length 16;
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Pred. No. 5e+02;
                                                                                                              Indels
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PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
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                                  AF21407D063B9462 CRC64;
                                                                             Score 29.5; DB 1;
Pred. No. 2.9e+02;
2; Mismatches 5;
                                                                                                                                                                                                                                                    17 AA
                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
-!- INDUCTION: BY BACTERIAL INFECTION.
Antibiotic; Insect immunity.
SEQUENCE 16 AA; 2040 MW; AF21407D0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROBABLE
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001245; Tyr_kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93141260; PubMed=8423992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN TYROSINE PHOSPHATE.
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                                                                               16.5%;
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83.3%;
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Best Local Similarity 83...
5; Conservative
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1 VDKPDYRPRP---WPRN 14
                                                                                                                                         8 VOKGEYRTNPEDIYPSN 24
                                                                                              Best Local Similarity 41.2
Matches 7; Conservative
                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                  (Rel. 29,
(Rel. 29,
(Rel. 39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shin S., Steffen D.L:;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=FISCHER;
                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                   01-JUN-1994
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30-MAY-2000
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SEQUENCE
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Q01621;
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LCK_RAT
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STANDARD;
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NCBI_TaxID=55431;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 VQKGEYRTNP 17
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                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Hemolymph;
                                                                                                                                                                                                                                                                                 METALNIKOWIN IIA.
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                                                          BACTERIA
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P80411;
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MK3_PALPR
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SO CC REFER
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                                                                                                                                                                                   Gaps
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0
                                                                                                                                                Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                               -1- SUBUNTT: COMPOSED OF AT LEAST 11 SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
Heteroptera; Panheteroptera; Pentatomomorpha; Pentatomoidea;
Pentatomidae; Palomena.
                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CYTOCHROME C OXIDASE POLYPEPTIDE VI (EC 1.9.3.1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 28; DB 1; Length 23, Pred. No. 7.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                          25 AA; 2870 MW; 4D8206C608122EEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       Oxidoreductase; Heme; Mitochondrion; Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                            25 AA.
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                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S
or send an email to license@isb-sib.ch).
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01-NOV-1995 (Rel. 32, Last seq
15-JUL-1998 (Rel. 36, Last ann
METALNIKOWIN I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.6%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M12118; AAA33576.1; -.
                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
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                                                                                                                                                                                                                                                                                        4 FERRICYTOCHROME C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                      Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=55431;
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TISSUM HEMOLYMPh;
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                                                                                                                                                                 NCBI_TaxID=5141;
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6 SNPEDD 11
       23 SNPTDD
                                                                           COX6_NEUCR
Q01359;
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P80408;
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SEQUENCE
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COX6_NEUCR
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MK1_PALPR
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Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;
"The inducible antibacterial peptides of the hemipteran insect
Palomena prasina. Identification of a unique family of proline-rich
peptides and of a novel insect defensin.";
J. Insect Physiol. 42:81-89(1996).
-:- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera; Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidea; Pentatomona.
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Pred. No. 5.9e+02;
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                                                                                                                                                                                                                                                                                                                                               Score 27.5; DB 1;
Pred. No. 5.1e+02;
1; Mismatches 6;
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
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50.0%;
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Best Local Similarity 41.2
Matches 7; Conservative
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STRAIN=0157:H7 / EDL933 / ATCC 700927
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22 YPQNP 26
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                                                                                                                                                                                                                                                                                                                                                              21 YPSNP
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P03053;
                    SEQUENCE.
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Eukaryota; Metazoa; Arthroda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;

Noctuoidea; Lymantriidae; Lymantria.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae;
Triticeae, Hordeum.
                                                   Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.; "The inducible antibacterial peptides of the hemipteran insect Palomena prasina. Identification of a unique family of proline-rich peptides and of a novel insect defensin."; Jusect Physiol. 42:81-89(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Naturally occurring analogs of Lymantria testis ecdysiotropin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gonadotropin isolated from brains of Lymantria dispar pupae.";
Arch. Insect Biochem. Physiol. 36:37-50(1997).
-!- FUNCTION: STIMULATES SYNTHESIS OF ECDYSTEROID IN THE TESTES
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MEDLINE-97387807; PubMed-9243792;
Loeb M.J., Wagner R.M., Woods C:W., Gelman D.G., Harrison D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.1%; Score 27; DB 1; Length 23; 50.0%; Pred. No. 9.5e+02;
                                                                                                                                                                                                                                                                                                    Score 27; DB 1; Length 16; Pred. No. 6.4e+02;
                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                 Antibiotic; Insect immunity. SEQUENCE 16 AA; 2024 MW; A9E3835D063B9462 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF LARVAE AND PUPAE.
JENCE 23 AA; 2550 MW; 21AF7C84232032A6 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
10-NOV-1990 (Rel. 16, Last annotation update)
C-HORDEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
TESTIS ECDYSIOTROPIN PEPTIDE B (TE).
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                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                  15.1%;
50.0%;
                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 50.00
دمر 5; Conservative
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Best Local Similarity
5; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                        27
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                                     TISSUE=Hemolymph;
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P02864;
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P80939;
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Shewry P.R., Autran J.-C., Nimmo C.C., Lew E.J.-L., Kasarda D.D.;
"N-terminal amino acid sequence homology of storage protein components from barley and a diploid wheat.";
Nature 286:520-522(1980).
-!- FUNCTION: SULFUR-POOR SEED STORAGE PROTEIN.
-!- TRSUE SPECIFICITY: DEVELOPING ENDOSPERM.
PIR; A03355, A03355.
Seed storage protein; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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MEDLINE=80101455; PubMed=118451;
Oxender D.L., Zurawski G., Yanofsky C.;
Attenuation in the Escherichia coli tryptophan operon: role of RNA secondary structure involving the tryptophan codon region.";
Proc. Natl. Acad. Sci. U.S.A. 76:5524-5528(1979).
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MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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MEDLINE=82150258; PubMed=7038627;
Yanofsky C., Platt T., Crawford I.P., Nichols B.P., Christie G..
Horowitz H., van Cleemput M., Wu A.M.;
"The complete nucleotide sequence of the tryptophan operon of Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Nucleotide sequence of the 5' end of tryptophan messenger RNA
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                                                                                                                                                                                                                                                                                                                                                                      Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                               28 AA; 3333 MW; 8DBA2DF2494775AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                   Score 27; DB 1; I
Pred. No. 1.2e+03;
0; Mismatches 1;
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21-JUL-1986 (Rel. 01, Last sequence update)
20-JUL-1986 (Rel. 40, Last annotation update)
TRP OPERON LEADER PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 AA
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MEDLINE=76240562; Pubmed=781271;
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                                                                                                                                                                                                                                                                                                                                                                   15.1%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                            Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli oli5:H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).
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                 Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; "Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7."; Nature 409:529-533(2001).
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EcoGene; EG11274; trpL.
Tryptophan biosynthesis; Leader peptide; Complete proteome.
SEQUENCE 14 AA; 1723 MW; 5B79306E3E804A37 CRC64;
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Pred. No. 7.6e+02;
3; Mismatches 2; Indels
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MEDLINE=21156231; PubMed=11258796;
MEDLINE-21074935; PubMed=11206551;
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Search completed: February 21, 2002, 16:37:51 Job time: 181 sec

7 YVQKGEYRIN 16 :| || :||: 5 FVLKGWWRTS 14

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Copyright (c) 1993 - 2000 Compugen Ltd.
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BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

473505 seqs, 146272329 residues Searched:

Total number of hits satisfying chosen parameters:

13439

Minimum DB seq length: 0 Maximum DB seq length: 32

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

sp\_plant:\*
sp\_rodent:\*
sp\_rodent:\*
sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\* SPTREMBL\_17:\*

1: sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fungi:\*
4: sp\_human:\*
5: sp\_human:\*
6: sp\_man=1:\*
7: sp\_mc:\* sp\_organelle:\* sp\_phage:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Q9u6u9 plasmodium	033292 zea mays (m		Q38269 bacteriopha	Q9twi5 ceratitis c	086139 clostridium	09e1t3 rabies viru	Q9qv20 mus sp. per	Q9hmb0 halobacteri	O9twi8 ceratitis c	Ogtns5 homo sapien	Q9e1t4 rabies viru	Q9crf6 mus musculu	Q16218 homo sapien	Q9qui8 rattus norv	070125 mus musculu	Q23745 ctenodrilus	Q9t2k5 pisum sativ	Q9v2v2 methanobact
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## ALIGNMENTS

	09u6u9 PRELIMINARY; PRT; 26 AA.	2000 (TrEMBLrel.	(TrEMBLrel. 13,	OITE SURFACE PROTEIN 1 (FRAC	MSP1	falciparum.	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.	NCBI_TaxID=5833; [1]	SECULENCE FROM N.A.	STRAIN=94/98;	Kirchgatter K., Branquinho M.S., Salles T.M., Lian Y.C., Roberio J.,		"Nosocomial malaria transmission identified by molecular typing of	Plasmodium falciparum.";	Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.	EMBL; AF176817; AAD54320.1;	Merozoite.	-	26	SEQUENCE 26 AA; 2921 MW; B26309B1A2117127 CRC64;	Ouerv Match 21.8%; Score 39; DB 5; Length 26;	Similarity 47.4%; Pred. No. 1.1e+02; 9; Conservative 1; Mismatches	14 RTNPEDIYPSNPTDDDVSS 32	4 RTNPSDNSSDSDAKS 18	C		Q33292 PRELIMINARY; PRT; 25 AA.	01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)	. ( - )
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"Mutational analysis of the maize chloroplast ATPase-beta subunit gene
promoter: the isolation of promoter mutants in E. coli and their
characterization in a chloroplast in vitro transcription system.";
EMBC J. 4:5641-3648 (1985).
EMBL; X03396; CAA27131.1;
                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
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Denslow N.D., Ryan J.W., Nguyen H.P.;
"Guinea pig membrane-bound aminopeptidase P is a member
peptidase family.";
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2603 MW; A987B062A134C6AE CRC64;
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A9F6A61854E44A25 CRC64;
01-NOV-1998 (TrEMBLrel. 08, Last annotation update) CHLOROPLAST ATPASE-BETA SUBUNIT GENE N (FRAGMENT).
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SEQUENCE 30 AA; 3411 MW; A9
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38.9%;
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"DNA sequences necessary for packaging of bacteriophage lambda DNA.";
Proc. Natl. Acad. Sci. U.S.A. 80:7456-7460(1983).
SEQUENCE FROM N.A.
MEDGLINE-73215915; PubMed-4515613;
Weigel P.H., Englund P.T., Murray K., Old R.W.;
Wifte 3' terminal nucleotide sequences of bacteriophage lambda DNA.";
Proc. Natl. Acad. Sci. U.S.A. 70:1151-1155(1973).
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Ineichen K., Shepherd J.C., Bickle T.A.;
Pithe DNA sequence of the phage lambda genome between PL and the gene
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Daniels D.L., Schroeder J.L., Szybalski W., Sanger F., Coulson A.R., Hong G.F., Hill D.F., Petersen G.B., Blattner F.R.;

(In) Hendrix R.W., Roberts J.W., Stahl F.W., Weisberg R.A. (eds.);
Lambda II, pp.519-674, Cold Spring Harbor Laboratory Press, New York (1983).
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(In) Heddrix R.W., Roberts J.W., Stahl F.W., Weisberg R.A. (eds.);
Lambda II, pp.469-517, Cold Spring Harbor Laboratory Press,
New York (1983).
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Crafy N.L., Nash H.A.;
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Cell 39:707-716(1984).
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Frackman S., Siegele D.A., Feiss M.;
"A functional domain of bacteriophage lambda terminase for prohead
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"Nucleotide sequence of bacteriophage lambda DNA.";
J. Mol. Biol. 162:729-773(1982).
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Annu. Rev. Biochem. 47:967-996(1978).
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J. Mol. Biol. 179:351-365(1984).
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MEDLINE=83189071; PubMed=6221115;
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NCBI_TaxID=1492;
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01-NOV-1998 (
01-JUN-2001 (
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 14, Last annotation update)
MAJOR COTICULAR PROTEIN (FRACMBNT).
Ceratitis capitata (Mediterranean fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=85142185; PubMed=3156406; Peltz S.W., Brown A.L., Hasan N., Podhajska A.J., Szybalski W.; Peltz S.W., Brown A.L., Hasan N., Podhajska A.J., Szybalski W.; "Thermosenstitivity of a DNA recognition site: activity of a truncated nutt antiterminator of coliphage lambda."; Science 228:91-93(1985).
                                                                               MEDIINE-84119555; Pubmed-6229793; Wulff D.L., Mahoney M., Shatzman A., Rosenberg M.; "Mutational analysis of a regulatory region in bacteriophage lambda that has overlapping signals for the initiation of transcription and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                       Warren F., Das A.; "Formation resistant transcription complex at phage lambda nut locus: effects of altered translation and a ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Colectough C., Erlitz F.L.; "Use of primer-restriction-end adapters in a novel cDNA cloning
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MEDLINE-87280224; PubMed=3038914;
Chen C.Y., Richardson J.P.;
Chen C.Y., Richardson J.P.;
Sequence elements essential for rho-dependent transcription termination at lambda tR1.";
J. Biol. Chem. 262:11292-11299(1987).

EMBL; J02459; AAA96576.1;
SEQUENCE 28 AA; 3699 MW; 2011F5C89C669BE2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                mutation.";
Proc. Natl. Acad. Sci. U.S.A. 81:3612-3616(1984).
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MEDLINE=85232076; PubMed=2408965;
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                  Mol. Biol. 180:865-880(1984).
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7; Conserva
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                                                                                                                                                                            translation.";
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"Distribution of the rubredoxin gene among the Clostridium butyricum
                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae; Clostridium.
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NON_TER 28 28
SEQUENCE 28 AA; 2953 MW; 2E330EA9ABBF3C6A CRC64;
                    Length 20;
                    Score 32; DB 5; Length 20;
Pred. No. 7.8e+02;
2; Mismatches 6; Indels
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Rhabdoviridae; Lyssavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          species.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ010147; CAA09017.1;
HSSP; P00268; ITRO.
InterPro; IPR001052; Rubredoxin.
InterPro; IPR003252; Rubredxin.domain.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
L PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                            (TrEMBLrel. 08, Created)
(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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Pred. No. 1e+03;
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58.3%;
                    17.9%;
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Query Match
Best Local Similarity 42.5
Best Local 6; Conservative
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Best Local Similarity 58...
7; Conservative
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                                                                                                                                       6 VIRSESEVNPDSIY
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                                                                                                  8 VOKGEYRTNPEDIY
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5.

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Length 30;

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Score 31.5; DB 1;
Pred. No. 1.4e+03;
                                     Mismatches
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J. Clin. Invest. 90:2355-2361(1992).
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                                                           10 KGEYRTNP----EDIYPSNPTDD 28
                                                                                  RGLLYTTPTDSDQSDTTPAQPADD 30
             17.6%;
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ilarity 71.4%;
Conservative
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Best Local Similarity
Matches 6; Conserv
               Query Match
Best Local Similarity
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Matches 5; Conserv
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01-MAY-2000
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SEQUENCE
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                                     Gaps
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                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10095;
                                                                                                                                                                                                                                                                                               Stark A., Meijer J.; "Purification and characterization of multifunctional enzyme from
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                                                                                                                                                                                                                                                                                                                                                                                                       Score 31.5; DB 11; Length 19;
Pred. No. 8.6e+02;
1; Mismatches 5; Indels
             Length 28;
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Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
          Score 32; DB 12; Length 28
Pred. No. 1.1e+03;
3; Mismatches 3; Indels
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U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
PEROXISOMAL MULTIFUNCTIONAL ENZYME (FRAGMENT).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                         mouse liver peroxisomes.";
Comp. Biochem. Physiol. 108B:471-480(1994).
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            17.9%;
27.8%;
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                                                          16 NPEDIY -- PSNPTDDDVS 31
                                     Conservative
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Best Local Similarity 53.3
Matches 8; Conservative
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Query Match
Best Local Similarity
..... 5; Conserve
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SEQUENCE 30 AA;
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NCBI_TaxID=64091;
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SEQUENCE
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MEDLINE=93107319; PubMed=1469092;
Meyand C.M., Hicok K.C., Hunder G.G., Goronzy J.J.;
"The HLA-PRB1 locus as a genetic component in giant cell arteritis.
Mapping of a disease-linked sequence motif to the antigen binding site
                                                                          01-MAY-2000 (TrEMBERE) 13, Last sequence update)
01-JUN-2000 (TrEMBERE) 14, Last annotation update)
MAJOR CUTICULAR PROTEIN (FRAGMENT).
Ceratitis capitata (Mediterranean fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Tephritoidea; Tephritidae; Ceratitis.
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Tsiliras A., Koromantzou E., Allen G., Dimitriadis G.;
Partial N-terminal sequences of larval cuticular proteins from the dipteran Ceratitis capitata.";
Hereditas 122:79-83(1995).
SEQUENCE 20 AA; 2408 MW; 2BC25E2F9EC15A80 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
HUMAN LEUCCCYTE ANTIGEN BETA CHAIN DR MOLECULE HLA-DRB1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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Pred. No. 1.1e+03;
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Pred. No. 1.3e+03;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4A23BF7821BACCE0 CRC64;
20 AA.
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17 YLQKGRY 23
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B8D701C9E3DDB4E0 CRC64;
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                                                                                                                                                                                 PRT;
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PRINTS; PR01078; AMINACHANNEL.
Ionic channel.
                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; S73204; AAB31484.2; -. NON_TER 1 1
                                      17.0%;
46.7%;
2979 MW;
                         Ouery Match
Best Local Similarity 46...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 16.8
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-VARIOUS STRAINS;
                                                                                         17 PEDIYPSNPTDDDVS 31
                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 TNPEDIYP 22
                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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2 TDPVDYYP 9
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SEQUENCE
 SEQUENCE
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KEDLINE=21085660; PubMed=11217851;

REDLINE=21085660; PubMed=11217851;

Redwai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Stauki R., Tomita B., Kochiwa H.,

Radota K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Radorstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M.,

Radorstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M.,

Radotinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Radotin H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Sakai H., Toyo-oka K., Wang K.H., Weitz C., Wilming L.,

Nyanawa Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nyanawa Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                        ij
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashizaki Y.;
"Functional amotation of a full-length mouse cDNA collection.";
Nature 409:665-690(2001).
EMBL: AK010771; BAB27171.1;
                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                                   Score 31; DB 12; Length 28; Pred. No. 1.6e+03;
                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                              Viruses; ssRNA negative-strand viruses; Mononegavirales;
Rhabdoviridae; Lyssavirus.
NCBI_TaxID=11292;
                                                                                                                                                                                                                                                                       SEQUENCE 28 AA; 2939 MW; 2E2267A9AB8F3C6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
2410117E06RIK PROTEIN (FRAGMENT).
                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                      4;
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                                                                                                                                                                                                                                                                                                                                       7; Mismatches
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                                       PRT;
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                                                                                                                                                                                                                                                                                                              17.3%; 27.8%;
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                                                                                                                                                                                                                                                                                                                                                                16 NPEDIY--PSNPTDDDVS 31
                                                                                                                                                                                                                                                                                                              Query Match 17.3
Best Local Similarity 27.8
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                       PRELIMINARY;
                                                                                                      PROTEIN (FRAGMENT).
                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                                                                                                  rabies virus
                                                                                                                                                                                              STRAIN=40389
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                                      Q9E1T4
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              RESULT 12
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                           09E1T4
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                   Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Expression and alternative splicing of the deleted in colorectal cancer (DCC) gene in normal and malignant tissues."; Cancer Res. 54:4493-4501(1994).
                                                                   1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-94220088; PubMed-8044801;
Reale M.A., Hu G., Zafar A.I., Getzenberg R.H., Levine S.M.,
Fearon B.R.;
      Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.8%; Score 30; DB 4; Length 21; 62.5%; Pred. No. 1.5e+03; cive 1; Mismatches 2; Indels
                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U35177; ABD103981; -
EMBL; U35177; ABD10397.1; -
INTEFPTO; IPR001873; ASC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 AA; 2337 MW; D2C3578D41548440 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
SODIUM CHANNEL BETA SUBUNIT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) DELETED IN COLORECTAL CANCER PROTEIN (FRAGMENT).
Score 30.5; DB 11;
Pred. No. 1.8e+03;
4; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                   21 AA
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26 AA; 3145 MW; B8E117C76575979C CRC64; SQ SEQUENCE

Η; 2; Gaps Query Match
Best Local Similarity 44.4%; Pred. No. 2e+03;
Matches 8; Conservative 2; Mismatches 6; Indels

7 YVQKGEYRINPEDIYPSN 24 | | | | | | | | | 1: | 10 YFQEFNYRTIEES--PAN 25 δλ

qq

Search completed: February 21, 2002, 16:37:14 Job time: 194 sec

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February 21, 2002, 16:31:15; Search time 23.74 Seconds (without alignments) 99.846 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | SIDSB/gcgdata/geneseqp/ah1980.DAT:*
| SIDSB/gcgdata/geneseqp/Ah1981.DAT:*
| SIDSB/gcgdata/geneseqp/Ah1981.DAT:*
| SIDSB/gcgdata/geneseqp/Ah1981.DAT:*
| SIDSB/gcgdata/geneseqp/Ah1983.DAT:*
| SIDSB/gcgdata/geneseqp/Ah1983.DAT:*
| SIDSB/gcgdata/geneseqp/Ah1981.DAT:*
| SIDSB/gcgdata/geneseqp/Ah1991.DAT:*
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| SIDSB/gcgdata/geneseqp/geneseqp/Ah1992.DAT:*
| SIDSB/gcgdata/geneseqp/aeneseqp/Ah1992.DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSS 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
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179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                                                                                                                                                                                           Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

15: 116: 119: 220: 221:

SUMMARIES

	Description	CD44 beetide CD44-	CD44 peptide CD44-	CD44 peptide CD44-	Surrounding seguen	Timothy grass alle	Timothy grass alle	Yeast Nup2 protein	Yeast YNup2 protei	Anticoagulant pept	Polypeptide fragme	Protein sequence 2
	ID		AAR53477	AAR53481	AAY15201	AAR86983	AAR86980	AAY08793	AAY08821	AAY53086	AAY01162	AAG64195
	DB	15	15	15	20	17	17	20	20	21	20	22
	Length	32	21	30	28	29	30	24	24	12	20	20
ф	Query e Match Length DB 1	100.0	62.0	53.6	45.3	22.3	22.3	21.8	21.8	21.2	21.2	21.2
	Score	179	111	96	81	. 40	40	39	39	38	38	38
	Result No.	1	7	٣	4	5.	9	7	8	6	10	11

Use of CD44 protein and new peptide derivs - for developing prods for inflammation, immune-mediated tissue damage and tumour cell

WPI; 1994-167121/20.

metastasis

Peptide sequence 2	·	toxin	derived	T helper cell (Th)	fied	Amino acid sequenc	ARH1 peptide mimet	Multisubunit 1mmun	BS106 synthetic po	BS106 polypeptide	GTF antigenic epit	Lolium perenne pro	LPI-22, peptide fr		AMB 1-2.15. Ambro	AMB 1-2.15 compris	Bacteriophage T4 f		Fragment of p53 bi	Human WBP1 immunog	Peptide #8936 enco	-	Human Stat6 antige		Streptavidin resid	Peptide derived fr	Human antithrombin	Adenovirus E1A pro	Peptide #11260 enc	Neurotrophic facto	Peptide derived fr
AAB99270	AAR82577	AAW05603	AAY80060	AAY 54543	AAY58771	AAB84439	AAR80000	AAY52323	AAW42092	AAY13470	AAY43350	AAR60736	AAR71561	AAR54411	AAR54414	AAW02492	AAB74004	AAR81762	AAW13184	AAW57352	AAM34899	AAB06281	AAY05230	AAB28824	AAW18505	AAW66705	AAW14612	AAY25353	AAM37223	AAR51725	AAW66707
22 15	19	17	21	21	21	22	16	21	19	20	20	15	16	14	14	17	22	16	16	19	22	21	20	21	18	19	18	20	22	15	19
20	24	24	24	24	24	24	56	32	21	21	16	20	20	24	24	24	56	12	19	19	31	10	18	19	21	23	24	25	25	56	28
21.2	20.7	20.7	20.7	20.7	20.7	20.7	20.7	20.7	20.4		19.8	19.6	19.6				19.3			19.0	19.0	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4
38	37	37	37	37	37	37	37	37		36.5		35	35	34.5	4	34.5	34.5	34	34	34	34	33	33						33		
12	14	12	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44

## ALIGNMENTS

Cell adhesion molecule; CD44; antiinflammatory; rheumatoid; arthritis; tumor cell metastasis; autoimmune disease; Telen MJ; Patton KL, AAR53475 standard; peptide; 32 AA. Liao H, 93WO-US10412. 92US-0973339. (first entry) Hale LP, Haynes BF, CD44 peptide CD44-3. immunosuppressive. (UYDU-) UNIV DUKE. Homo sapiens. 29-OCT-1993; 30-OCT-1992; WO9409811-A. 01-DEC-1994 11-MAY-1994. . AAR53475; AAR53475 

Claim 4; Page 14; 83pp; English.

SXXCCCCCCXX SXXCCCCCCCC

ò g

us-08-753-851-3.rag

2.yrtnpediypsnptdddvss 21

AA.

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The peptide can be used for treating inflammation and immune-mediated tissue damage such as occurs in the course of autoimmune diseases, e.g. rheumatoid arthritis. It can also be used for determining metastatic potential or to treat or prevent tumor cell metastasis. This peptide corresponds to AA 150-161, 170-177 and 189-180 of the CD44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of CD44 protein and new peptide derivs - for developing prods for inflammation, immune-mediated tissue damage and tumour cell
                                                                                                                                                                                         Cell adhesion molecule; CD44; antiinflammatory; rheumatoid;
                                                                                                                                                                                                        arthritis; tumor cell metastasis; autoimmune disease; immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 14; 83pp; English.
                                                        AAR53481 standard; peptide; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liao H,
                                                                                                                                                                                                                                                                                                                                                            93WO-US10412.
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                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hale LP, Haynes BF,
                                                                                                                                                          CD44 peptide CD44-8.
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                             (UYDU-) UNIV DUKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 AA;
                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                            29-OCT-1993;
                                                                                                                         01-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                              30-OCT-1992;
                                                                                                                                                                                                                                                                                           WO9409811-A.
                                                                                                                                                                                                                                                                                                                           11-MAY-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  metastasis
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                                                                                                                                                                                                          Gaps
The peptide can be used for treating inflammation and immune-mediated tissue damage such as occurs in the course of autoimmune diseases, e.g. rheumatoid arthritis. It can also be used for determining metastatic potential or to treat or prevent tumor cell metastasis. This peptide corresponds to AA 150-180 of the CD44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The peptide can be used for treating inflammation and immunemediated tissue damage such as occurs in the course of autoimmune diseases, e.g. rheumatoid arthritis. It can also be used for determining metastatic potential or to treat or prevent tumor cell metastasis. This peptide corresponds to AA 161-180 of the CD44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of CD44 protein and new peptide derivs - for developing prods for inflammation, immune-mediated tissue damage and tumour cell
                                                                                                                                                                                                          ;
0
                                                                                                                                                                         Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell adhesion molecule; CD44; antiinflammatory; rheumatoid; arthritis; tumor cell metastasis; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 21;
                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Telen MJ;
                                                                                                                                                                      Score 179; DB 15;
Pred. No. 1.8e-19;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.0%; Score 111; DB 15; 100.0%; Pred. No. 1.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patton KL,
                                                                                                                                                                                                                                       1 CRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSS 32
                                                                                                                                                                                                                                                          1 crdgtryvqkgeyrtnpediypsnptdddvss 32
                                                                                                                                                                                                                                                                                                                                                         AAR53477 standard; peptide; 21 AA.
                                                                                                                                                                      Query Match 100.0%; Sc
Best Local Similarity 100.0%; Pr
Matches 32; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 14; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liao H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92US-0973339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hale LP, Haynes BF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1994-167121/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD44 peptide CD44-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYDU-) UNIV DUKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                        32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein sequence
                                                                                     protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21
                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9409811-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  metastasis
                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                         AAR53477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                         AAR53477
                                                                                                                                                                                                                                                                                                                          RESULT
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Telen MJ;

Patton KL,

1; Gaps Surrounding sequence of potential assembly site E5-Rg, in CD44. .; 8 isoform; CD44; expression vector; exon; modification; proteoglycan; glycosaminoglycan binding protein; rheumatoid; arthritis; asthma; immunological disorder; assembly site. DB 15; Length 30; 53.6%; Score 96; DB 15; Length 30 illarity 67.9%; Pred. No. 2.8e-07; Conservative 0; Mismatches 1; Indels 1 CRDGTRYVQKGEYRTNPEDIYPSNPTDD 28 AAY15201 standard; Peptide; 28 AA.

6

Gaps

; 0

Indels

,0

13 YR THEDIYPSNPTDDDVSS 32

ò

Valent P;

3

us-08-753-851-3.rag

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Recombinant DNA encoding epitope(s) of timothy grass allergen PhlpI - useful in diagnosis and treatment of allergies, partic. to grass
                                                                                                                                                                                                           timothy grass allergen PhlpI
allergies, partic. to grass
                                                                                                                                                                                                                                                                                                                                                                                    protection of the contract of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Timothy; grass; allergen; Phl p I; epitope; clone c86; diagnosis; allergy; pollen; plant protein; immunoassay; detection; antibody; treatment; immunotherapy; immunodominant; IgE hapten;
                                                                                                                                                                                                                                                                                                                                                                    The present sequence is the Timothy grass allergen Phl p I
                                                                                Susani M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Susani M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Timothy grass allergen Phl p I epitope clone c86.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 17;
Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sperr W,
                                                                             Sperr W,
                                                                                                                                                                                           Recombinant DNA encoding epitope(s) of - useful in diagnosis and treatment of pollen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anaphylactic shock; hyposensitisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR86980 standard; Peptide; 30 AA.
                                                                                                                                                                                                                                                                                                                 Claim 1; Page 19; 25pp; English.
                                                                             aft D, Laffer S,
Vrtala S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kraft D, Laffer S,
R, Vrtala S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.3%;
41.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       || :| :| ||: |
| rytteggtkteaedvip 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 41.2 Matches 7; Conservative
                             (PHAA ) PHARMACIA AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PHAA ) PHARMACIA AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-049622/05.
                                                                                                                                                        WPI; 1996-049622/05
                                                                             Kraft D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phleum pratense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09534578-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Valenta R,
                                                                                                   Valenta R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR86980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ball T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pollen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR86980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The fusion protein may be used to target proteoglycans to a given site, which causes local accumulation of GAG-binding proteins. Therefore the protein may be used as adjuvants for vaccination and in the targeting of chemokines to non-immunogenic tumour cells to enhance cellular antitumour responses. In addition, the fusion protein can also enhance the half-life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  assembly sites in a CD44 exon.

The recombinant fusion protein may be administered to a patient to enhance the biological activity of a GAG-binding protein within the body. The protein also enhances wound healing and may be used to treat rheumatoid arthritis, asthma, chronic obstructive pulmonary disorder, Lupus, inflammatory bowel disease, psoriasis, osteoarthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis;
antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is part of the surrounding sequence of one of the potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                       New artificial proteoglycans useful for treating rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.3%; Score 81; DB 20; Length 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Timothy, grass; allergen; Phl p I; epitope; clone c108; allergy; pollen; plant protein; immunoassay; detection; treatment; immunotherapy; immunodominant; IgE hapten;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Timothy grass allergen Phl p I epitope clone c108.
                                                                                                                                                                                                                                                                                                                                         Wolff EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.le-05;
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Mismatches
                                                                                                                                                                                                                                                                                                                                       Bennett KL, Greenfield WB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anaphylactic shock; hyposensitisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 30; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.52,
100.0%; Piv
0;
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                                                                                                                                                                                                                                                                                    (BRIM ) BRISTOL-MYERS SQUIBB
                                                                                                                                                                                                                                 98US-0072416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95WO-SE00724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 45.3
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-478982/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phleum pratense
Synthetic.
Homo sapiens
                                                                           WO9937317-A1
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                                                                                                                                                                              21-JAN-1999;
                                                                                                                                                                                                                                 24-JAN-1998;
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                                                                                                                           29-JUL-1999
                                                                                                                                                                                                                                                                                                                                       Aruffo AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR86983;
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AAR86983

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Gaps

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7; Indels

Valent

Length 29;

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us-08-753-851-3.rag

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Buergin A,
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                                                                                                                                                                   Sequence
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δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel nucleic acid construct comprising the following components (a) an activation sequence for the transcription of component b, (b) component b which is constructed from component bl (a transcription factor activating domain), component b2 (murine pl63 or p27 binding protein) and component b3 (a transcription factor DNA binding domain), (c) an activation sequence which is activated by binding of the expression product of component (b) and which induces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Activation sequence; transcription factor; murine; p163; p27; treatment; binding protein; DNA binding domain; effector gene; disease; infection; tumour; leukaemia; autoimmune disease; allergy; arthritis; inflammation; transplant rejection, graft-versus-host disease; circulatory disorder; blood clot; anaemia; hormonal disorder; CNS injury; yeast; Nup2.
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid construct comprising promoter, transcription factor gene, activation sequence and effector gene - useful for gene therapy treatment of allergies, inflammation, transplant disorders
                                                               epitope clone c86, which was isolated by screening a random DNase I digested Phl p I E. coli expressed lambda gill cDNA library, with serum IgE from Phl p I allergic patients. The epitope can be used to (pref. in vitro) diagnose allergy to plant proteins, esp. grass pollen, by immunoassay detection of specific antibodies, for the treatment of pollen allergy, by passive admin. Or active immunotherapy and for measuring (pref. in vitro) cellular reactions against the Phl p I epitope. The epitope is an immunodominant IgE hapten, and is therefore less likely to cause anaphylactic shock during hyposensitisation treatment.
                                                                                                                                                                                                                                                                                                                                                                    ö
                                                The present sequence is the Timothy grass allergen Phl p I
                                                                                                                                                                                                                                                                                                                            Score 40; DB 17; Length 30;
Pred. No. 48;
3; Mismatches. 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY08793 standard; Protein; 24 AA.
              Claim 1; Page 19; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sedlacek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HMRI ) HOECHST MARION ROUSSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yeast Nup2 protein fragment 1.
                                                                                                                                                                                                                                                                                                                            22.3%;
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| 2 rytteggtkteaedvip 18
                                                                                                                                                                                                                                                                                                                                                                                                   6 RYVQKGEYRINPEDIYP 22
                                                                                                                                                                                                                                                                                                                                                                  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buergin A, Eilers M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-349238/30
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                        30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leukaemia
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This invention describes (1) a protein that inhibits p27 and thereby arrests p27-induced inhibition of cell proliferation, (2) the protein of (1) comprising at least part of the amino acid sequence of murine p163. (3) a protein that can be derived from the protein of (2) by deletion of the p27 binding domain or the Ran binding domain, (4) a protein that can be derived from the protein of (2) by deletion of all amino acid sequences other than the p27 binding domain, (5) a protein that is the bind to the p17 binding domain, (5) a protein that is the human or other mammalian species homologue of a protein as in (1)-(4), (6) DNA encoding the p163 protein, (7) antibodies and antibody fragments that bind to the Ran binding domain of a protein as above, (9) antisense nucleic acids complementary to portions of the DNA of (6) between codons 121 and 467, (10) a nucleic acid construct coding for an antisense nucleic acid as in (9) for inhibiting the proliferation of a cell, in which DNA coding for the antisense nucleic acid as in (2) for the antisense uncleic acid sequence is linked to at least one activation sequence and is introduced into the target cell as naked DNA or as an insert in a
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transcription of component (d) and (d) an effector gene. The construct, preferably in a plasmid or viral vector, or cell can be used to treat a disease selected from infections, tumours, leukaemia, autoimmune diseases, allergies, arthritis, inflammations, transplant rejection, graft-versus-host disease, blood clotting disorders, circulatory disorders, anammia, hormonal disorders and CNS injuries. This sequence represents a fragment of the Saccharomyces cerevisiae Nup2 protein which is used to describe the method of the invention.
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Pred. No. 52;
2; Mismatches 3; Indels
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58.3%;
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Best Local Similarity 58.3
Matches 7; Conservative
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13 etydsnesdddv
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conviral or viral vector and (11) a nucleic acid construct containing the DNA of (6) linked to an activation sequence that permits expression of a protein as above in a cell. The DNA of (6) can be used for detection and/or quantification of p163 mRNA in cells and/or tissues, preferably by Northern blotting, PCR or fluorescent in-situ hybridisation. The proteins of an be used to produce antibodies, which can be used to detect the corresponding protein in cells, tissues or body fluids. The antisense nucleic acids can be used to inhibit cell proliferation in vitro or in vivo. The proteins can be used to screen for substances that inhibit the interaction between the proteins and their cellular binding partners, preferably using a two hybrid system or using an affinity system in which phase is incubated with a test substance, and the inhibition of the binding of a labelled binding partner of p163 (especially p27 or Ran) is measured. Assays for p163 can be used to assess the malignancy of
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                                                                                                                                                                                                                                                                            Score 39;
Pred. No.
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890S-0388725.
900S-0559438.
910S-0774126.
920S-0989998.
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Best Local Similarity 58.5
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13 etydsnesdddv 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; secreted protein; gene therapy; protein therapy; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; autoimmune disease; AIDS; developmental abnormality; foetal deficiency; Alzheimer's disease; cognitive disorder; schizophrenia: immunological disorder; moder disorder; immune deficiency disease; respiratory disorder; arthritis; skeletal; haematopoietic disorder; neural; osteoporosis; metabolic disorders; cardiovascular; endocrine; gastrointestinal; asthma; diagnosis.
                               represent peptide derivatives given in examples from the present invention. The peptide derivatives have a thrombin recognition site binder mechanism of action. The peptide derivatives can be used as anticoagulants. They can bind to the thrombin recognition site without binding to the cleavage site of thrombin.
AAY53062 to AAY53093 represent specifically claimed anticoagulant peptide derivatives from the present invention. AAY53094 to AAY53125
                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                              Score 38; DB 2
Pred. No. 32;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                  AAY01162 standard; Protein; 20 AA.
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97US-0051381.
97US-0051480.
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50.0%;
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Matches 6; Conservative
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                                                                                                                                           12 AA;
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01-JUL-1997;
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for peptide mimetics and as

medicinal chemistry manipulation,

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                                                                                                                                                  AIDS), mood disorders, respiratory disorders, arthritis, asthma, haematopoietic disorders, neural disorders, skeletal disorders, societal disorders, osteoporosis, metabolic disorders, cardiovascular disorders, endocrine disorders or gastrointestinal disorders. The polypeptides are also useful for identifying their binding partners. The present sequence represents a polypeptide fragment encoded by a gene of the invention (see descriptor
be also diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, developmental abnormalities and foetal deficiencies, autoimmune diseases, lymphonas, Alzheiner's and cognitive disorders, schizophrenia, immunological disorders, immune deficiency diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complementary peptide ligands as reagents and drugs for drug discovery programs and as lead ligands to facilitate drug design and development, are generated from microbial genome sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a set of complementary peptide ligands generated from Mycoplasma genitalium genome sequences. These specific complementary peptides interact with their relevant target proteins encoded by the microbial genome. They are capable of antagonising or agonising specific interaction of a protein with another protein or receptor and are thus useful as reagents and drugs, and as lead ligands to facilitate drug design and development. They are useful as tools for functional genomic studies, reagents for the configuration of high-throughput screens, as a starting point for
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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59;
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                                                                                                                                                                                                                                                                                                                                                                    Score 38;
Pred. No.
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Best Local Similarity 37.5
Matches 6; Conservative
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2 dpkktigmgsfrinpd 17
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                                                                                                                                                                                                                                                                       line for gene number).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-514238/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified.
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                                                                                                                                                                                                                                                                                                              Sequence
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            therapeutic agents. The analysis and acquisition of peptide sequences facilitates understanding of protein-protein interactions. The method allows for analysis of an entire database at a time, thus overcoming sampling problems. The present sequence is provided as an example protein sequence in a description of the invention.
                                                                                                                                                                             Gaps
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                                                                                                                                                                           8; Indels
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Pred. No. 59;
2; Mismatches
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59;
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Pred. No.
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                                                                                                                                             21.2%;
ilarity 47.4%;
Conservative
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| gtfrtsredstysgdtdfd 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-DEC-2000; 2000WO-GB04781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 GEYRTNPEDIYPSNPTDDD 29
                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                        11 GEYRTNPEDIYPSNPTDDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roberts GW, Heal JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PROT-) PROTEOM LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-381629/40.
                                                                                                                                            Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                Peptide sequence 2.
                                                                                                   20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200142279-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                                                    11-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JUN-2001.
                                                                                                                                                                                                                                                                                                                                      AAB99270;
                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                               RESULT 12
                                                                                                                                                                                                                                                                                              AAB99270
8888888
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10-DEC-1996
                                                                                                24 - MAR-1995;
                                                                                                                    25-OCT-1994;
                                                                                                                             28-MAR-1994;
                                                                             05-OCT-1995.
                                                                                                                                                                                                                                 treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW05603;
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                     Wang CY;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW05603
q
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0
                                                                                                                                                                                                                                                                                                                                                                      Synthetic immunogenic peptides are provided in which a universal immune stimulator is linked to a peptide or protein hapten containing B cell and/or cytotoxic T lymphocyte epitopes, giving a product which causes potent immune responses to the coupled peptide or protein. The stimulator consists of (A) a promiscuous helper T cell epitope (Th) which elicits an immune response to the coupled peptide in members of a heterogeneous population expressing diverse HLA phenotypes, and (B) an adjuvant peptide sequence from the invasin protein of Yersinia. Spacer amino acid sequences (e.g. Gly-Gly) can be provided between the invasin and Th domains and between the immune stimulator and hapten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         components. When the hapten is LHRH, then optionally the invasin domain can be omitted from the immune stimulator component.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a pertussis toxin helper T cell epitope which can be used as Th in the immune stimulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                               Helper T cell epitope; universal immune stimulator; invasin; hapten;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                            Helper T cell epitope for use in universal immune stimulator.
                                                                                                                                                                                                                                                                                                                       Immunogenic luteinising hormone releasing hormone peptide(s) that suppress LHRH activity in males and females
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; DB 15;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pertussis toxin helper T cell epitope, PT2
                   AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ¥.
                                                                                                                                                                                                                                                                                                                                                     Claim 7; Page 25; 213pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24
                AAR62696 standard; peptide; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.78;
                                                                                                                                                                                        94WO-US04832
                                                                                                                                                                                                           93US-0057166.
94US-0229275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR82577 standard; peptide;
                                                                                                                                                                                                                                                                                 Zamb T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :||| : | | | |
6 cpngtraltvaelrgnae 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRDGTRYVQKGEYRTNPE 18
                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 44.4.
                                                                                                          vaccine; pertussis toxin,
                                                                                                                           Bordetella pertussis.
                                                                                                                                                                                                                                                                                                    WPI; 1994-357910/44.
                                                                                                                                                                                                                                                                                 Wang CY,
                                                                                                                                                                                                                                       (LADD/) LADD A E. (WANG/) WANG C Y. (ZAMB/) ZAMB T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 AA;
                                                                                                                                                                                                           27-APR-1993;
14-APR-1994;
                                                                                                                                                                                       28-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-JUN-1996
                                                        10-SEP-1995
                                                                                                                                                WO9425060-A.
                                                                                                                                                                   LO-NOV-1994
                                     AAR62696;
                                                                                                                                                                                                                                                                                Ladd AE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR82577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR82577
        AAR62696
                           EX AX SX B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     membrane anchoring domain; helper T cell; surface antigen; core antigen; pertussis toxin; tetanus toxin; measles virus F protein; immunotherapy; Chlamydia trachomatis major outer membrane protein; immunogen; vaccine; diphtheria toxin; plasmodium falciparum; circumsporozoite; E. coli TraT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preparation of a peptide immunogen that is useful in vaccines for treating allergic reactions. In the immunogen an IGE CH4 peptide is atteached C-terminally to a series of amino acids including a helper T cell epitope. The immunogen may also opt. contain a farty acid derivative, an invasin domain or alpha-NH2. The immunogen produces high titres of antibodies to the effector site in human IGE heavy chain (the CH4 domain peptide) which inhibit mast cell activation and reduce allergen-induced IgE prodn. The immunogens may be used in either a radially branching multimeric form or a linearly arranged monomeric form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     schistosoma mansoni, triose phosphate isomerase, allergenic reaction, allergic rhinitis; food allergy; anaphylaxis; virally-induced asthma; antihistamine; decongestant; beta-2 agonist; immunosuppression;
IgE: CH4; immunoglobulin; epsilon; immunogen; helper T cell; epitope; vaccine; allergy; antibody; constant heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic peptide-based immunogen contg. IgE CH4 peptide and helper \mathbb T cell epitope \cdot useful for eliciting antibody prodn. for allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW05603 standard; peptide; 24 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 58; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UNBI-) UNITED BIOMEDICAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                   94US-0328912.
94US-0218461.
                                                                                                                                                                                                                                                                                                                              95WO-US03741.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                          Bordetella pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-351297/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 8; Conserv
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WO9612740-A1.

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AAW05957-W05616 represent helper T cell epitopes used in the peptide immunogens of the invention. This sequence represents the pertussis toxin helper T cell antigen. The peptides of the invention contain one of these sequences, and a membrane-bound immunoglobulin E (IgE) fragment (see AAW05595 and AAW05596). The peptide immunogens of the invention can be used in vaccines for the immunotherapeutic treatment of allergenic reactions, including allergic rhinitis, food allergies, anaphylaxis, or period of anthhistamines, decongestants, and beta-2 agonists, while preventing the broad immunosuppression of corticosteroids. The peptides do not have the potential side effects of restlessness or sedation (associated with antihistamines), associated increased morbidity in asthmatics (as seen with beta-2 agonists) and adverse hormonal activities (observed in corticosteroid users).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                             Peptide immunogen useful in treatment of allergy - comprises membrane-bound IgE epsilon-chain peptide synthesised linearly in tandem with T helper epitope peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37; DB 17; Length 24; Pred. No. 1e+02; 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.7%; Scor.
44.4%; Pred
2;
                                                                                                                                                                                                                                                                                                                      Claim 2; Page 18; 53pp; English.
                                                                                                                                        (UNBI-) UNITED BIOMEDICAL INC.
                                                                     95WO-US13841
                                                                                                      94US-0328519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 44.4
Matches 8; Conservative
                                                                                                                                                                         Walfield AM, Wang CY;
                                                                                                                                                                                                            WPI; 1996-230555/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 AA;
                                                                 25-OCT-1995;
                                                                                                      25-OCT-1994;
                                  02-MAY-1996.
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Search completed: February 21, 2002, 16:34:28 Job time: 193 sec

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ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFRENCE/CDCKET NUMBER: 1575
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 703-010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: peptide US-08-143-3118-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                     (without alignments) 57.701 Million cell updates/sec
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Sequence 5, Appli
Sequence 9, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                      February 21, 2002, 16:32:55; Search time 12.48 Seconds
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Sequence 3
Sequence 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/pCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/pCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                     US-08-753-851-3
179
1 CRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSS 32
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US-08-143-311B-5
US-08-143-311B-9
US-08-750-419A-30
US-09-215-221-11
US-08-446-692-8
US-09-100-409A-44
PCT-US55-1344-11
US-09-100-409A-11
US-08-55-1341-11
US-08-55-1341-11
US-08-55-1341-11
US-08-55-1341-11
US-08-93-92-15
US-08-93-92-15
US-08-93-93-15
US-08-93-15
US-08-93-13
US-08-93-13
US-08-17-205-13
US-08-17-205-13
US-08-17-205-13
US-08-017-205-83
US-09-017-205-83
US-09-017-205-83
US-09-017-205-83
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-08-484-296-22
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US-08-264-030-11
                                                                                                                                                                                                                                                                                                                                                     212252 seqs, 22503292 residues
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    protein search, using sw model

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                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0% Maximum Match 100%
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Match Length
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Perfect score:
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Maximum DB
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Patent No. 5240706
Patent No. 5252328
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Sequence 4, Appli
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Sequence 73,
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
US-09-258-754-186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AN ADHESION MOLECULE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32,955
FR: 1579-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08143311B Patent No. 5863540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HAYNES, BARTON F.
APPLICANT: HALE, LAURA P.
APPLICANT: PATTON, KAREN L.
APPLICANT: TELEN, MARILIN J.
APPLICANT: LIAO, HUA-XIN
TITLE OF INVENTION: AN ADHESIO
NUMBER OF SEQUENCES: 28
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/143,311B
FILING DATE: 29-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 96; DB 2;
Pred. No. 1.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                  APPLICANT: HALE, LAURA P.
APPLICANT: PATTON, KAREN L.
APPLICANT: TELEN, WARLEYN J.
APPLICANT: LIAO, HUA-XIN
TITLE OF INVENTION: AN APHESION MOLECULE
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                              10MBER: US/08/143,311B
29-OCT-1993
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                                                                                                                                                                                                                                ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,339
FILING DATE: 30-OCT-1992
CLASSIFICATION: 436
APPLICATION NUMBER: 07/669,730
FILING DATE: 15-MAR-1991
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 30, Application US/08750419A Patent No. 6008340 GENERAL INFORMATION: APPLICANT: BALL, TANJA APPLICANT: VRTALA, SUSANNE APPLICANT: SPERR, WOLFGANG
Sequence 9, Application US/08143311B Patent No. 5863540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: WILSON, MARY J. REGISTRATION NUMBER: 32,955 REFERENCE/DOCKET NUMBER: 157 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.6%;
                                                                 BARTON F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VALENT, PETER
SUSANI, MARKUS
KRAFT, DIETRICH
LAFFER, SYLVIA
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 53.69
Best Local Similarity 67.99
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 703-816-400
TELEFAX: 703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                    CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-750-419A-30
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APPLICANT:
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                         Length 32;
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Pred. No. 5.3e-10;
0; Mismatches 0; Indels
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COUNTER: VICALIAN
COUNTER READBALE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATA:
APPLICATION NUMBER: US/08/143,311B
FILING DATE: 29-OCT-1993
CLASSITCATION: 436
PALICATION NUMBER: 07/973,339
FILING DATE: 30-OCT-1992
CLASSIFICATION: 436
APPLICATION: 436
APPLICATION: WHERE: 07/973,339
FILING DATE: 30-OCT-1992
CLASSIFICATION: 436
APPLICATION: WHERE: 07/669,730
FILING DATE: 15-MAR-1991
                   Query Match 100.0%; Score 179; DB 2; Best Local Similarity 100.0%; Pred. No. 1e-19; Matches 32; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                            APPLICANT: HAYNES, BARTON F.
PAPLICANT: HALE, LAURA P.
APPLICANT: PATCON, KAREN L.
APPLICANT: TELEN, MARILYN J.
APPLICANT: LIAO, HUA-XIN
TILE OF INVENTION: AN ADHESION MOLECULE
NUMBER OF SEQUENCES: 28
                                                                                                     1 CRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSS 32
                                                                                                                               1 CRDGTRYVQKGEYRTNPEDIYPSNPTDDDVSS 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : NIXON & VANDERHYE P.C. 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                   Sequence 5, Application US/08143311B Patent No. 5863540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.0%; Sco.
100.0%; Pre
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ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-
TELECOMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 703-816-4100 INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 YRTNPEDIYPSNPTDDDVSS 32
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Best Local Similarity 100.0
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & V
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                                                                                                                                                                                                             RESULT 2
US-08-143-311B-5
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RECOMBINANT ALLERGEN, FRAGMENTS THEREOF,

TITLE OF INVENTION:

RESULT

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GENERAL INFORMATION:
APPLICANT: BILERS, MARTIN
APPLICANT: BILERS, AND AND APPLICANT: BUBRGIN, ANDREA
APPLICANT: SEDLACEK, HANS-HARALD
TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
FILE REFERENCE: 026083/019215, 221
CURRENT APPLICATION NUMBER: US/09/215, 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 20;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Indels
                      SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40; DB 3;
Pred. No. 19;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMBER: 197 56 975.7
1997-12-20
                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,419A
                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 1614-175
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPHONE: (703) 205-8000
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: Saccharomyces cerevisiae US-09-215-221-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 11, Application US/09215221
; Patent No. 6265562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 8, Application US/08446692; Patent No. 5759551; GENERAL INFORMATION:
                                                                                              CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.3%;
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58.3%;
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Zamb, Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 41.27
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Best Local Similarity که ی
آن Conservative
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PRIOR FILING DATE: 1997-1
                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ladd, Anna
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13 ETYDSNESDDDV 24
    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                           linear
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SOFTWARE: Patentin V
                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                US-08-750-419A-28
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-215-221-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-446-692-8
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LENGTH: 24
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CORRESPONDING RECOMBINANT DNA MOLECULES, VECTORS AND HOSTS CONTAINING THE DNA MOLECULES, DIAGNOSTIC AND THERAPEUTIC USES OF SAID ALLERGENS AND FRAGMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDING RECOMBINANT DNA MOLECULES, VÈCTORS AND HOST CONTAINING THE DNA MOLECULES, DIAGNOSTIC AND THERAPEUTIC USES OF SAID ALLERGENS AND FRAGMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ore 40; DB 3; Length 29;
ed. No. 18;
Mismatches 7; Indels
                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,419A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                              ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH STREET: PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1614-175
                                                                                                                                                                                        ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 28, Application US/08750419A Patent No. 6008340 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 1614
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BALL, TANJA
APPLICANT: VRTALA, SUSANNE
APPLICANT: SPERR, WOLFGANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: VALENT, PETER
APPLICANT: SUSANI, MARKUS
APPLICANT: KRAFT, DIETRICH
APPLICANT: LAFFER, SYLVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-08-750-419A-30
                                      TITLE OF INVENTION: US
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                    FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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Best Local Similarity
'-hac 7; Conserva
    TITLE OF INVENTION:
                        INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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ZIP: 22040-0747
                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                                                                                                                                                          COUNTRY:
                                                                                                                                    CITY: F
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Sequence 44, Application US/09100409A

Patent No. 6090388
GENERAL INFORMATION
GENERAL INFORMATION: DEPTIDE COMPOSITION FOR
TITLE OF INVENTION: PREVENTION AND TREATMENT OF HIV INFECTION AND
TITLE OF INVENTION: IMMUNE DISORDERS
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
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Pred. No. 39;
2; Mismatches
                                                                                  PILING DATE: 14 APR-1994
CLASSIPICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,166
FILING DATE: 27-APR-1992
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAIA C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/COCKET NUMBER: 1151-4146 US2
TELECOMMUNICATION INFORMATION:
TELEFRAN: (516/751-6849)
INFORMATION FOR SEQ. ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
LENGTH: 24 amino acids
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    FILING DATE: 424
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,275
TING DATE: 14-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, v SOFTWARE: #1.25 USOFTWARE: #1.25 APPLICATION DATA: APPLICATION NUMBER: US/09/100,409A
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: MORGAN & FINNEGAN STREET: 345 Park Avenue CITY: New York STATE: N
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TELECOMMUNICATION INFORMATION
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
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Best Local Similarity 44.4%;
Matches 8; Conservative
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ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: peptide US-08-488-351A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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10154-0054
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US-09-100-409A-44
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TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SECURES: 114
CORRESPONDENCE ADDRESS:
ADDRESSE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,692
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAMME: MATIA C.H. Lin
RECISTRATION NUMBER: 1151-4146 US2
TELEPHONE: (212)415-975
TELEPHONE: (212)415-975
TELEPHONE: (212)415-975
TELEPHONE: (212)415-975
TELEPHONE: (212)415-975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/488,351A
FILING DATE: 7-JUN-1995
CASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/08488351A Patent No. 5843446 GENERAL INFORMATION:
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COUNTRY: 10S
ZIP: 10164-0053
COMPUTER READABLE FORM:
....TIM TYPE: FLORMy disk
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STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CRDGTRYVQKGEYRTNPE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 20.7
Best Local Similarity 44.4
Matches 8; Conservative
                                                                                                                                                                        COUNTRY: US
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide US-08-446-692-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                CITY:
STATE:
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Gaps

GENERAL INFORMATION:

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Gaps
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GENERAL INFORMATION:
APPLICANT: United Biomedical Inc: Walfield, Alan M.;
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: Synthetic IgE Membrane Anchor
TITLE OF INVENTION: Peptide Immunogens for the Treatment of Allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                             Length 24;
                                                                                                                                 8; Indels
                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                             Score 37;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION NATA: APPLICATION NUMBER: PCT/US95/13841 FILING DATE: 25-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1151-4117
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US-08-563-892A-10
; Sequence 10, Application US/08563892A
; Patent No. 5976819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/328,519
FILING DATE: 25-0CT-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNET/AGENT INFORMATION:
NAME: Lin, Maria C.H.
REGISTRATION NUMBER: 29,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 32
CORRESPONDEMES ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
                                                                                         20.7%;
ilarity 44.4%;
Conservative
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                                                                                                                                                                  1 CRDGTRYVQKGEYRTNPE 18
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6 CPNGTRALTVAELRGNAE 23
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Best Local Similarity 44.*
Best Conservative
Annual Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-409A-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide PCT-US95-13841-11
                                                                         Query Match
Best Local Similarity
`~hes 8; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY:
STATE:
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Peptide Production as Fusion Protein in Transgenic Mammal Milk
APPLICANT: Finkel, Terri H.

PEDLICANT: Rozdaial, Moshe M.

TITLE OF INVENTION: PRODUCT AND PROCESS TO REGULATE ACTIN
TITLE OF INVENTION: POLYMERIZATION IN T LYMPHOCYTES
TUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. 1100 New York Avenue, Suite 600 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,595
FILING DATE: (Herewith)
                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 2;
Pred. No. 55;
1; Mismatches
                                                                                                                               E: Sheridan Ross & McIntosh
1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/563,892A
FILING DATE: 21-NOV-1995
                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08938595
Patent No. 6197946
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 21-NOV-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KOVATIK, JOSEPH E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2879
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cottingham, Ian R. APPLICANT: Garner, Ian TITLE OF INVENTION: Peptide P TITLE OF INVENTION: Transgeni NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 GEYRTNPEDIYPSNPTDDD 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 GGYMT----LNPRAPTDDD 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 303/863-9700
TELEFAX: 303/863-0223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 303/863-0223
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 20.7
Best Local Similarity 47.4
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 amino acids
                                                                                                                                                                                              STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                              Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20005
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                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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APPLICANT: Griffith, Irwin J.
APPLICANT: Kuo, Mei-Chang
APPLICANT: Lugman, Mohammad
TITLE OF INVENTION: T CELL EPITOPES OF RYEGRASS POLLEN
TITLE OF INVENTION: ALLERGEN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/POCKET NUMBER: IPC-075 (IMI-040cp)
TELECOMMUNICATION INFORMATION:
TELEBHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 52:
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35; DB 4;
Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                            0623.0460001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,861
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: US 08/106,016
FILING DATE: 31-AUG-1993
ATTORNEY AGENT INFORMATION:
MANNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: LAHIVE & COCKFIELD 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-440-861-52; Sequence 52, Application US/08440861; Patent No.:5710126; GENERAL INFORMATION:
                                                                 NAME: Fleshner, Raz E. REGISTRATION NUMBER: 34,331
                                                                                                       REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                       19.68;
75.08;
                                                                                                                                                                           TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARGTERIZE:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-440-861-52
                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: peptide US-08-727-153-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Massachusetts
                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 PSNPTDDD 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 PAFPTDDD 10
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CITY: Boston
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TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Patent No. 6211427
GENERAL INFORMATION:
APPLICANT: Cottingham, Ian R.
APPLICANT: Garner, Ian
TITLE OF INVENTION: Peptide Production as Fusion Protein in
TITLE OF INVENTION: Transgenic Mammal Milk
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.6%; Score 35; DB 4; Length 12; 75.0%; Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 New York Avenue, Suite 600 STREET: Washington STATE: DC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM:

PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/727,153

FILING DATE: 08-0CT-1996

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/718,523

FILING DATE: 06-0CT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/GB95/00769

NELING DATE: 05-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9406974.7
                                                                              FILING DATE: 08-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/718,523
FILING DATE: 08-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB95/00769
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9406974.7
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                             NAME: Fleshner, Raz E.
REGISTRATION NUMBER: 34,331
REFERENCE/DOCKET NUMBER: 0623.0460003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/727,153
TITLE OB-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 19.6
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 PSNPTDDD 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |: ||||||
3 PAFPTDDD 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE:
US-08-938-595-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-727-153-5
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us-08-753-851-3.rai

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                                                      0; Gaps
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0
Score 35; DB 1; Length 20;
pred. No. 62;
4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 1; Length 18;
Pred. No. 77;
3; Mismatches 6; Indels
                                                                                                                                                                                                           US-07-729-099-15

Sequence 15, Application US/07729099

Sequence 15, Application US/07729099

Patent No. 5403581

GENERAL INFORMATION:

APPLICANT: Binger, Mary-Helen

APPLICANT: Basemontes, Luis

TITLE OF INVENTION: Coccidiosis Vaccines

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hoffmann-La Roche Inc.

STREET: 340 Kingsland Street

CITY: Nutley

STATE: New Jersey

COUNTRY: U.S.

ZIP: O7110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBMP C compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PATENTIN RELEASE #1.0, Ver CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/729,099
FILING DATE: 19910712
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ROSEMAN, Catherine R
REGISTATION NUMBER: 34,240
REFERENCE/DOCKET NUMBER: 8514
TELECOMMUNICATION INFORMATION:
TELEFAN: (201) 235-6208
TELEFAN: (201) 235-6208
TELEFAN: (201) 235-5300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
TOPOLOGY: 11near
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.0%;
40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Eimeria tenella
US-07-729-099-15
          19.6%;
35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
FRACHENT TYPE: C-terminal
ORIGINAL SOURCE:
      Query Match
Best Local Similarity 35.3°
Matches 6; Conservative
                                                                                          6 RYVOKGEYRTNPEDIYP 22
                                                                                                                    2 RYTTEGGTKSEVEDVIP 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 19.0
Best Local Similarity 40.0
Matches 6; Conservative
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Search completed: February 21, 2002, 16:34:47 Job time: 112 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

February 21, 2002, 16:37:20 ; Search time 13.26 Seconds (without alignments) 241.277 Million cell updates/sec Run on:

Title:

Perfect score:

US-08-753-851-4 223 1 CRDGTRYVQKGEYRINPEDI......SNPTDDDVSSGSSSERSSTS 42 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

9284 Total number of hits satisfying chosen parameters:

219241 seqs, 76174552 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 42

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR\_68:\* Database :

pir1:\* pir2:\* pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ecei	NADH dehydrogenase	X-Pro aminopeptida	chlorophyll a/b-bi		elastase inhibitor	hypothetical prote	synexin, long form	T-cell receptor al	pollen allergen An	omega-qliadin - ei	Kex2/subtilisin-li	vitellogenin - tur	cytochrome-c oxida	Kex2/subtilisin-li	2-phosphinomethylm	T-cell receptor ga	zona pellucida pro	1 osm	ribosomal protein	long-chain-fatty-a	allophycocyanin al	poly-Ig receptor -	hypothetical prote	$\sim$	T-complex protein	seed protein ws-25	.calmodulin - elect	hypothetical prote
SUMMARIES	ΩΙ	A41683	I49732	PC2307	9	A44862	S54329	T07488	C39513	A41299	637396	A03356	E45357	A29184	S77983	C45357	PS0106	S35924	S35572	A32112	S78757	PQ0050	73	6	17	S78722				₹
	DB	7	7	7	~	~	7	7	7	7	~	~	~	~	7	7	~	~	~	~	~	~	7	7	7	7	7	7	7	7
	Length	29	29	30	38	38	35	40	31	19	26	28	34	40	20	24	28	29	36	38	38	40	40	36	36	42	19	20	22	30
	!		٥.		9.9					•	٠	4.8	•	4.8		٠	٠		4.3		4.3	•	•	•	•	3.7	•			
æ	Query	ĕ	H		ĭ				ä	7	7	ä	7	7	7	7	7	Ä	7	Ä	ń	ñ	H	H	H	H	H	H	ä	ä
	Score	75	40	40	37	36.5	36	m	35.5	33	33	33	33	33	32	32	32	32	32	32	32	32	m	30.5	。	ö	30	30	30	30
	Result No.	1	7	ю	4	Ŋ	9	7	80	6	10	11	12	13	. 14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

neuropeptide Y - s corticotropin - sp	endometrial secret	ribosomal protein	hemoglobin alpha-2	protein phosphatas	L protein - rabies	ATPase-beta chain	pollen allergen Po	pollen allergen Ag	annexin V - rat (f	photosystem I chai	hypothetical prote	hypothetical prote	hypothetical prote	Kex2/subtilisin-li
S07052 CTDFAS	A61377	S32387	A05301	A32917	PQ0369	T01689	F37396	E37396	D53507	B56817	S13994	T01701	F82394	B45357
7 -	7	7	~	N	7	~	7	7	~	7	7	7	7	7
36 39	19	20	40	18	25	25	56	56	56	59	30	31	34	34
13.5	13.2	13.2	13.2	13.0	13.0	13.0	13.0	13.0	13.0	13.0	13.0	13.0	13.0	13.0
30	29.5	29.5	29.5	29	29	29	29	29	29	29	29	29	29	29
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

```
A41683
hyaluronate receptor CD44 (version 2) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 30-Sep-1993
C;Accession: A41683
R;Shivelman, E; Bishop, J.W.
Mol. Cell. Biol. 11, 5446-5453, 1991
A;Title: Expression of CD44 is repressed in neuroblastoma cells.
A;Reference number: A41683 MUID:92017823
A;Accession: A41683
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-29 cSHT?
A;Cross references: GB:M69215
C;Keywords: cell adhesion
```

Gaps ; 33.6%; Score 75; DB 2; Length 29; 100.0%; Pred. No. 0.0028; ive 0; Mismatches 0; Indels Query Match 33.6 Best Local Similarity 100. Matches 16; Conservative

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27 DDDVSSGSSSERSSTS 42 δλ

1 DDDVSSGSSSERSSTS 16 q

A:Status: preliminary
A:Status: preliminary
A:Molecule type: protein
A:Molecules: 1-29 < HER>
C:Genetics:
A:Genome: mitochondrion
C:Keywords: electron transfer; hydrogen ion transport; mitochondrial inner membrane;

ö 0; · Gaps Query Match 17.9%; Score 40; DB 2; Length 29; Best Local Similarity 46.7%; Pred. No. 89; Matches 7; Conservative 3; Mismatches 5; Indels

17 PEDIYPSNPTDDDVS 31

δy

us-08-753-851-4.rpr

1;

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Exp. Parasitol. 73, 451-459, 1991
A;Title: Trypanosoma cruzi: antibodies to a MAP-like protein in chronic Chagas' disea
A;Reference number: A44862; MUID:92070444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: chloroplast Pinus thumbergiana (Japanese black pine)
C; Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 18-Aug-2000
C; Dates 107488
R; Wakasugi, T: Tsudzuki, J:; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiura, M. Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994
A; Title: Loss of all ndh genes as determined by sequencing the entire chloroplast gen A; Accession: T07488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elastase inhibitor (elastasin) - goat
C:Species: Capra aegagrus hircus (domestic goat)
C:Date: 27-0ct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C:Accession: S54329
R:Potempa, J.; Enghild, J.J.; Travis, J.
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                                                                                                                                                                                                                    A; Experimental source: epimastigotes, Tulahuen 2 strain
A; Note: sequence extracted from NCBI backbone (NCBIN:68286, NCBIP:68287)
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C;Species: chloroplast Pinus thunbergiana (Japanese black pine)
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                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-38 </br><br/>A;Cross-references: GB:S68286; NID:g239898; PID:g239899
                                                                                                                                                                                                                                                                                                                            Score 36.5; DB 2;
Pred. No. 3.4e+02;
5; Mismatches 10;
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Pred. No. 3
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A:Title: The primary elastase inhibitor (¢
A:Reference number: S54329; WUID:95169053
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10 GPRHVDPDHFRSTTQDAYRPVDPS 33
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5 VTPEDQHKGTAVDDHALASSNTD 27
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26.1%;
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Best Local Similarity 33.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 1-35 <POT>
C;Superfamily: antithrombin III
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Best Local Similarity
Matches 6; Conserv
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Matches 9; Conserv
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C;Keywords: chloroplast
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A; Residues: 1-40 <WAK>
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                                                                              A; Accession: A44862
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T07488
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                                                                                                                                                       X-Pro aminopeptidase (EC 3.4.11.9) L13K - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Species: Cavia porcellus (guinea pig)
C;Date: 25-Feb-1995 #sequence_revision 26-May-1995 #text_change 17-Nov-2000
C;Accession: PC2307; PC310
R;Denslow, N.D.; Ryan, J.W.; Nguyen, H.P.
Blochem: Biophys. Res. Commun. 205, 1790-1795, 1994
A;Title: Guinea pig membrane-bound aminopeptidase P is a member of the proline peptidase
A;Reference number: PC2307; MUID:95110325
A;Accession: PC2307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Comment: This enzyme is a membrane bound protein.
C;Comment: This enzyme hydrolyzes imido bonds.
C;Comment: This enzyme acts as an aminoacylproline hydrolase and is a member of the prol C;Superfamily: pig X-Pro aminopeptidase
C;Keywords: alpha-aminoacylpeptide hydrolase; membrane protein
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C;Species: Physcomitrella patens
C;Species: Physcomitrella patens
C;Species: O6-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 01-May-1998
C;Accession: S40096
R;Reski, R.; Faust, M.; Wang, X.H.; Wehe, M.; Abel, W.O.
submitted to the EMBL Data Library, December 1993
A;Description: Genome analysis of a moss Physcomitrella patens (Hedw.) B.S.G. A;Reference number: S40096
A;Accession: S40096
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Pred. No. 93;
3; Mismatches
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46.7%;
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Matches 7; Conservative
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Best Local Similarity 50.0
Matches 8; Conservative
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A, Residues: 1-26 CDE2>
A, Experimental source: kidney
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13 PDDFDPNNPYKKDVA 27
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A.Residues: 1-30 AbEN>
A.Experimental source: lung
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A; Residues: 1-38 <RES>
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C;Species: Mus musculus (house mouse)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994
R;Sedah, N.G.; Day, R.; Hamelin, J.; Gaspar, A.; Collard, M.W.; Chretien, M.
Mol. Endocrinol 6, 1559-1570, 1992
A;Title: Testicular expression of PC4 in the rat: molecular diversity of a novel germ A;Reference number: A45357; MUID:93078790
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A;Title: The primary structure of avian phosvitins. Contributions through the Edman d
A;Reference number: A91754; MUID:86056531
A;Accession: A29184
                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Species: Triticum monococcum (einkorn wheat)
C.Species: Triticum monococcum (einkorn wheat)
C.Species: Un-1991 #sequence_revision 30-Jun-1991 #text_change 18-Jun-1993
C.Sacession: A03356
R.Shewry, P.R.; Autran, J.C.; Nimmo, C.C.; Lew, E.J.L.; Kasarda, D.D.
Nature 286, 520-522, 1980
A.Reference number: A93228
A.Reference number: A93328
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N:Contains: phosvitin
C;Species: Meleagris gallopavo (common turkey)
C;Date: 0.3 Jun-1988 #sequence_revision 05-Jun-1988 #text_change 13-Sep-1996
C;Accession: A29184
R;Clark, R.C.
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Pred. No. 8.5e+02;
2; Mismatches 10; Indels
                                                                           Score 33; DB 2; Length 26;
Pred. No. 6.2e+02;
; Mismatches 7; Indels
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42.9%;
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31.2%;
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Best Local Similarity 42.97
Local Similarity 42.97
Local Similarity 42.97
Local Similarity 42.97
                                       Query Match
Best Local Similarity 31.2.
Best S; Conservative
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                                                                                                                                                                                                                                                                                    1 YTTEGGKKVEAEDVIP 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 1-28 <SHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 NPEDIYPSNP 25
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13 SPQQLYPQQP 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: gliadin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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                                                                                                                                        Synoria, long form, brain - rhesus macaque (fragment)
Synoria, long form, brain - rhesus macaque (fragment)
C;Species: Macaca mulatta (rhesus macaque)
C;Species: Macaca mulatta (rhesus macaque)
C;Species: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 09-May-1997
C;Accession: C39513
Biol. Chem. 266, 3228-3232, 1991
A;Ritle: Alternative splicing of human synexin mRNA in brain, cardiac, and skeletal musc A;Reference number: A39513; MUID:91131630
A;Accession: C39513
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-31 cAMG>
C;Superfamily: annexin VII; annexin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               741299
T-cell receptor alpha chain precursor V region (17.2) - human (fragment)
T-cell receptor alpha chain precursor V region (17.2) - human (fragment)
C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 23-Jul-1999
C;Accession: A41299
R;Udematsu, Y: Wege, H.; Straus, A.; Ott, M.; Bannwarth, W.; Lanchbury, J.; Panayi, G.;
R;Udematsu, Y.; Wege, H.; Straus, A.; Ott, M.; Bannwarth, W.; Lanchbury, J.; Panayi, G.;
A;Title: The T-cell-receptor repertoire in the synovial fluid of a patient with rheumatc
A;Reference number: A41299
A;Accession: A41299
A;Accession: A41299
A;Accession: A41299
A;Accession: A41299
A;Accession: A41299
A;Cession: A41299
A;Cession: Title of A patient with rheumatc
A;Cession: A patient with rheumatc
A;Cession: Title of A patient with rheumatc
A;Cession: Title of A patient
A;Cession: Title of A patient
A;Cession: A 
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G37396

pollen allergen Ant o I - sweet vernal grass (fragment)

C;Species: Anthoxanthum odoratum (sweet vernal grass)

C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 09-Jun-2000

C;Accession: G37396

Mol. Immunol. 26, 557-561, 1989

A;Title: Isolation and characterization of a major cross-reactive grass group I allergen

A;Reference number: A37396; MUID:89364850

A;Reference of 37396

A;Molecule type: protein

A;Molecule type: protein

A;Residues: 1-26 <ESC>

C;Superfamily: expansin

C;Keywords: pollen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35.5; DB 2;
Pred. No. 3.7e+02;
2; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 RINPEDIYPSNPTDDDVSSGSSSE 37
7 YQEKGSNRV-----PCNGSDSDTVS
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Matches 7; Conservative
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Best Local Similarity
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Job time: 100 sec
A;Molecule type: protein
A;Residues: 1-40 <CLA>
C;Superfamily: vitellogenin
C;Keywords: phosphoprotein
F;12,13,14,15,16,17,19,20,24,25,26,27,28,29,31,32/Binding site: phosphate (Ser) (covalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Pathway: oxidative phosphorylation; respiratory chain
C; Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Seidah, N.G.; Day, R.; Hamelin, J.; Gaspar, A.; Collard, M.W.; Chretien, M. Mol. Endocrinol. 6, 1559-1570, 1992
Myl: Endocrinol. 6, 1559-1570, 1992
A;Title: Testicular expression of PC4 in the rat: molecular diversity of a novel germ ce A;Reference number: A45357; MUID:93078790
A;Accession: C45357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B. submitted to the Protein Sequence Database, June 1997
A;Reference number: S77980
A;Accession: S77983
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C;Species: Thunnus obeeus (bigeye tuna)
C;Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 30-Jan-1998
C;Accession: S77983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C;Accession: C45357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.3%; Score 32; DB 2; Length 24; 33.3%; Pred. No. 7.6e+02; Live 2; Mismatches 12; Indels
                                                                                                                                                                                       Query Match 14.8%; Score 33; DB 2; Length 40; Best Local Similarity 42.9%; Pred. No. 1e+03; Matches 9; Conservative 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.3%; Score 32; DB 2; Length 20; 55.6%; Pred. No. 6.2e+02; ive 3; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                              22 PSNPTDDDVSSGSSSERSSTS 42
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Best Local Similarity 33.3
Matches 7; Conservative
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Best Local Similarity
Matches 5; Conserv
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# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

February 21, 2002, 16:38:46 ; Search time 10.05 Seconds (without alignments) 153.226 Million cell updates/sec

Title: Perfect score: Sequence:

US-08-753-851-4
223
1 CRDGTRYVQKGEYRINPEDI.....SNPTDDDVSSGSSSERSSTS 42

Scoring table:

100059 seqs, 36664827 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

2877 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 42

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SIIMMARIES

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	pti	P80267 solanum tub	P34421 caenorhabdi	25	P56531 meleagris g	_	.0	φ.			_		~	_		~	P01196 struthio ca		P80329 oncorhynchu	7	-		P81079 desulfuromo	0	P80167 gadus morhu		7	0	σ	m	~	27 chloroflex	m	001359 neurospora
SUMMARIES	ID	NUO1_SOLTU	YLZ8_CAEEL	GDO_TRIMO	VIT_MELGA	COXB_THUOB	PAHO_RABIT	PHAC_MASLA	NEUY_SHEEP	PYY_RAJRH	COLI_SQUAC	HBA2_UROHA	PSAF_SYNP6	VG8_SPV4	COLI_BALPH	REV_SIVM2	COLI_STRCA	LCK_RAT	COXF_ONCMY	FEDG_AMYME	PHAC_ANASP	HOXY_RHOOP	CY35_DESAC	COXL_ONCMY	NEUY_GADMO	NEUY_ONCMY	NPF_MONEX	MK2B_PALPR	SCX9_BUTOC	DEF7_RABIT	YDRB_STRPE	YMDB_CHLAU		COX6 NEUCR
	DB	-	-		Н		Н	-		m	Н		<del>, -  </del>	<del></del>	1	-	H	Н	-	⊣	-	Н	٦	1	7	٦	7	Н	٦		Н	-+		
	Query Match Length	29	37	28	40	20	36	40	36	36	39	40	29	38	39	37	39	17	20	24	28	29	30	33	36	36	39	16			40	18	23	25
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	Score	40	33.5	33	33	32	31	31	30	30		29.5	29	29	$\sim$	28.5		28	28	28	28	28	28	28	28	28	28	27.5	27.5	27.5	27.5	27	27	27
	Result No.	1	7	က	4	Ŋ	9	7	ထ	Ø.	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	22	56	27	28	29	30	31	32	33

	P37999 ceratotheri P82036 uperoleia i P37300 conus magus P49975 streptomyce	P43511 lymantria d P01304 sus scrofa P09640 oryctolagus P29949 rana ridibu	
HORC_HORSP ITRY_TRIKI PHNA_STRMU	PAHO_CERSI UP51_UPEIN CXOC_CONMA RL15_STRLI	PBAN_LYMDI NEUY_PIG NEUY_RABIT NEUY_RANRI PMY PETHAA	ALIGNMENTS
28 1 41 1 33 1	36 13 29 1	33 36 1 36 1 36 1	
12.1 12.1 11.9	11.9 11.7 11.7	7.1.1	
27 27 26.5	26.5 26 26 26	20000	
34 35	37 38 39 40	4 4 4 4 4 11 4 6 4 8	

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RESULT 1 NUO1_SOLTU SOLTU STANDARD; PRT; 29 AA.	,	OS Solanum tuberosum (Potato).  OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  OX NCBL_TaxID-4113;  RN [1]	SEQUENCE. STRAIN=CV. BINTJE; TISSUE=Tuber; MEDLINE=94124587; PubMed=8294484; Herz U., Schroeder W., Liddell A., Leaver C.J., Brennicke A. Grohmann L.; "Purification of the NADH-ubiquinone oxidoreductase (complex	the respiratory chain from the inner mitochondrial membrane of Solanum tuberosum."; J. Biol. Chem. 269:2263-2269(1994)!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELL TO BE UBLOUINONE.	-!- -!- -!- PIR; Oxid	Que Bes Mat	QY       17 PEDIYPSNPTDDDVS 31          :   :    :          :         Db       13 PDDFDPNNPYKKDVA 27	RESULT 2 YLZ8_CAEEL ID YLZ8_CAEEL STANDARD; PRT; 37 AA.  AC P34421; DT 01-FEB-1994 (Rel. 28, Last sequence update) DT 01-FEB-1994 (Rel. 29, Last annotation update) DT 01-TEP-1994 (Rel. 29, Last annotation update) DF WYPOTHETICAL 4.4 KDA PROTEIN F42H10.8 IN CHROMOSOME III.  GN F42H10.8. Caenorhabditis elegans.
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16 NPEDIYPSNP 25
                                            13 SPOOLYPOOP 22
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                                                                                                                                                                                                                                                          NCBI_TaxID=9103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kadenbach B.;
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P80974;
                                                                                                                        VIT_MELGA
                                                                                                                                                                                                                                                                                         SEQUENCE.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                   Wilson R., Anacour, M., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Sulston N., Smith A., Smith M., Sonnhammer E., Staden R.,
Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Wohldman P.,
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Triticum monococcum (Einkorn wheat) (Small spelt).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
                                                                                                                                                                                                                                                                        "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.0%; Score 33.5; DB 1; Length 37; 42.1%; Pred. No. 3.7e+02; ive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33; DB 1; Length 28;
Pred. No. 3.1e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4433 MW; 1F7C5F19F020105C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EA368C84E893FAA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1992 (Rel. 03, Last annotation update)
OMEGA-GLIADIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, L08403; -; NOT_ANNOTATED_CDS.
Wornbep; F42H10.8; CE00558.
Hypothetical protein.

SEQUENCE 37 AA; 4433 MW, 1F7C5F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                          STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery March 14.8%;
Best Local Similarity 40.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 HKILP-DLYPLEPLQQAVS 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 AA; 3343 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 YRINPEDIYPSNPTDDDVS 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 286,520-522(1980).
PIR, A03356, A03356.
Seed storage protein.
NON_TER 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                   Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Triticeae; Triticum.
NCBI_TaxID=4568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                          FROM N.A.
                             NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDO_TRIMO
P02865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                      elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
GDO_TRIMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Gaps

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Thunnus obesus (Bigeye tuna).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
Scombridae; Thunnus
                                                                                                                        Meleagris galiopavo (Common turkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
                                                                                                                                                                                                                                                                                                "The primary structure of avian phosvitins. Contributions through the Edman degradation of methylmercaptovitins prepared from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBRYO.

-!- PTM: PHOSVITIN, AN EGG YOLK STORAGE PROTEIN, IS ONE OF THE MOST HIGHLY PHOSPHORYLATED (10%) PROTEINS IN NATURE.
                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: PHOSVITIN IS BELIEVED TO BE OF IMPORTANCE IN SEQUESTERING CALCIUM, IRON AND OTHER CATIONS FOR THE DEVELOPING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          liver.";
Eur. J. Biochem. 248:99-103(1997).
-!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The subunit structure of cytochrome-c oxidase from tuna heart and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Heart, and Liver;
MEDLINE=97454291; PubMed=9310366;
Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NoV-1997 (Rel. 35, Created)
01-NoV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CYTOCHROME C OXIDASE POLYPEPTIDE VB (EC 1.9.3.1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F736301BDCFE708B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 1; I
Pred. No. 4.7e+02;
                                     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
40 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-SER.
PRT;
                                                                                                                                                                                                                                                                                                                                         constituent phosphoproteins.";
Int. J. Biochem. 17:983-988(1985).
                                                                                                                                                                                                                                                      MEDLINE-86056531; PubMed-4065410;
Clark R.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |: | || || || || || || 7 PNAKTSSSSSSSSSSSSS 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 PSNPTDDDVSSGSSSERSSTS 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3935 MW;
                                                                                                       PHOSVITIN (PV) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40
40 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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SECRETION OF GONADOTROPHIN-RELEASE HORMONE.
-!- SUBCELLULLAR LOCATION: SECRETED.
-!- TISSUE SPECIFICITY: ONE OF THE MOST ABINDANT PEPTIDES IN THE NERVOUS SYSTEM. ALSO FOUND IN SOME CHROMAFFIN CELLS OF THE ADRENAL
                                                                                                                                                                                                      FEBS Lett. 217:279-282 (1987).

-1 FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN FROM THE PHYCOBILIPROTEIN COMPLEX. ALLOPHYCOCYANIN HAS A MAXIMUM ABSORPTION AT APPROXIMENTELY 650 NANOMETERS.

-1 SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
-1 - PRIN: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE. PIR; B27398; B27398; B27398; B27398; B127398; B12801659; Phycobilisome.

Promise PRO0502; Phycobilisome.

Phycobilisome = Electron transport; Photosynthesis; Bile pigment.

NON_TER 40

SEQUENCE 40 AA; 4506 MW; 2FC4F66D3F091D54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sillard R., Agerberth B., Mutt V., Joernvall H.;
"Sheep neuropeptide Y. A third structural type of a highly conserved
                                                                                                                                                    Suter F., Fueglistaller P., Lundell D.J., Glazer A.N., Zuber H.; "Amino acid sequences of alpha-allophycocyanin B from Synechococcus 6301 and Mastigocladus laminosus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide.";
FEBS Lett. 258:263-265(1989).
-!- FUNCTION: NPY IS IMPLICATED IN THE CONTROL OF FEEDING AND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31; DB 1; Length 40;
Pred. No. 8.4e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY; BELONGS TO THE NPY / PPY / PYY FAMILY.
01-JUL-1989 (Rel. 11, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
ALLOPHYCOCYANIN ALPHA-B CHAIN (FRAGMENT).
Mastigocladus laminosus (Fischerella sp.).
Bacteria; Cyanobacteria; Stigonematales; Fischerella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NEUROPEPTIDE Y (NPY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00278; PANCHORMONE.
ProDom; PD001267; Pancreatic_hormn; 1.
SMART; SM00309; PAH; 1.
PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
PROSITE; PS50276; PANCREATIC_HORMONE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S07052; S07052.
HSSP; P01303; IRON.
InterPro; IPR001955; Pancreatic_hormn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90092485; PubMed=2599092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 13.9
Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00159; hormone3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 TRYVQKGEYRI 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 TEFLOTGEORV 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ovis aries (Sheep).
                                                                                            NCBI_TaxID=1191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEUY_SHEEP
P14765;
                                                                                                                                SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEUY_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
     δy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
                                                     -!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VB FAMILY.
InterPro; IPR002134; COX58;
PROSITE; PS00848; COX58; PARTIAL.
                   -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 \text{ H}(2)O 4 FERRICYTOCHROME C.
                                                                                                                                                                                                                         Score 32; DB 1; Length 20;
Pred. No. 2.8e+02;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 36 AMIDATION.
36 AA; 4197 MW; A14A4E0831A7759D CRC64;
                                                                                                                                                                 20 AA; 2158 MW; 76F1473E1F392BD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 13.9%; Score 31; DB 1; Ler
Best Local Similarity 33.3%; Pred. No. 7.5e+02;
Matches 7; Conservative 3; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PANCREATIC HORMONE (PANCREATIC POLYPEPTIDE) (PP).
                                                                                                                                Oxidoreductase; Inner membrane; Mitochondrion.
NON TER 20 20
                                                                                                                                                                                                                                                                                                                                                                                                                                       36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00265; PANCREATIC_HORMONE_1; 1. PROSITE; PS50276; PANCREATIC_HORMONE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00278; PANCHORMONE.
ProDom; PD001267; Pancreatic_hormn; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001955; Pancreatic_hormn. Pfam; PF00159; hormone3; 1.
 MITOCHONDRIAL ELECTRON TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Pancreas;
MEDLINE=94130533; PubMed=8299350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHAC_MASLA STANDARD;
p11389;
01-JUL-1989 (Rel. 11, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hormone; Amidation; Pancreas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 PEPVYPG----DDATPEQMAE 19
                                                                                                                                                                                                                           14.3%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEDIYPSNPTDDDVSSGSSSE
                                                                                                                                                                                                        Query Match
Best Local Similarity 55.6۷
نامح 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P01302; 1BBA.
                                                                                                                                                                                                                                                                                                                                     7 PIDDEQATG 15
                                                                                                                                                                                                                                                                                                  25 PTDDDVSSG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                   PAHO_RABIT
P41336;
                                                                                                                                                  NON_TER
SEQUENCE
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SEQUENCE
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PAHO\_RABIT

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PHAC\_MASLA ID PHAC\_M AC P11389 DT 01-JUL

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HBA2_UROHA
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HBA2_UROHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                       PEPTIDE YY-LIKE (PYY).
Raja rhina (Skate).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COLI_SQUAC STANDARD; PRT; 39 AA.
P01197;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
CORTICOTROPIN (ACTH).
Squalus acanthias (Spiny dogfish).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Squalea; Squaloidei; Squalidae; Squalus.
NCBL_TaxID=7797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-91296574; Pubmed=2067973;
Conlon J.M., Bjenning C., Moon T.W., Youson J.H., Thim L.;
Conlon J.M., Bjenning C., Moon T.W., Youson J.H., Thim L.;
"Neuropeptide Y-related peptides from the pancreas of a teleostean (eel), holostean (bowfin) and elasmobranch (skate) fish.";
eel), holostean (bowfin) and elasmobranch (skate) fish.";
-: SUBCELLULAR LOCATION: SECRETED.
-: SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE.

BEDGINES-5127389; PubMed-4375977;

LOWIY P.J., Bennett H.P.J., McMartin C., Scott A.P.;

The igolation and amino acid sequence of an adrenocorticotrophin
                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
Rajiformes; Rajidae; Raja.
NCBI_TaxID=30478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                             Length 36;
                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30; DB 1; Length 36;
Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
0D069303C8BD0DD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMIDATION.
07A7D9DC196660B6 CRC64;
                                                             Score 30; DB 1;
Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                              01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                        36 AA.
                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00265; PANCREATIC_HORMONE_1; 1. PROSITE; PS50276; PANCREATIC_HORMONE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0278; PANCHORMONE.
ProDom; PD001267; Pancreatic_hormn; 1.
SMART; SM00309; PAH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P01303; 1RON.
InterPro; IPR001955; Pancreatic_hormn
                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.5%;
71.4%;
                                                             13.5%;
71.4%;
4241 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 AA; 4251 MW;
                                                        Query Match 13.5
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hormone; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
    AA;
                                                                                                                                         22 PSNPTDD 28
                                                                                                                                                                    | || || 5
| PDNPGDD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 PSNPTDD 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | || || ||
5 PENPGDD 11
36
                                                                                                                                                                                                                                                                                                                            01-DEC-1992
01-DEC-1992
                                                                                                                                                                                                                                                                                      PYY_RAJRH
P29206;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
COLI_SQUAC
                                                                                                                                                                                                                                                RESULT 9
PYY_RAJRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
SO
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REVISION TO MELANOTROPIN ALPHA.
MEDLINE-7512730; Pubmed-4375978;
Bennett H.P.J., Lowry P.J., McMartin C., Scott A.P.;
"Structural studies of alpha-melanocyte-stimulating hormone and a novel beta-melanocyte-stimulating hormone from the neurointermediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HORMONE; Cleavage on pair of basic residues; Amidation.
PEPTIDE 1 39 CORTICOTROPIN (ACTH).
PEPTIDE 1 13 MELANOTROPIN ALPHA (ALPHA-MSH).
CORTICOTROPIN-LIKE INTERMEDIARY PEPTIDE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Uromastyx hardwickii (Indian spiny-tailed lizard).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Uromastycinae;
from the pars distalis and a corticotrophin-like intermediate-lobe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CLIP).
AMIDATION (G-14 PROVIDE AMIDE GROUP)
4B6E5794F6D78E71 CRC64;
                           peptide from the neurointermediate lobe of the pituitary of the dogfish Squalus acanthias.";
                                                                                                                                                                                                        Lowry P.J., Chadwick A.;
"Purification and amino acid sequence of melanocyte-stimulating
hormone from the doglish Squalus acanthias.";
Biochem. J. 118:713-718(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
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Naqvi S., Zaidi Z.H., von Bahr-Lindstroem H., Carlquist M.,
Joernvall H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lobe of the pituitary of the dogfish Squalus acanthias.";
Biochem. J. 141:439-444(1974).
-!- SIMILARITY: BELONGS TO THE POMC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Characterization of hemoglobin from the lizard Uromastix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 30; DB 1; Length 39;
Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heme; Oxygen transport; Respiratory protein; Erythrocyte. NoN. TER 1 1 0 40 8 EROUENCE 40 AA, 4508 MW; 15853F091D1EBB87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
HEMOGLOBIN ALPHA-2 CHAIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A01462; CTDFAS.
InterPro; IPR001941; Melanocortin_ACTH.
Pfam; PF00976; ACTH_domain; 1.
ProDom; PD003250; Melanocortin_ACTH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                             SEQUENCE OF 3-13.
MEDLINE=71026863; PubMed=5476715;
                                                                                   Biochem. J. 141:427-437(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.5%;
31.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hardwickii.";
FFR Lett. 162:290-295(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A05301; A05301.
InterPro; IPR000971; Globin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4686 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00042; globin; 1.
PROSITE; PS01033; GLOBIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 PEDIYPSNPTDDDVSS 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | :||:: |: |: PIKVYPNSFEDESVEN 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=40250;
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send an email to license@isb-sib.ch).
                                                 PIR; A29825;
                                                                                                                                                                                                                           COLI_BALPH
P01195;
                                                                                                                                                                                                                                                   21-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPIATES
                                                                                                                                                                                                                                                                                                                           (FRAGMENT)
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NON_TER
SEQUENCE
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                                                            SEQUENCE
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PEPTIDE
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COLI_BALPH
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              SORRES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                      Photósystem I core protein from Synechococcus sp. PCC 6301.";
Biochim. Biophys. Acta 1059:215-225(1991)
-!- FUNCTION: PROBABLY PARTICIPATES IN EFFICIENCY OF ELECTRON TRANSFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                      Gaps
                                                                                                                                                                                                                                                                                               Li N., Warren P.V., Golbeck J.H., Frank G., Zuber H., Bryant D.A.; "Polypeptide composition of the Photosystem I complex and the
                                                                                                                                                                                                                                                                                                                                                         FROM PLASTOCYANIN TO P700 (OR CYTOCHROME C553 IN ALGAE AND CYANOBACTERIA). THIS PLASTOCYANIN-DOCKING PROTEIN CONTRIBUTES TO THE SPECIFIC ASSOCIATION OF PLASTOCYANIN TO PS I. SIMILARITY: BELONGS TO THE PSAF FAMILY.

Photosynthesis; Photosystem I. 29 29 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ő
                                    .;
                                                                                                                                                               01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PHOTOSYSTEM I REACTION CENTRE SUBUNIT III (PSI-F) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-88032809; PubMed-2822658;
Renaudin J., Pascarel M.-C., Bove J.-M.;
"Spiroplasma virus 4: nucleotide sequence of the viral DNA,
regulatory signals, and proposed genome organization.";
J. Bacteriol. 169:4950-4961(1987).
            Length 40;
                                                                                                                                                                                                                          Synechococcus sp. (strain PCC 6301) (Anacystis nidulans).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 29; DB 1; Length 29;
Pred. No. 1e+03;
5; Mismatches 7; Indels
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spiroplasma virus 4 (SpV4).
Viruses; ssDNA viruses; Microviridae; Spiromicrovirus.
NCBI_TaxID=10855;
                                                                                                                                                                                                                                                                                                                                                                                                                                29 AA; 3040 MW; 535DDC7A63B18711 CRC64;
            Score 29.5; DB 1;
Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-JUL-1989 (Rel. 11, Last annotation update)
GENE 8 PROFEIN.
                                                                                                                                            29 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 AA
                                   Mismatches
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                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                     MEDLINE=91355213; PubMed=1653017;
           13.2%;
35.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.0%;
                                                                               18 EVYPOTKTYFPHFDASAGSN 37
Query Match
Best Local Similarity 35.v.
7; Conservative
                                                         19 DIYPSNPT---DDDVSSGSS
                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 DGTRYVQKGEYRINPE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : |::|: | |:
ESPRFIQRAEAAATPQ 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    NCBI_TaxID=1139;
                                                                                                                                          PSAF_SYNP6
P31083;
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P11340;
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                                                                                                                   RESULT 12
PSAF_SYNP6
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20-AuG-2001 (Rel. 40, Last annotation update)
CORTICOTROPIN-LIPOTROPIN (PRO-OPIOMELANOCORTIN) (POMC) (CONTAINS:
CORTICOTROPIN (ADRENOCORTICOTROPIC (AGRANDAE); MELANORROPIN ALPHA (ALPHA-MSH); CORTICOTROPIN-LIKE INTERMEDIARY PEPTIDE (CLIP)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pankov Y.A., Nikolaeva O.P., Elisarova G.P.,
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MELANOTROPIN ALPHA.
CORTICOTROPIN-LIKE INTERMEDIARY PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORTISOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDITRE-78061046; Pubmed=201308; Particle Town Selwhale (Balaenoptera Pankov Y.A., Nikolaeva O.P., Elizarova G.P.; Pankov Y.A., Nikolaeva O.P., Elizarova G.P.; Pankov Y.A., Nikolaeva O.P., Elizarova G.P.; Pankov Y.A., Nikolaeva O.P.; Elizarova G.P.; Porcalis) and pinwhale (Balaenoptera physalus)."; Biokhimiia 42:2044-2050,1977).

-i. FUNCTION: ACTH STIMULATES THE ADRENAL GLANDS TO RELEASE CORTISCIPLE FUNCTION: MSH (MELANCXTE-STIMULATING HORMONE) INNERASES THE PIGMENTATION OF SKIN BY INCREASING MELANIN PRODUCTION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .!- TISSUE SPECIFICITY: ACTH AND MSH ARE PRODUCED BY THE PITUITARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMIDATION (G-14 PROVIDE AMIDE GROUP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Balaenoptera borealis (Sei whale).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: BETA-ENDORPHIN AND MET-ENKEPHALIN ARE ENDOGENOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Balaenoptera physalus (Finback whale) (Common rorqual), and
                                                                                                                               Length 38;
                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00976; ACTH_domain; 1.
Probom; PD003250; Melanocortin_ACTH; 1.
Hormone; Cleavage on pair of basic residues; Amidation.
                                                      58E00837B14DF2C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  461FD46C28945A6E CRC64;
                                                                                                                               Score 29; DB 1; 1
Pred. No. 1.4e+03;
1; Mismatches 4,
                                                                                                                                                                                                                                                                                                                                                                                                                          39 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- SIMILARITY: BELONGS TO THE POMC FAMILY.
PIR; A01458; A01458.
PIR; PN0127; PN0127.
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EMBL; M17988; -; NOT_ANNOTATED_CDS.
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NCBI_TaxID=9770, 9768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Balaenoptera physalus).";
Bioorg. Khim. 2:855-856(1976).
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39
4541 MW;
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54.5%;
                                                      4629 MW;
                                                                                                    Query Match
Best Local Similarity 54.5v
That 6; Conservative
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                           G8BPSV
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                                                      38 AA;
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                                                           Gaps
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Kestler H.W. Li Y., Naidu Y.M., Butler C.V., Ochs M.F., Jaenel G.,

King N.W., Daniel M.D., Desrosiers R.C.;

"Comparison of simian immunodeficiency virus isolates.";

Nature 331:1619-627(1988).

-!- FUNCTION: REV APPEASS TO ACT POST-TRANSCRIPTIONALLY TO RELIEVE

NEGATIVE REPRESSION OF GAG AND ENV PRODUCTION.
-!- SUBCELLUAR LOCATION: NUCLEAR; ACCUMILATES IN THE NUCLEOLI.
-!- PTM: PHOSPHOPROTEIN WHOSE STATE OF PHOSPHORYLATION IS MEDIATED

BY A SPECIFIC SERINE KINASE ACTIVITY PRESENT IN THE NUCLEUS.
-!- MISCELLANBOUS: THIS IS A MACAQUE ISOLATE.
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01-NOV-1988 (Rel. 09, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
REV PROTEIN (ANTI-REPRESSION TRANSACTIVATOR PROTEIN) (ART/TRS)
                  Score 29; DB 1; Length 39;
Pred. No. 1.5e+03;
4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                 Simian immunodeficiency virus (Mm251 isolate) (SIV-MAC).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11734;
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                                                                                                                                                                                                                        37 AA.
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HUY; X06879; REVSAMA51.
INTELPO: IPRO0625; REV.
Pfam: PF00424; REV; 1.
                    13.0%;
25.0%;
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Query Match
Best Local Similarity 25.ur
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19 PVKVYPNGAEDESAEA 34
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7; 12.8%; Score 28.5; DB 1; Length 37; 30.0%; Pred. No. 1.6e+03; 2; Indels Mismatches 2 19 DIYPSNPTDDDVSSGSSSER 38 1 DSYPTGP-----GTANOR 13 6; Conservative Query Match Best Local Similarity Matches δy

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Gaps

Search completed: February 21, 2002, 16:41:45 Job time: 179 sec

Q9wrl4 avian pneum

Q9ucs9 homo sapien

Q9qxh0 rattus norv Q9crf6 mus musculu porcine cir

streptomyce chlamydia t homo sapien homo sapien

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Scoring table:

Searched:

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protein

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Run on:

salmonella

Q86818 influenza

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Q9tx41 cryptospori
Q9qw82 rattus norv
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Q9tns5 homo sapien
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Q9twe3 ascaris suu
                                                091866 porcine ci:
096851 bombyx mori
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Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysla;
Bombycoidea; Bombycidae; Bombyx.
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Last annotation update)
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
SERICIN MRNA, PARTIAL CDS (FRAGMENT).
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Copyright (c) 1993 - 2000 Compugen Ltd
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Gaps

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48.5

Score

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Result

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SEQUENCE FROM N.A.
MEDLINE=8828832; PubMed=3135494;
Ibanez C.F., Affranchino J.L., Macina R.A., Reyes M.B., Leguizamon S., Camargo M.E., Aslund L., Pettersson U., Frasch A.C.,
"Multiple Trypanosoma cruzi antigens containing tandemly repeated amino acid sequence motifs.",
Mol. Biochem. Parasitol. 30.27-33(1988).
EMBL; M21331; AAA75430.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma
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Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
NCBL_TaxID=3350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

STRAIN=TULAHUEN 2;

MEDLINE=92070444; PubMed=1959572;

Kerner N., Liegeard P., Levin M.J., Hontebeyrie-Joskowicz M.;

Kerner N., Liegeard P., Levin M.J., Hontebeyrie-Joskowicz M.;

Trypanosoma cruzi: antibodies to a MAP-like protein in chronic Chagas' disease cross-react with mammalian cytoskeleton.";

Exp. Parasitol. 73:451-459(1991).

EMBL; S68286; AAB20531.2; -.

NON_TER 38

SEQUENCE 38 AA, 4428 MW; D53D1F64DBCFD19F CRC64;
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Last annotation update)
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Pred. No. 8.2e+02;
5; Mismatches 10;
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Local Similarity 33.3%;
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38 AA;
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MICROTUBULE P
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Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=CV. (HEDW.)B.S.G.;
MEDLINE=94359457; PubMed=8078460;
MESKI R., Faust M., Mang X.H., Wehe M., Abel W.O.;
"Genome analysis of the moss Physcomitrella patens (Hedw.) B.S.G.";
Mol. Gen. Genet. 244:352-359(1994).
EMBL. X76632; CAA54081.1; -..
EMBL. X76632; CAA54081.1; -..
InterPro; IRB2: Phypa;LhC0:182.
InterPro; IRPR001344; Chloro_AB_bind.
Pfom; PF00504; chloroa_b-bind; 1.
             Cavia (guinea pigs).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Physcomitrella patens (Moss).
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
NCBI_TaxID=3218;
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Pred. No. 2.3e+02;
3; Mismatches 5; Indels
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
ANTIGEN DNA (TANDEM REPEAT SEQUENCE), CLONE 36 (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                             Biochem. Biophys. Res. Commun. 205:1790-1795(1994). SEQUENCE 30 AA; 3411 MW; A9F6A61854E44A25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69BA0C1296FBC1EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CHLOROPHYLL-A,B,-BINDING PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 10;
Pred. No. 7.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38
                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                     MEDLINE=95110325; PubMed=7811266;
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46.78;
 AMINOPEPTIDASE P (FRAGMENT).
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50.0%;
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Best Local Similarity 46.7
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                7 YVQKGEYRINPEDIY 21
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Matches 8; Conserv
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                                                         NCBI_TaxID=10140;
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01-NOV-1998
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Amanatides P.G., Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Ceniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Ceniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A manatides P.G., Scherer S.E., Holt R.A., Evans R.A., Galle R.F.,
R. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Briton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
R.A. Brandon R.C., Rogers Y.-H.C., Blazes J. K.G., Champe M., Pfelifer B.D.,
Ran K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Ran Bril J.F., Agbayania A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ran Ballew R.M., Basu A., Baxendale J., Bayraktaroqlu L., Beasley E.M.,
Ballew R.M., Basun A., Barwan B.P., Bhandari D., Bolshakov S.,
Ballew R.M., Basun D.A., Buller H., Cadieu E., Center A., Chandra I.,
Ran Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
Ran Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
Ran Burtis K.C., Busam D.A., Buller H., Cadieu E., Dunn P.,
Ran Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Ran Borson K., Doup L.E., Garg N.S., Gelbart W.M., Glasser K.,
Ran Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Ralush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison D.,
Ran Merkulov G., Milshina N.V., Mobarry C., Morris S., Mulp Y., Machelson D.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Ran Ralazzolo M., Pittman G.S., Pan R., Panceler F., Shen H.,
Ralesto P., Leis W., Seunders R.D.C., Scheeler F., Shen H.,
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
MAJOR CUTICULAR PROTEIN (FRAGMENT).
Ceratitis capitata (Mediterranean fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopteryota; Diptera; Brachycera; Tephritoidea; Tephritidae; Ceratitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                      Taillras A., Koromantzou E., Allen G., Dimitriadis G., Partial N-terminal sequences of larval cuticular proteins from the
                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 5; Length 20;
Pred. No. 6.4e+02;
                                                                                                                                                                                                                                                                                                                                                 C6ABB0B44ED70B88 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                    MEDLINE=95279142; PubMed=7759285;
                                                                                                                                                                                                                                                                                                    dipteran Ceratitis capitata.";
Hereditas 122:79-83(1995).
SEQUENCE 20 AA; 2329 MW; C6
                                                                                                                                                                                                                                                                                                                                                                                                              15.7%;
42.9%;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
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Best Local Similarity 42.3
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6 VIRSESEVNPDSIY 19
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CG13666.
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                                                      Tsudzuki J., Nakashima K., Tsudzuki T., Hiratsuka J., Shibata M., Wakasugi T., Sugiura M.;
"Chloroplast DNA of black pine retains a residual inverted repeat lacking rRNA genes: nucleotide sequences of trnQ, trnK, psbA, trnI and trn and the absence of rps16.";
Mol. Gen. Genet. 232:206-214(1993).
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                                                                                                                                                                                                                                                      Tsudzuki J., Ito S., Tsudzuki T., Wakasugi T., Sugiura M.; "A new gene encoding tRNA(Pro) (GGG) is present in the chloroplast genome of black pine: a compilation of 32 tRNA genes from black pine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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MEDLINE-95024047; PubMed-7937893;
Wakasugi T., Tsudzuki J., Ito S., Nakashima K., Tsudzuki T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35.5; DB 4; Length 42; Pred. No. 1.2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Loss of ""." In the genes as determined by sequencing the enchloroplast genome of the black pine Pinus thunbergil."; Proc. Natl. Acad. Sci. U.S.A. 91:9794-9798(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL, BC003538; AAH03538.1; -. SEQUENCE 42 AA, 4698 MW; 3546E5D63068E503 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 AA; 4449 MW; 6FF723BF47470E3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09BTP5;
0-JUNN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 8;
Pred. No. 1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 YQEKGSNRV-----PCNGSDSDTVS 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 YVQKGEYRINPEDIYPSNPTDDDVSS 32
                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-95094312; PubMed-8001170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=PANCREATIC ADENOCARCINOMA;
                                        MEDLINE=92212283; PubMed=1557027;
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Э.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                            Curr. Genet. 26:153-158(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.1%;
34.6%;
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47.1%;
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Best Local Similarity 34.6'
Matches 9; Conservative
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Best Local Similarity 47.1°
Matches 8; Conservative
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               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                            chloroplasts."
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Tsiliras A., Koromantzou E., Allen G., Dimitriadis G.; "Partial N-terminal sequences of larval cuticular proteins from the dipteran Ceratitis capitata."; Hereditas 122:79-83(1995). SEQUENCE 20 AA; 2408 MW; 2BC25E2F9EC15A80 CRC64;
                  MEDLINE=95279142; PubMed=7759285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 INPEDIY -- PSNPTDDDVS 31
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                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                            PRELIMINARY;
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Best Local Similarity
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01.MAY-2000 (TrEMBLrel. 13, Last sequence update)
01.MA-2000 (TrEMBLrel. 14, Last annotation update)
01.JUN-2000 (TrEMBLrel. 14, Last annotation update)
MAJOR CUTICULAR PROTEIN (FRAGMENT)
CETALILIS capitata (Mediterranean fruit fly).
Eukaryota; Metazoa; Arthropda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Tephritoidea; Tephritidae; Ceratitis.
[l/t]:
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Wainstock G.M., Waissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Zhong X., Xeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zhong K.H., Zhong W., Zhou K., Zhu S., Zhu K., Smith H.O., The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000)
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Bombycoidea; Bombycidae; Bombyx.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 silk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=87076763; PubMed=3024742; Michaille J.-J., Couble P., Prudhomme J.-C., Garel A.; "A single gene produces multiple sericin messenger RNAs in the
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                                                                                                                                                                                                      15.7%; Score 35; DB 5; Length 42; 66.7%; Pred. No. 1.4e+03; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 AA; 3793 MW; 71F3C0B347D7BD4C CRC64;
                                                                                                                                                                 D30246980893E46F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
SERICIN MRNA, PARTIAL CDS (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 15.5%; Score 34.5; DB 5; Best Local Similarity 47.6%; Pred. No. 1.5e+03; Matches 10; Conservative 3; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                                                           38 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                    FBgn0035882; CG13666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gland of Bombyx mori.";
Biochimie 68:1165-1173(1986).
EMBL; M26105; AAA27847.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 SKSRDENVSTTGSSSNTDSNS 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 SNPTDDDVS-SGSSSERSSTS 42
                                                                                                                                                                 4295 MW;
                                                                                                                                                                                                        Query Match 15.7
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Bombyx mori (Silk moth).
                                                                                                                                                                                                                                                                            42 AA;
                                                                                                                                                                                                                                                             31 SSGSSSERSSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7091;
                                                                                                                                                      FlyBase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                        096852;
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096852
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, ALL63529; CAB86546.1: -.
NON_TER
SEQUENCE 42 As. 3953 MW; 262E24C5F241951C CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 12; Length 28;
Pred. No. 1.2e+03;
9; Mismatches 3; Indels
  Length 20;
                                         Indels
                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA negative-strand viruses; Mononegavirales;
Rhabdoviridae; Lyssavirus.
NCBI_TaxID=11292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2E330EA9AB8F3C6A CRC64;
                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL SERINE-RICH PROTEIN (FRAGMENT).
Score 34; DB 5; Pred. No. 8.6e+02;
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                                       Mismatches
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  15.2%;
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Best Local Similarity 26.3%;
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                                 Gaps
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MEDLINE=96082572; PubMed=7581667; Michael T., Spena A.;
Michael T., Spena A.;
Michael T., Spena A.;
Michael T., Spena A.;
Effects on morphology, development, and hormone metabolism.";
Methods Mol. Biol. 44:207-222(1995).
SEQUENCE 38 AA; 3927 MW; F90FA27E17C90AB7 CRC64;
                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ROLA PROTEIN (FRAGMENT).
Agrobacterium rhizogenes.
Bacteria: Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
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Waltregny D., Loda M.;
"Homo sapiens cyclin-dependent kinase inhibitor p27 intron.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF213700; AAF21058.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.0%; Score 33.5; DB 2; Length 38; 36.8%; Pred. No. 2e+03;
15.2%; Score 34; DB 3; Length 42; 40.0%; Pred. No. 1.9e+03; tive 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 4; Length 42;
Pred. No. 1.9e+03;
5; Mismatches 5; Indels
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42 AA; 4461 MW; 92B374982A590CD9 CRC64;
                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR P27 (FRAGMENT)
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                                                                                                                                                               42 AA.
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| SYSSDSSASSSSSSHESSA 20
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                                                          23 SNPTDDDVSSGSSSERSSTS 42
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24 ANRTEENVSDGSPNAGS 40
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Best Local Similarity 36.83
Matches 7; Conservative
Query Match 15.2
Best Local Similarity 40.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 SNPTDDDVSSGSSSERS 39
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Matches 7; Conservative
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NON_TER
SEQUENCE
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Q9R5U8
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Search completed: February 21, 2002, 16:41:29
Job time: 184 sec
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Phosphopeptide #4 Anticariogenic pho Casein phosphopept Phosphopeptide 4. Phosphopeptide der Sequence of casein Sodium caseinate t

9hosphopeptide

Human gene 11-enco

Human secretory pe Human Zsig9 secret Fragment of human Zinc finger 2 sequ Rabbit polymeric i

Bos alpha-s2-casei Phosphopeptide T4.

Yeast Nup2 protein

bladd

Yeast YNup2 protei Human normal bladd

Peptide #4901 enco

Sequence of a new Linker amino acid

Title: Perfect score:

Sequence:

protein

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Run on:

Scoring table:

Searched:

Database

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Use of CD44 protein and new peptide derivs - for developing prods for inflammation, immune-mediated tissue damage and tumour cell
                                                                                                                                                                                                                                                                                                                                                                                                           Cell adhesion molecule; CD44; antiinflammatory; rheumatoid; arthritis; tumor cell metastasis; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patton KL,
                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                      AAR32930
AAR31240
AAR32311
               AAP71323
AAR14450
                                                                AAR47817
AAR68939
AAW66601
AAB12803
                                                                                                       AAY15133
AAB38408
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AAY08793
AAY08821
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AAY90828
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AAM16778
         AAB48726
                                AAR28428
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                                                                                                                                                                                                                                                                                                                                         AAR53476 standard; peptide; 42
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93WO-US10412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92US-0973339
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Hale LP, Haynes BF,
                                                                                                                                                                                                                                                                                                                                                                                            CD44 peptide CD44-4
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                                                                                                                                                                                                                                                                                                                                                                                                                           immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYDU-) UNIV DUKE.
Homo saplens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                           01-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9409811-A
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metastasis
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36.5
36.5
36.5
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                Surrounding sequen
CD44 peptide CD44-
CD44 peptide CD44-
Erythropoietin rec
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Peptide #8898 enco
BS106 synthetic po
BS106 polypeptide
Polypeptide fragme
                                                               (without alignments)
131.825 Million cell updates/sec
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CD44 peptide CD44-
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                                                      February 21, 2002, 16:35:10; Search time 23.6 Seconds
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                                                                                     US-08-753-851-4
223
1 CRDGTRYVQKGEYRINPEDI......SNPTDDDVSSGSSSERSSTS
                                                                                                                                                                                                                                              /SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1982.DAT:*
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       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                Potal number of hits satisfying chosen parameters:
                                                                                                                                               522463 seqs, 74073290 residues
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    protein search, using sw model

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AAB21600
AAM34861
AAW42089
AAY13467
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Gapop 10.0 , Gapext 0.5
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228
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Match 1
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116:
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Human TrkA protein BS106 synthetic po BS106 polypeptide Peptide #3212 enco Peptide #3300 enco

Telen MJ;

46.5 44 43.5 43.5 43

3 5 6 7 7 10 11

Score

٠ 9 Result

223 173 126 105 96 47

EPOa-hSA fusion pr Peptide derived fr Alpha V beta 3 rec H. insolens family Humanised anti-p18

Peptide recognised

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8 x 5 5 5 5 5 5 5 X 8

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Lupus, inflammatory bowel disease, psorlasis, osteoarthritis or HIV infection.

HIV infection.

The fusion protein may be used to target proteoglycans to a given site, which causes local accumulation of GAG-binding proteins. Therefore the protein may be used as adjuvants for vaccination and in the targeting of chemokines to non-immunogenic tumour cells to enhance cellular antitumour responses. In addition, the fusion protein can also enhance the half-life of non-GAG binding growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The recombinant fusion protein may be administered to a patient to enhance the biological activity of a GAG-binding protein within the body. The protein also enhances wound healing and may be used to treat rheumatoid arthritis, asthma, chronic obstructive pulmonary disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           part of the surrounding sequence of one of the potential \prime sites in a CD44 exon.
                                                                                                                                                                                             Surrounding sequence of potential assembly site E5-Rg, in CD44
                                                                                                                                                                                                                            isoform; CD44; expression vector; exon; modification; proteoglycan; glycosaminoglycan binding protein; rheumatoid; arthritis; asthma; immunological disorder; assembly site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New artificial proteoglycans useful for treating rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 126; DB 20;
Pred. No. 4.7e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
     1 crdgtryvqkgeyrtnpediypsnptdddvss 32
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                                                                                      AAY15201 standard; Peptide; 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bennett KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   W09937317-A1
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Best Local Simi
Matches 25;
                                                                                                                                                            26-0CT-1999
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                                                                                                                                                                                                                                                                                                                                                                                  29-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aruffo AA,
                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                        AAY15201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR53477;
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                                                                        AAY15201
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                                                                                                                                                                                                                                               Gaps
                               The peptide can be used for treating inflammation and immune-mediated tissue damage such as occurs in the course of autoimmune diseases, e.g. rheumatoid arthritis. It can also be used for determining metastatic potential or to treat or prevent tumor cell metastasis. This peptide corresponds to AA 150-190 of the CD44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The peptide can be used for treating inflammation and immune-mediated tissue damage such as occurs in the course of autoimmune diseases, e.g. rheumatoid arthritis. It can also be used for determining metastatic potential or to treat or prevent tumor cell metastasis. This peptide corresponds to AA 150-180 of the CD44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of CD44 protein and new peptide derivs - for developing prods for inflammation, immune-mediated tissue damage and tumour cell
                                                                                                                                                                                                                                             .;
0
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0
                                                                                                                                                                                                             Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adhesion molecule; CD44; antiinflammatory; rheumatoid; ritis; tumor cell metastasis; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 32;
                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Telen MJ;
                                                                                                                                                                                                                                                                                               Score 223; DB 15;
Pred. No. 1.2e-24;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 173; DB 15;
Pred. No. 1.1e-17;
0; Mismatches 1;
                                                                                                                                                                                                                                                                             1 CRDGTRYVQKGEYRINPEDIYPSNPTDDDVSSGSSSERSSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.16
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patton KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. CRDGTRYVQKGEYRINPEDIYPSNPTDDDVSS 32
                                                                                                                                                                                                                                                                                                                                                                                                  AAR53475 standard; peptide; 32 AA.
Claim 4; Page 14; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 14; 83pp; English.
                                                                                                                                                                                                          Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 42; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liao H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.68;
96.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93WO-US10412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1994-167121/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD44 peptide CD44-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYDU-) UNIV DUKE.
                                                                                                                                                            42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 AA;
                                                                                                                        protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-OCT-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR53475;
                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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AAR53475 RESULT

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Gaps

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Length 28; Indels

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New ligands for human erythropoietin receptor, useful for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the erythropoietin receptor (EPOR)-binding peptide Base and a startide B6. This peptide was identified as baing able to bind a recombinant erythropoietin receptor via biopanning methods. The peptide is a product of an ERB1 (erythropoietin receptor (EPOR)
                                                                                                                                                                             The peptide can be used for treating inflammation and immune-
mediated tissue damage such as occurs in the course of autoimmune
diseases, e.g. rheumatoid arthritis. It can also be used for
determining metastatic potential or to treat or prevent tumor cell
metastasis. This peptide corresponds to AA 150-161, 170-177 and
189-198 of the CD44
                                                                                Use of CD44 protein and new peptide derivs - for developing prods for inflammation, immune-mediated tissue damage and tumour cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPO; receptor; erythropoietin receptor; EPOR; immunoglobulin G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fusion protein; vector; cloning; synthetic peptide; biopanning; evolved library; mimetic; proliferation; biological activity; chronic renal failure; malignancy; cancer; chemotherapy; HIV; rheumatoid arthritis; treatment; anaemia.
                                                                                                                                                                                                                                                                                                                                                                       Length 30;
                                                                                                                                                                                                                                                                                                                                                                          Db 12. . 9.4e-07; . 1; Indels
               Telen MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Erythropoietin receptor (EPOR)-binding peptide B6.
                                                                                                                                                                                                                                                                                                                                                                       Score 96; DB 15;
Pred. No. 9.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
               Patton KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                           28
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRDGTRYVQKGEYRINPEDIYPSNPTDD
                                                                                                                                                 Claim 4; Page 14; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 7; Fig 4; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY42816 standard; peptide; 38
               Liao H,
                                                                                                                                                                                                                                                                                                                                                                        43.0%;
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                                                                                                                                                                                                                                                                                                                                                                       Query Match 43.0
Best Local Similarity 67.9
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McConnell SJ, Spinella
               Hale LP, Haynes BF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-601069/51
                                               WPI; 1994-167121/20
                                                                                                                                                                                                                                                                                                                       30 AA;
                                                                                                                                                                                                                                                                                      protein sequence
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                                                                                                                   metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY42816;
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Db
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The peptide can be used for treating inflammation and immune-mediated tissue damage such as occurs in the course of autoimmune diseases, e.g. rheumatoid arthritis. It can also be used for determining metastatic potential or to treat or prevent tumor cell metastasis. This peptide corresponds to AA 161-180 of the CD44
                                                                                                                                                                                                                                                                                                                                                                                      Use of CD44 protein and new peptide derivs - for developing prods for inflammation, immune-mediated tissue damage and tumour cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                             Cell adhesion molecule; CD44; antiinflammatory; rheumatoid; arthritis; tumor cell metastasis; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adhesion molecule; CD44; antiinflammatory; rheumatoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arthritis; tumor cell metastasis; autoimmune disease;
                                                                                                                                                                                                                                                                                                                     Telen MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.1%; Score 105; DB 15; 95.0%; Pred. No. 3.2e-08; ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                    Patton KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR53481 standard; peptide; 30 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 14; 83pp; English.
                                                                                                                                                                                                                                                                                                                     Liao H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32
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Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                    Hale LP, Haynes BF,
               CD44 peptide CD44-5.
                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-167121/20.
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                                                                              immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunosuppressive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein sequence.
                                                                                                                                                                                                                                                                                  (UYDU-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                   30-OCT-1992;
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AAR53481 RESULT

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and for treating disorders regulated at the neuronal nicotinic acetylcholine receptors, including cardiovascular disorders, gastric motility disorders, urinary incontinence, nicotine addiction, mood disorders such as bipolar disorder, unipolar depression, dysthymia and seasonal affective disorder, and small cell lung carcinoma.
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                                                                                               Sequence
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                                                                                                                                                                       Matches
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binder 1) evolved library which was constructed using redundant oligonucleotides AA23086 and AA23085, and then screened for EPOR-binding activity. Such EPOR-binding peptides are unrelated to the amino acid sequence of EPO and contain a consensus sequence necessary for EPOR binding, CXXGWGXCXXW (AAY42845). Shorter peptides (AAY42846, AAY42847) based on EPOR-binding peptides already shown to bind EPOR with high affinity (AAY4881, AAY42881) were found to stimulate proliferation of an EPO- responsive cell line, thus demonstrating that they had EPO biological activity. Such EPO mimetric peptides can be used in the treatment of anaemia associated with pathological conditions including chronic renal failure, malignancy, the effects of chemotherapy, HIV and rheumatoid arthritis. The peptides are smaller than recombinant EPO used in prior art treatment, and thus less expensive and easier to deliver as a therapeutic agent, compared to prior art methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a number of alpha-conotoxin peptides and their coding sequences from a number of different species of cone snail. These peptides are found in minute quantities in the venom of the snails, fund are targeted at the neuronal nicotinic acetylcholine receptors of the nervous system. They usually contain two disulphide bonds, which give them defined conformations, a arxity in molecules this small. The alpha conotoxins can be used as neuromuscular blocking agents in surgery,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha-conotoxin polypeptides derived from the venom of cone snails useful e.g. as neuromuscular blocking agents for use in surgery and for
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuronal nicotinic acetylcholine receptor; cardiovascular disorder; gastric motility disorder; urinary incontinence; nicotine addiction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                            Score 47; DB 20; Length 38;
                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McIntosh JM,
                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cone snail alpha-conotoxin SEQ ID NO: 328
                                                                                                                                                                                                                                                                                                                                                                  34
                                                                                                                                                                                                                                                                                                                                  1 CRDG----TRYVQKGEYRINPEDIYPSNPTDD 28
                                                                                                                                                                                                                                                                                                                                                      Olivera BM, Hillyard DR,
                                                                                                                                                                                                                                                                                          Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 39; Page 57; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB21600 standard; Peptide; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treating unipolar depression -
                                                                                                                                                                                                                                                                           21.18; 37.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JAN-2000; 2000WO-US01979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            small cell lung carcinoma
                                                                                                                                                                                                                                                                                                        12; Conservative
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (COGN-) COGNETIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-505965/45.
                                                                                                                                                                                                                              38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAA89496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200044776-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Watkins M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB21600;
                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                      Peptide #8898 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to single exon nucleic acid probes (SENP:
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful for
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    Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22; Length 42;
                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                            microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5,
    21;
    DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ore 44; DB 2
ed. No. 35;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           analyzing gene expression in human placenta
                                        Mismatches
                                                                                                        3 DGTRYVQKGEYRINPEDIYPSNP---TDDDVSSG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 27; SEQ ID No 35130; 654pp; English.
  Score 46.5;
Pred. No. 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.78; Score 44; 40.78; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 PSNPTDDDVSSGSS----SERSSTS 42
                                                                                                                                                                                                                    A.
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2
                                                                                                                                                                                                                    AAM34861 standard; Protein; 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
20.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000GB-0024263
                                                                                                                                                                                                                                                                                                (first entry)
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    numan genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-488897/53
    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157272-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-OCT-2000;
                                                                                                                                                                                                                                                                                                17-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001
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AAW42089

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tumour; neurodegenerative disorder; leukaemia; autoimmune disease; AIDS; developmental abnormality; foetal deficiency; Alzheimer's disease; cognitive disorder; schizophrenia; immunological disorder; mod disorder; immune deficiency disease; respiratory disorder; arthritis; skeletal; haematcopoietic disorder; neural; osteoporosis; metabolic disorders; cardiovascular; endocrine; gastrointestinal; asthma; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                            polypeptides (AAV13466-470). The BS106 nucleic acids correspond to a breast tissue gene and can be used as markers for breast tissue disease. The products can be used for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining diseases or conditions associated with BS106, especially breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted protein; gene therapy; protein therapy; tissue; cancer;
                                                                                                                                                                                                                                                                                                                                                                BS106 polynucleotides (AAX55578-82) and
                                                                                                                                                                                                                  Kratochvil JD;
                                                                                                                                                                                                  Friedman PN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 20;
                                                                                                                                                                                   Colpitts TL, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43.5; DE Pred. No. 38; 7; Mismatches
                                                                                                                                                                                                                  SC, Klass Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptide fragment encoded by gene 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 PEDIYP-SNPTDDDVSSGSSSERSSTS 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 17; Page 92; 105pp; English.
                                                                                                                                                                                                                                                                                              New isolated BS106 nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY01162 standard; Protein; 20
                                                                                                                                                                                                                   Hodges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.5%;
29.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0058663.
97US-0051381.
97US-0051480.
97US-0058598.
                                                                                                                                                                                                 Cohen M,
                                                                                                                                                                                                                               Roberts-rapp L, Russell JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                  98WO-US22020
                                                                                                                                97US-0962094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US13608
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Best Local Similarity 29...
Best Local Similarity 29...
                                                                                                                                                                                                                                                                                                                                                                The invention provides
                                                                                                                                                                                                                   Granadose,
                                                                                                                                                                                                                                                               WPI; 1999-326991/27
                                                                                                                                                                                                 Billiing-Medel PA,
                                                                                                                                                                 (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JAN-1999.
   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09901020-A2
                                WO9923230-A1
                                                                                                                                  31-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                19-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-SEP-1997;
                                                                  14-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1997;
01-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-SEP-1997
                                                                                                                                                                                                                   Gordon J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY01162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BS106 is a breast tissue gene with which breast cancer and related diseases are associated. The BS106 polypeptides AAW42088-W42092 can be utilized in a variety of of assays for the detection of antibodies to breast tissue. They can also be used as immunogens for the detection of antibodies to breast tissue. The products and methods discussed in this invention can be used for detecting, diagnosing, staging, preventing or treating, or determining predisposition to diseases or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting BS106 gene products - useful for developing products for detecting, staging, preventing, treating or determining predisposition to e.g. breast cancer
                                                                                                                                                                                                                              Human; BS106; breast tissue gene; breast cancer; detection marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Cohen M, Colpitts TL, Friedman PN;
dos EN, Hodges SC, Klass MR, Kratochvil JD;
Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BS106; breast; marker; detection; diagnosis; breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conditions of the breast such as breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43.5;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 PEDIYP-SNPTDDDVSSGSSSERSSTS 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | | | : | | | : : ::|:
padtypatgpaddeapdaettaaatta 35
             15 psppssqtasagstatcgspsqrsats 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; Page 93; 114pp; English.
                                                                                             AAW42089 standard; Peptide; 39 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY13467 standard; Protein; 39
                                                                                                                                                                                             BS106 synthetic polypeptide 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.5%;
29.6%;
                                                                                                                                                                                                                                                                                                                                                             97WO-US19836
                                                                                                                                                                                                                                                                                                                                                                                               96US-0742067
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                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Granados EN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-272234/24
                                                                                                                                                                                                                                                                                                                                                                                                                               (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Billing-Medel PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roberts-Rapp L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39
                                                                                                                                                               25-SEP-1998
                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                            WO9818945-A1
                                                                                                                                                                                                                                                                                                                                                             31-OCT-1997;
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Gordon

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AAY13467

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Gaps

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Length 39; Indels 9

99WO-US13418.

15-JUN-1999;

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The invention relates to nucleic acid sequences (AAX22111 to AAX22134) encoding human secreted proteins (AAY01135 to AAY01159). The secreted proteins are deposited with the ATCC under deposit number ATCC 200118. Host cells comprising recombinant vectors containing the nucleic acid sequences are used for the recombinant production of the secreted proteins. The polynucleotide and amino acid sequences are useful for preventing, treating or amino acid sequences are useful for are useful for preventing, treating or amino acid sequences are useful for are useful for preventing, treating or amino acid sequences are useful conditions e.g. by protein or gene therapy. Pathological conditions can be also diagnosed by determining the amount of the mew polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the polynucleotides. Specific uses are described for each of the polynucleotides based on which tissues they are most highly expressed in, and include developmental abnormalities and foetal deficiencies, autoimmune diseases, lymphomas, Alzheimer's and cognitive disorders, cancormalities and foetal disorders, autoimmune diseases, lymphomas, Alzheimer's and cognitive disorders, haematopoietic disorders, inmune deficiency asthma, hamunological disorders, immune disorders, entratidis asthma, hamunological disorders, immune disorders, entratidis asthma, haematopoietic disorders, respiratory disorders, arthritis, asthma, cateoporosis, metabolic disorders, cardiovascular disorders, endocrine disorders or gestroprotes for identifying their binding partners. The present sequence represents a company of the invention (see descriptor is appropriate fragment encoded by a gene of the invention (see descriptor
                                                                                                                                                                      New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, immune deficiency diseases or blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 20; Length 20;
                             Ruben SM;
                             Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.3%; Score 43;
                                                                                                                                                                                                                                                                                                                           Disclosure; Page 7; 179pp; English.
                             Feng P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.8%;
                             Endress GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ine for gene number).
                                                                                   WPI; 1999-105683/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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.; 0 Gaps .; 0 5; Indels Pred. No. 20; 4; Mismatches Query Match 19.3 Best Local Similarity 43.8 Matches 7; Conservative

3 DGTRYVQKGEYRINPE 18 | ::| |:||||: 2 dpkktigmgsfrinpd 17

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AAY86368 standard; peptide; 38 AA. AAY86368

19-APR-2000 (first entry) 

Human gene 11-encoded protein fragment, SEQ ID NO:283.

Human; secreted protein; cancer; tumour; developmental abnormality; foetal deficiency; blood disorder; immune system disorder; inflammation; autoimmune disease; allergy; Alzheimer's disease; cognitive disorder; schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder; digestive disorder; endocrine disorder; infection; AIDS; leukaemia; therapy; chromosome 3.

Homo sapiens

WO9966041-A1

23-DEC-1999

ds snw

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AAX86215 to AAX86333 are the secreted human secreted protein genes.
AAX86215 to AAX86333 are the secreted proteins encoded by the 94 human genes. This sequence represents a fragment of one of the human secreted proteins. This sequence represents a fragment of one of the human secreted proteins. The genes and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Also pathological conditions an bediagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 94 genes, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, developmental abnormalities and feetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney disorders, digestive/endocrine disorders, indections and AIDS. The polypeptides are also useful for identifying their binding partners.
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                                                                                                                                                                                                                Ebner R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                    New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                              CA, Wei Y, Young PE, Florence KA;
Endress GA, Carter KC, Mucenski M,
Shi Y, Moore PA, Komatsoulis G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41; DB 21; Length 38;
Pred. No. 84;
7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse liver growth hormone-induced clone 5 ORF #3.
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                                               98US-0089508.
98US-0089509.
98US-0089510.
98US-0090112.
                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.48;
41.28;
                                  98US-0089507
                                                                                                                      98US-0090113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                Ni J, Rosen
                                                                                                                                                                                                                Brewer LA,
Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     open reading frame; ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity
The 7; Conserve
                                                                                                                                                                                                                                                                   WPI; 2000-106100/09
                                                                                  16-JUN-1998;
22-JUN-1998;
22-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-MAR-2001
                                                                   16-JUN-1998
                                                                                                                                                                                                                                 Lafleur DW,
                                                     .6-JUN-1998
                                                                                                                                                                                                                Soppet DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB48726;
                                                                                                                                                                                              Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
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periodontal disease; osteoporosis; osteomalacia,

'label= phosphoserine 'label= phosphoserine label= phosphoserine /label= phosphoserine

Location/Qualifiers

us-08-753-851-4.rag

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New phosphopeptides contg. defined aminoa cid sequence - useful in treatment of dental, rarefying bone diseases and disease relating to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Page 17; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          malabsorption of minerals.
                                                                                                                                                                                              Caries; gingivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1987-362707/51.
                                                                                                                                          Phosphopeptide 4.
                                                                                                                                                                                                                                                                                                                                Modified-site
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                                                                                     07-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-JUN-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO8707616-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-DEC-1987,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reynolds EC;
                                                                                                                                                                                                                                                  Synthetic.
                                      AAP71323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (VICT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (REYN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UYME-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR14450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
           δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method of diagnosing abnormal levels of growth hormone (GH) activity in the liver, or predicting a change in the condition of the liver in response to abnormal GH activity. The method involves correlating the level of expression of certain specific genes with the level of GH activity in the liver, or with an expected change in the condition of the liver as the result of GH activity. Excessive GH activity in the liver is thought to be deleterious to health, causing an increase in liver size as a consequence of both hyperplasia and hepatocyte hypertrophy, and hepatocellular lesions which progress with eage. Studies in transgenic mice which express high levels of bovine growth hormone identified a number of genes whose expression in the liver is altered by high GH levels. The genes which are upregulated are liver is altered by high GH levels. The genes which are upregulated are thus, rab8-interacting protein, controsteroid binding globulin, fetuin, rab8-interacting protein, paraoxonase-3, cytochrome P450IIIA, S-2 hydroxyacid oxidase, interferon alpha/beta receptor, growth hormone cenceding are submit, and coagulation factor V. Two novel genes, clone 5 (AAC87257) and clone 45 (AAC87258) are also upregulated in response to abnormally high GH levels. Conversely, expression of the formance are conding 3-beta-hydroxysteroid dehydrogense/delta-5-delta-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis of liver pathologies associated with gigantism or acromegaly or with diabetes, as other causative agents may act directly or indirectly upon the same genes. Sequence ABAH0724-B48739 represent the open reading frames (ORFS) of the novel mouse liver cDNA clone 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isomerase appears to be downregulated. The invention also relates to transgenic nonhuman mammals comprising a GH-induced transgene which exhibit or have a propensity to develop a liver pathology; an assay for drugs which inhibit the development of, or which treat a liver pathology; preventing a diversaling the drug to the transgenic animal; and preventing or treating a liver pathology in a patient comprising administering a drug which inhibits the expression of a GH-induced gene. The method of the invention is used for diagnosing abnormal levels of GH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity in the liver or predicting a change in the condition of the liver in response to abnormal levels of GH activity. The GH-regulatable liver genes and proteins are useful as diagnostic markers of liver pathology. Assays for the expression of these genes is useful for the
                                                                                                                                                                                                                                                                                                                                                                                                     abnormal levels of growth hormone activity in liver assaying growth transcriptional activity and protein level of hormone-regulatable liver genes, as diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
18.2%; Score 40.5; DB 22; Length 35;
Best Local Similarity 35.5%; Pred. No. 89;
Matches 11; Conservative 7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 53; 65pp; English.
                                                                                                        05-MAY-2000; 2000WO-US12366
                                                                                                                                                             99US-0132663
                                                                                                                                                                                                                                                                                                                                                                                                                                   comprising assaying growth expression level of hormone markers of liver pathology
                                                                                                                                                                                                                                                                   Kopchick JJ, Tiong J;
                                                                                                                                                                                                                                                                                                                       WPI; 2001-007239/01.
N-PSDB; AAC87257.
                                                                                                                                                                                                                 (UYOH-) UNIV OHIO.
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WO200066787-A2
                                                                                                                                                             05-MAY-1999;
                                                       09-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                          Diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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VICTORIA DAIRY INDUSTRY AUTHORITY. UNIVERSITY OF MELBOURNE. EC REYNOLDS.

87WO-AU00172. 86AU-0006385

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Gaps
                                                                                                                                                                                                                                                                                                                        carles; gingivitis; periodontal disease; osteoporosis; osteomalacia;
anaemia.
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The phosphopeptide is used in compsns. at a conc. of 0.01-5 See also \mbox{AP7}1320\mbox{-}P71324\mbox{.}
                                                                               Length 25;
                                                                                                         Indels
                                                                                                                                                                                                                                                                                                    Phosphopeptide #4 for increasing mineral absorption.
                                                                             17.9%; Score 40; DB 8;
47.1%; Pred. No. 70;
Live 4; Mismatches
                                                                                                                                                                                                                           AA.
                                                                                                                                                                                                                        AAR14450 standard; Protein; 25
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                                                                                                                                24 NPTDDDVSSGSSSERSS 40
                                                                                                                                                1 naneeeysigssseesa 17
                                                                                                         Conservative
                                                                                         Local Similarity
les 8; Conser
                                          AA;
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                                                                                                                                                                                                                                                                                                                                                                 Synthetic
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                                          Sequence
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Gaps

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14 RINPEDIYPSNPTDDDVSSGSSSE----RSS 40 

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AAP71323 standard; peptide; 25

AAP71323 ID AAP7 RESULT

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Novel phosphopeptides - useful for treating dental diseases, rarefying diseases or diseases relating to malabsorption of minerals
                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is an example of a highly generic formula for a phosphopeptide of length 5-13 amino acids. The peptides can be made synthetically (e.g. chemical synthesis or genetic engineering) or they can be extracted from cereals, nuts or vegetables or by fractionating a digest of casein, alpha-s-casein, beta-casein or a salt of it. Compositions comprising the peptide may take the form of foodstuff or confectionery, dentifrices; mouthwashes and preparations for topical application to teeth or gingival tissue. The peptides significantly increase absorption of calcium, phosphate and iron in the gut. See AAR1447-R14451.
                         /label= OTHER
/note= "phosphoserine (Pse)"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                 (UYME-) UNIV OF MELBOURNE.
(VICT-) VICTORIAN DAIRY INDUSTRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Column 11; 8pp; English.
                                                                /label= OTHER
                                                                                                                                                /label= OTHER
/note= "Pse"
                                                                                                         /label= OTHER
                                                                                                                      'note= "Pse"
                                                                                                                                                                                                                                               900S-0563798
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                                                                                                                                                                                                                                                                                                                                                                     WPI; 1991-316875/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 AA;
 Key
Modified-site
                                                     Modified-site
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                                                                                                                                                                                                                                             03-AUG-1990;
                                                                                                                                                                                                                                                                       03-AUG-1990;
                                                                                                                                                                                                                                                                                                                                         Reynolds EC;
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                                                                                                                                                                                        US5015628-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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Search completed: February 21, 2002, 16:38:21 Job time: 191 sec

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Gaps

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17.9%; Score 40; DB 12; Length 25; 47.1%; Pred. No. 70; ive 4; Mismatches 5; Indels

Qy Dp us-08-753-851-4.rai

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COUNTRY INC.

ZIP: 22201-4714

ZIP: 22201-4714

COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACHALIN RCLease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/143,311B
FILING DATE: 29-OCT-1993
CLASSIFICATION 1436
PRICATION NUMBER: 07/973,339
FILING BAPLICATION UMBER: 07/973,339
FILING DATE: 30-OCT-1992
CLASSIFICATION: 436
APPLICATION NUMBER: 07/669,730
FILING DATE: 15-MAR-1991
CLASSIFICATION: UMBER: 07/669,730
FILING DATE: 15-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HAYNES, BARTON F.
APPLICANT: HALE, LAURA P.
APPLICANT: PATTON, KAREN L.
APPLICANT: TELEN, MARILYN J.
APPLICANT: LIAO, HOANIN MOLECULE
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: NIXON & VANDERHYE P.C. 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08143311B Patent No. 5863540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY FAGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REPERENCE/DOCKET NUMBER: 1579-
TELECOMMUNICATION INFORMATION:
TELEFONE: 703-816-4100
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
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MOLECULE TYPE: peptide
US-08-143-311B-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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Sequence 12, Appl
Sequence 4, Appli
Sequence 6, Appli
Sequence 11, Appl
Sequence 8, Appli
Sequence 8, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence 85, Appli
Sequence 85, Appli
Sequence 81, Appli
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Sequence 3, Appli
Sequence 5, Appli
Sequence 9, Appli
                                                                                                                                                                     (without alignments)
75.793 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                            February 21, 2002, 16:36:50; Search time 12.47 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
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223
1 CRDGTRYVQKGEYRINPEDI.....SNPTDDDVSSGSSSERSSTS
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6: /cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-437-607A-48
US-08-931-858E-175
US-08-726-306A-88
US-08-645-641-83
US-08-645-641-83
US-08-696-762-83
US-08-308-865-83
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US-08-143-311B-5
US-08-143-311B-5
US-08-143-311B-9
US-08-143-44B-4
US-08-954-985A-4
US-08-955-383-6
US-08-133-804-8
US-08-461-838-8
US-08-159-34-8
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                                                                                                                                                                                                                                                                                                                                                                                    212252 segs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                     protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
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Match Length
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Perfect score:
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Maximum DB s
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US-09-042-353-280
US-08-758-417A-128
PCT-U52-10918-38
US-09-082-279B-828
US-08-373-159-5
US-08-77-153-5
US-08-373-190-3
US-08-373-190-3
US-08-38-190A-3
US-08-38-190A-3
US-08-38-190A-4
US-08-38-190A-4
US-08-373-190-4
US-08-350-215-3
US-08-373-190-4
US-08-38-190A-4
US-08-38-190A-4
US-08-38-190A-4
US-08-38-190A-4
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US-09-100-409A-44
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Pred. No. 2.9e-08;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARES PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/143,311B
FILING DATE: 29-OCT-1993
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,339
FILING DATE: 30-OCT-1992
CLASSIFICATION: 436
APPLICATION NUMBER: 07/669,730
FILING DATE: 15-MAR-1991
CLASSIFICATION: 436
CLASSIFICATION: 436
                                                     GENERAL INFORMATION:
APPLICANT: HAVNES; BARTON F.
APPLICANT: HALLE, LAURA P.
APPLICANT: PATTON, KAREN L.
APPLICANT: TELEN, MARILYN J.
APPLICANT: LIAO, HOA-XIN
APPLICANT: LIAO, HOA-XIN
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HALE, LAURA P.
APPLICANT: HALE, LAURA P.
APPLICANT: PATTON, KAREN L.
APPLICANT: TELEN, MARILIN J.
APPLICANT: LIAO, HUA-XIN
TITLE OF INVENTION: AN ADHESION MOLECULE
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                      ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
               Sequence 5, Application US/08143311B
Patent No. 5863540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/08143311B Patent No. 5863540 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 YRINPEDIYPSNPTDDDVSS 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 YRTNPEDIYPSNPTDDDVSS 21
                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 703-610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 703-816-4100 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                             STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 19; Conserv
US-08-143-311B-5
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0
                                        Length 42;
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Pred. No. 2.2e-17;
0; Mismatches 1; Indels
                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/143,311B
FILING DATE: 29-0CT-1993
CLASSIFICATION: 436
PRIOR APPLICATION NUMBER: 07/973,339
FILING DATE: 30-0CT-1992
CLASSIFICATION NUMBER: 07/669,730
FILING DATE: 31-0CT-1992
CLASSIFICATION: 436
APPLICATION NUMBER: 07/669,730
FILING DATE: 15-MAR-1991
CLASSIFICATION: 436
                                                                                                                                            1 CRDGTRYVQKGEYRINPEDIYPSNPTDDDVSSGSSSERSSTS 42
                                                                                                                      1 CRDGTRYVQKGEYRINPEDIYPSNPTDDDVSSGSSSERSSTS 42
                                    ch .100.0%; Score 223; DB 2;
1 Similarity 100.0%; Pred. No. 4.2e-24;
42; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                             APPLICANT: HAVES, BARTON F.
APPLICANT: HALE, LAURA P.
APPLICANT: PATTON, KAREN L.
APPLICANT: TELEN, MARILYN J.
APPLICANT: LIAO, HUA-XIN
TITLE OF INVENTION: AN ADHESION MOLECULE
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CRDGTRYVQKGEYRINPEDIYPSNPTDDDVSS 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :: NIXON & VANDERHYE P.C. 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                Sequence 3, Application US/08143311B Patent No. 5863540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.6%;
96.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 96.99
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: VIRGINIA
COUNTRY: U.S.A.
2IP: 22201-4714
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARLINGTON
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Gaps

CORRESPONDENCE ADDRESS

RESULT

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DB 1; Length 42; 43;
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Patent No. 5227154
GENERAL INFORMATION:
APPLICANT: REYNOLDS, ERIC CHARLES
TITLE OF INVENTION: PHOSPHOPEPTIDES FOR THE
TITLE OF INVENTION: TREATMENT OF DENTAL CALCULUS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: ANDRUS, SCEALES, STARKE & SAWALL STREET: 100 EAST WISCONSIN AVE., SUITE 1100 CITY: MILWAUKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.4%; Score 41;
62.5%; Pred. No. 4
                                                   ATTORNEY AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CME-062
RELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEG ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DC
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: SARA, CHARLES S
REGISTRATION NUMBER: 30,492
REFERENCE/COCKET NUMBER: C.84
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 255-2022
              FILING DATE: 17-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (608) 255-2182
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TELEX: 26832 ANDSTARK
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 18.4
Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19910822
                                                                                                                                                                                                                                                                                                                                peptide
internal
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                             linear
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                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53202
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                                                                                                                                                                                                                                                                                        TYPE: ami
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
US-07-748-344B-4
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Pred. No. 7.8e-07;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Saunders, Scott
APPLICANT: Bernfield, Merton
APPLICANT: Bernfield, Merton
APPLICANT: Kato, Masato
TITLE OF INVENTION: Construction and USe of Synthetic
TITLE OF INVENTION: Constructs Encoding Syndecan
NUMBER OF SEQUENCES: 43
ADDRESSE: AANTVE & COCKFIELD
STREET: A COCKFIELD
STREET: Boston
CITY: Boston
                                                                                         STATE: VIGALINIA
COUNTER: VIGALINIA
ZIP: 22201-4714
COMPUTER READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RGlease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/143,311B
FILING DATE: 29-OCT 1993
CLASSIFICATION NUMBER: US/08/143,311B
FILING DATE: 30-OCT -1992
CLASSIFICATION: 436
PILING DATE: 30-OCT -1992
CLASSIFICATION NUMBER: 07/973,339
FILING DATE: 15-MAR-1991
CLASSIFICATION NUMBER: 1579-50
FILING DATE: 15-MAR-1991
CLASSIFICATION NUMBER: 1579-50
RESISTRATION NUMBER: 1579-50
TELEDROMENICATION INFORMATION:
NAME: WILSON, MARY J.
RESISTRATION NUMBER: 1579-50
TELEDROMENICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZUP: 102.109
ZUP: 102.109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: ISM PC COMPATIBLE
SOFTWARE: ASCII (text)
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/078,683A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRDGTRYVQKGEYRINPEDIYPSNPTDD 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/08078683A Patent No. 5486599 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.0%;
67.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 67.99
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 703-010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-143-311B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sin
                                                   ARLINGTON
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US-08-078-683A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MA
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Gaps
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                                                                               FEATURE:
NAME/KEY: Phosphoserine
LOCATION: 13
OTHER INFORMATION: Post-translationally phosphorylated serine
FEATURE:
                                                                                                                                                                                   NAME/KEY: Phosphoserine

LOCATION: 16

CHER INFORMATION: Post-translationally phosphorylated serine

US-08-954-9854-4
                                                           OTHER INFORMATION: Post-translationally phosphorylated serine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08856383
Patent No. 6042833
GENERAL INFORMATION:
APPLICANT: Mostov, Keith E.
APPLICANT: Richman-Eisenstat, Janice
TITLE OF INVENTION: Cellular Internalization of pigR Stalk
TITLE OF INVENTION: and Associated Ligands
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 40;
                                                                                                                                                                                                                                                                                                             Length 25;
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APPLICATION NUMBER: US/08/856,383 FILING DATE: No. 6042833 yet assigned CLASSIFICATION: 530 RELOR APPLICATION DATA:
APPLICATION NUMBER: US 60/018,958 FILING DATE: 04 -UN-1996 ATTORNEY/AGENT: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3;
                                                                                                                                                                                                                                                                                                                  5
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                                                                                                                                                                                                                                                                                                               DB
31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02307E-067910PC
                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                               Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Weber, Kenneth A.
REGISTRATION INDMBER: 31,677
REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEFAN: (415) 576-0200
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                             17.98;
47.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 17.7%;
Best Local Similarity 34.3%;
Matches 12; Conservative
                       Phosphoserine
                                                                                                                                                                                                                                                                                                                                                                                               24 NPTDDDVSSGSSSERSS 40
                                                                                                                                                                                                                                                                                                                                                                                                                          1 NANEEEYSIGSSSEESA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: peptide US-08-856-383-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIT1.
STATE: Car.
COUNTRY: USA
TO: 94111-3834
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                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-08-856-383-6
                                          LOCATION
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                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                             ; LOCATION: 16
; OTHER INFORMATION:
: OTHER INFORMATION: Post-translationally phosphorylated serine
US-07-748-3448-4
                 OTHER INFORMATION: OTHER INFORMATION: Post-translationally phosphorylated serine
                                                                                                                                                                                                                            OTHER INFORMATION: Post-translationally phosphorylated serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 11 OST-translationally phosphorylated serine
                                                                                                                                             Post-translationally phosphorylated serine
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                                                                                                                                                                                                                                                                                                                                                                                                                                   17.9%; Score 40; DB 1; Length 25; 47.1%; Pred. No. 31; 5; Indels tive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
STREET: Dental School, The University of Melbourne STREET: 711 Elizabeth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: REYNOLDS, Eric Charles
TITLE OF INVENTION: A Treatment for Sensitive Teeth
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Ascii
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,985A
FILING DATE: 21-OCT-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 322-00033 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08954985A Patent No. 5981475 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362,479
FILING DATE: 22-FEB-1995
ATTORNEX/AGENT INFORMATION:
NAME: WOZDY, THOMMS M
REGISTRATION NUMBER: 28,922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (414) 271-7590
TELEFAX: (414) 271-5770
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                        MAME/KEY: Phosphoserine LOCATION: 12 OTHER INFORMATION: OTHER INFORMATION: POSt
                                                                                                                                                                                   NAME/KEY: Phosphoserine LOCATION: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Phosphoserine
                                                                                                                                                                                                                                                                                          NAME/KEY: Phosphoserine
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 3000
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: Australia
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LOCATION: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Exchange Place, 53 State Street
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; OTHER INFORMATION: /note= "LINKER 2"
US-08-461-838-8
                                                                                                                                                                             NAME/KEY: Protein
LOCATION: 1..15
OCHER INFORMATION: /note= "LINKER 2"
US-08-133-804-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08461838 Patent No. 5753204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION
TELEPHONE: 617-248-7477
TELEBRAX: 617-248-7100
                                                                                                                                                                                                                                                                                                    16.6%;
75.0%;
                                                        LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 75.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 15 amino acids
                                         SEQUENCE CHARACTERISTICS:
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617-248-7100
                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS: ADDRESSE: Testa, Hu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                 31 SSGSSSERSSTS 42
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  TELEFAX:
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                                                                                                                                                    Sequence 11, Application US/0921521
Patent No. 656552
GENERAL INFORMATION:
APPLICANT: EILERS, MARTIN
APPLICANT: EILERS, MARTIN
APPLICANT: ESDLACEK, HANS-HARALD
APPLICANT: SEDLACEK, UNCURIENT APPLICANTON: INVIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF FILE REFERENCE: 026083/0192
CURRENT APPLICATION NUMBER: 1979-12-18
PRIOR APPLICATION NUMBER: 197 56 975.7
PRIOR FILING DATE: 1997-12-20
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault/Patent Department
STREET: Exchange Place, 53 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.5%; Score 39; DB 4; Length 24; 58.3%; Pred. No. 40; 3; Indels Live 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/133,804
                                           8 VQKGEYRINPEDIYPSNPTDDDVSSGSSSERSSTS 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08133804 Patent No. 5534254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34,637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 58.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
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13 ETYDSNESDDDV 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02109
                                                                                                                  RESULT 9
US-09-215-221-11
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US-08-133-804-8
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Gaps
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Score 37; DB 1; Length 15; Pred. No. 42; 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVERTION: Biosynthetic Binding Proteins For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/461,838
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Sequence 3, Application US/08665202

Sequence 3, Application US/08665202

GENERAL INFORMATION:

APPLICANT: Marks, James D.

APPLICANT: Schier, Robert

TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to

TITLE OF INVENTION: Tumor Antigens

NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California
                 APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer TITLE OF INVENTION: Marker
                                                                                                                                   Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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1; Mismatches
                                                                                                                                                 STREET: Exchange Place, 53 State Street
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                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/356,786
                                                                                                                                                                                                                                                                                                           PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                         07/831,967
                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,96'
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: PItcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/COCKET NUMBER: CRP-(TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: ELOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
       Oppermann, Hermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.6%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 16.6
Best Local Similarity 75.0
Matches 9; Conservative
                                                                                              NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-356-786-12
                                                                                                                                                                                           Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 SSGSSSSGSSSS 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                        Boston
                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                02109
                                                                                                                                                                                           STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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US-08-665-202-3
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Exchange Place, 53 State Street
     DB 1; Length 15;
                                        Indels
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                                                                                                                                                                                                                                                                              APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                        1; Mismatches
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   Score 37;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: 1..15
; OTHER INFORMATION: /note= "LINKER 2"
US-08-461-386-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/461,386
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                                                                                                                                                                                                           Sequence 8, Application US/08461386
Patent No. 5837846
GENERAL INPORMATION: James S.
APPLICANT: Oppermann, Hermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFRENCE/DOCKET NUMBER: 2054
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
Query Match
Best Local Similarity 75.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 75.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 424
                                                                         31 SSGSSSERSSTS 42
                                                                                                3 SSGSSSSGSSSS 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 SSGSSSSGSSSS 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boston
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STREET: Ex
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US-08-356-786-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                         US-08-461-386-8
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Gaps ; 0

Length 15;

0; Gaps

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Length 15;
                                                                                                                                                                                       2; Indels
                                                                                                                      Score 37; DB 3;
Pred. No. 42;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: February 21, 2002, 16:38:40 Job time: 110 sec
                                                                                                                      16.6%;
75.0%;
                                                                                                                                                                                       9; Conservative
                                                                                                                                                                                                                                                       31 SSGSSSERSSTS 42
                                                                                                                                                                                                                                                                                            3 SSGSSSSGSSSS 14
                                                                                                                   Query Match
Best Local Similarity
Matches 9; Conserv
                       US-08-483-749A-31
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Sequence 31, Application US/08483749A
TUTLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY TITLE OF INVENTION: ANDLECULES SPECIFIC FOR CANCER ANTIGENS NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSE: CHIRON CORPORATION
STREET: INVELLECTUAL PROPERTY - R440, PO BOX 8097
COTAT: EMERYVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 75.0%; Pred. No. 42;
Matches 9; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:: INTELLECTUAL PROPERTY - R440, PO BOX 8097
CITY: EMERYVILLE
STATE: CA
COUNTRY: USA
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,749A
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 05/08/483,749A
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 36,914
REGISTRATION OF SED ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: TIPERED SINGER
TOPOLOGY: linear
                                                                                                  PRIOR APPLICATION: 474

PRIOR APPLICATION: 474

APPLICATION NUMBER: US 60/000,238

FILING DATE: 14-UN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250

FILING DATE: 15-UN-1995

ATTORNEY/AGENT INFORMATION:
NAME: HUNTER, TOM:
REGISTRATION NUMBER: 02307E-061410

TELEPHONE: (415) 576-0300

TELEPHONE: (415) 576-0300
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 SSGSSSERSSTS 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 SSGSSSSGSSSS 14
                                               FILING DATE: 13 CLASSIFICATION:
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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2002, 16:41:06; Search time 33.6 Seconds
(without alignments)

47.609 Million cell updates/sec
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Title: US-08-753-851-5
Perfect score: 120
Sequence: 1 CYRTNPEDIYPSNPTDDDVSS 21
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 404

Minimum DB seq length: 0 Maximum DB seq length: 21 Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Ig heavy chain C reapsid protein VP1 protein QF200051 - 26K kidney and gal Ig heavy chain DJ carboxylesterase ( proteinase inhibit ribosomal protein hemocyanin chain I trypsin (EC 3.4.21 ranatachykinin D cytochrome-c oxida melatin-ommochrome NADH dehydrogenase tryptophyllin-rela tryptophyllin-13 - alpha-conotoxin Au protein-tyrosine k protein phosphatas insulin-like growt protein kinase C i Jenzoyl-CoA ligase alpha-conotoxin Au major outer membra I-cell receptor al endometrial secret calliMIRFamide 1 Description SUMMARIES A54651 S72501 S78416 S00492 A61328 D61033 G37266 PQ0545 A61377 S24780 S27248 A39040 S77983 A23992 G49732 A41299 DB Query Match Length Score Result

manganese peroxida trypsin-like prote	acetyl-CoA synthet	pyrrhocoricin - Py	cytochrome b559 co	28K protein 4209 -	cycloinulooligosac	cytochrome-c oxida	metal-binding prot	urinary tract ston	alpha-conotoxin Au	pollen allergen Fe	alpha-conotoxin EI	beta-Gliadine 13 -	alpha-macroglobuli	dermatan sulfate p
S65434 S50022	T44453	S44465	S05031	PS0210	PC2330	S43626	PL0152	A56049	C59045	C37396	A58589	PN0149	S23971	A56798
77	7	7	7	7	7	7	7	7	7	~	Н	7	7	7
19	20	20	21	16	11	11	14	15	16	17	18	18	18	18
19.2	19.2	19.2	19.2	18.8	18.3	18.3	18.3	18.3	18.3	18.3	18.3	18.3	18.3	18.3
23	23	23	23	22.5	22	22	22	22	22	22	22	22	22	22

## ALIGNMENTS

ESOLIT 1
A41299
T-cell receptor alpha chain precursor V region (17.2) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 23-Jul-1999
C; Accession: A41299
; Uematsu, Y.; Wege, H.; Straus, A.; Ott, M.; Bannwarth, W.; Lanchbury, J.; Panayi, G
Proc. Natl. Acad. Sci. U.S.A. 88, 8534-8538, 1991
A; Title: The T-cell-receptor repertoire in the synovial fluid of a patient with rheum
A; Reference number: A41299; MUID:92020887
A; Accession: A41299
A;Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-19 <uem></uem>
A;Cross-references: GB:S57433; NID:9236318; PIDN:AAB19956.1; PID:9236319
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
Query Match 27.5%; Score 33; DB 2; Length 19;
Similarity 58.3%; Pred. No. 94;
Matches /; Conservative U; Mismatches 5; indeis U; daps U;
Qy 8 DIYPSNPTDDDV 19

A61377

endometrial secretory protein - sheep (fragment)

C; Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C; Species: O9-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 17-Mar-1999

C; Accession: A61377

R; Vallet, J.L.; Barker, P.J.; Lamming, G.E.; Skinner, N.; Huskisson, N.S.

J. Endocrinol. 130, R.R.A, 1991

A; Reference number: A61377; MUID:92013712

A; Reference number: A61377

A; Status: preliminary

A; Molecule type: protein

A; Residues: 1-19 < VAL>

Query Match 24.6%; Score 29.5; DB 2; Length 19; Best Local Similarity 46.2%; Pred. No. 3.1e+02; Matches 6; Conservative 3; Mismatches 3; Indels 1; Gaps

1;

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Gaps

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Length 18;

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A;Pathway: oxidative phosphorylation; respiratory chain
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membr
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N;Alternate names: melanization and reddish coloration hormone III; MRCH III
C;Species: Bombyx mori (silkworm)
C;Date: 30-Jan-1988 #sequence_revision 30-Jan-1988 #text_change 18-Jun-1993
C;Accession: A23992
                                                                                                                                                                                                                                                                                                                                                                                             protein phosphatase - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Bate: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 30-Sep-1993
C;Bate: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 30-Sep-1993
C;Accession: A32917
R;Tamura, S.; Yasui, A.; Tsuiki, S.
Biochem. Blophys. Res. Commun. 163, 131-136, 1989
A;Title: Expression of rat protein phosphatase 2C (IA) in Escherichia coli.
A;Reference number: A32917
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-18 <TAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytochrome-c oxidase (EC 1.9.3.1) chain Vb - bigeye tuna (fragment)
C;Species: Thunnus obesus (bigeye tuna)
C;Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 30-Jan-1998
C;Accession: S77983
R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenk submitted to the Protein Sequence Database, June 1997
A;Reference number: S77980
A;Accession: S77983
A;Accession: Protein
A;Residues: 1-20 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 26; DB 2; Length 18;
Pred. No. 9.8e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 26; DB 2; Ler
Pred. No. 1.1e+03;
                                                                                    Score 26; DB 2;
Pred. No. 9.8e+02;
C; Keywords: cardiac muscle; heart; phosphoprotein
                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: heart; liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.7%;
80.0%;
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44.48;
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41.78;
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5 DDDLPTINTEDD 16
                                                                                 Query Match
Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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7 PGDPLEDQV 15
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7 PTDDE
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C;Species: Canis lupus familiaris (dog)
R;Cala, S.E.; Jones, L.R.
J. Biol. Chem. 266, 391-398, 1991
A;Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by casein A;Reference number: A39040; MUID:91093153
A;Reference number: A39040
A;Reference number: A39040; MUID:91093153
A;Reference number: A39040; MID:91093153
A;Residues: 26-18 cCAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: lck
C; Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h
C; Keywords: ATP; blocked amino end; lipoprotein; myristylation; phosphotransferase; thic
F; 2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F; 3, 5/Binding site: palmitate (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                A;Title: Frequent activation of the lck gene by promoter insertion and aberrant splicing A;Reference number: I58370; MUID:93141260 A;Accession: I58370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rilane, B.G.; Cuning, A.C.; Fregeau, J.; Carpita, N.C.; Hurkman, W.J.; Bernier, F.; Drat Eur. J. Biochem. 209, 961-969, 1992
A;Title: Germin isoforms are discrete temporal markers of wheat development. Pseudogermi ated embryos, it is incorporated into cell walls.
A;Reference number: $27247; MUID:93049354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
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                                                                                                        C; Species: Rattus norvegicus (Norway rat)
C; Date: 19-Feb-1994 #sequence_revision 26-Jul-1996 #text_change 04-Mar-2000
C; Accession: 158370; S24780
C; Accession: 5.; Steffen, D.L.
Oncogene 8, 141-149, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Triticum aestivum (common wheat)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 29-Aug-1997
C;Accession: S27248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                      A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-18 <RES>
A:Cross-references: EMBL:215029; NID:956567; PIDN:CAA78748.1; PID:956568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 27; DB 2; Length 15;
Pred. No. 5.7e+02;
0; Mismatches 1; Indels
                                                                                 protein-tyrosine kinase (EC 2.7.1.112) lck - rat (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.3%; Score 28; DB 2; I
83.3%; Pred. No. 4.9e+02;
Live 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.5%;
80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-15 <LAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 5; Conserv
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7 SNPEDD 12
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Lottspeich, F.; Kadenbach,

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A. Accession: S72501
A. Molecule type: protein
A. Rocession: S72501
A. Molecule type: protein
A. Rocession: S72501
A. Molecule type: protein
A. Note: this protein was identified as biliverdin reductase; the identification is quarantee; M.D.; Polevoda, B.V.; Huang, T.J.; McCoubrey Jr., W.K.
Eur. J. Biochem. 235, 372-381, 1996
A. Fitle: Human biliverdin IX-alpha reductase is a zinc-metalloprotein. Characterizati
A. Reference number: S62622; MUID:96202961
A. Accession: S62623
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C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 01-Aug-1997
C;Accession: 800492
R;Makino, N.; Kimura, S.
Eur. J. Blochem. 173, 423-430, 1988
A;Title: Subunits of Panulirus japonicus hemocyanin. 1. Isolation and properties. A;Reference number: 800492; MUID:88196131
A;Accession: 800492
                                                                                                             protein kinase C inhibitor - human (fragment)
N:Alternate names: histidine triad nucleotide-binding protein
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S72501; S62623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
C;Accession: S78416
S;Goldschmidt-Reisin, S; Graack, H.R.
submitted to the Protein Sequence Database, February 1998
A;Reference number: S78411
                                                                                                                                                                                                                                                 R;Maines, M.D.; Trakshel, G.M.
Arch. Biochem. Biophys. 300, 320-326, 1993
A;Title: Purification and characterization of human biliverdin reductase.
A;Reference number: S29736; MUID:93143333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Note: the protein is designated as mitochondrial ribosomal protein L28 C;Keywords: mitochondrion; protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: protein kinase C inhibitor; histidine triad homology C;Keywords: homodimer; protein kinase inhibitor; zinc
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878416
ribosomal protein RL28, mitochondrial [validated] - rat (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.6e+03;
4; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.8%; Score 25; DB 2; I 62.5%; Pred. No. 1.5e+03; iive 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
649732
NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 20K chain - potato mitochondrion (fragment)
NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 20K chain; NADH-ubiquinone oxidoreductase 20K C; Species: mitochondrion Solanum tuberosum (potato)
C; Species: mitochondrion Solanum tuberosum (potato)
C; Species: mitochondrion Solanum tuberosum (potato)
C; Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 07-May-1999
C; Accession: 649732
R; Herz, U.; Schroeder, W.; Liddell, A.; Leaver, C.J.; Brennicke, A.; Grohmann, L.
J. Biol. Chem. 269, 2263-2269, 1994
A; Title: Purification of the NADH: ubiquinone oxidoreductase (complex I) of the respirato
A; Reference number: A49732; MUID:94124587
A; Accession: 649732
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-15 < HER>
C; Genetics:
A; Genetics:
A; Genetics:
A; Genome: mitochondrion
C; Keywords: electron transfer; hydrogen ion transport; mitochondrial inner membrane; mit
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C.Date: 13-0ct-1994 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995
C.Accession. A54651
A.Title: Purification from human cerebrospinal fluid of insulin-like growth factor bindi
A.Reference number: A54651; MUID: 93091816
A.Status: preliminary
A.Molecule type: procein
A.Residues: 1-18 < RGG>
A.Residues: 1-18 < RGG>
A.Residues: Lils < RGG>
A.Residues: Lils < RGG>
A.Residues: Note: sequence extracted from NCBI backbone (NCBIP:121074)
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                                                            an insect neurohormone, melanization and
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Pred. No. 1.1e+03;
2; Mismatches 1; Indels
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Pred. No. 1e+03;
4; Mismatches 3;
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Pred. No. 1.4e+03;
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R;Matsumoto, S.; Isogai, A.; Suzuki, A.
FEBS Lett. 189, 115-118, 1985
A;Title: N-terminal amino acid sequence of
A;Reference number: A23992; MUID:85285612
A;Reference roumber: Protein
A;Refocus: Protein
A;Residues: 1-16 < MAT>
C;Reywords: hormone
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1 DSFVPXEPSDEKALS 15
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Regul. Pept. 42(Suppl.1), S12, 1992
Regul. Pept. 100 of four novel tachykinins from frog (Rana catesbeiana) brain and inte
A; Reference number: A61033
A; Accession: D61033
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A; Residues: 1-11 <KAN>
R; Residues: 1-11 <KAN>
R; Rozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 177, 588-595, 1991
A;Title: Jobation of four novel tachykinins from frog (Rana catesbelana) brain and inte
A; Reference number: JE0426; MUID:91254337
A; Accession: JE0429
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R;Bricteux-Gregoire, S.; Schyns, R.; Florkin, M.; Emmens, M.; Welling, G.W.; Beintema, J
Biochim. Biophys. Acta 386, 244-255, 1975
A;Title: N-terminal amino acid sequence of trypsinogen from the lesser rorqual, Balaenog
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C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Rana catesbeiana (bullfrog)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000
C;Accession: D61033; JE0429
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A;Molecule type: protein
A;Residues: 1-8 <BRI>C;Keywords: hydrolase; protein digestion; serine proteinase; zymogen
F;1-8/Domain: activation peptide #status experimental <APT>
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C; Superfamily: unassigned animal peptides
C; Keywords: amidated carboxyl end; neuropeptide
F; 11/Modified site: amidated carboxyl end (Met) #status experimental
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Pred. No. 2.2e+05;
0; Mismatches 1; Indels
A;Molecule type: protein
A;Residues: 1-20 <MAK>
C;Superfamily: hemocyanin
C;Keywords: copper; hemolymph; hexamer; oxygen carrier
                                                                                                                                                              Score 24.5; DB 2;
Pred. No. 1.8e+03;
1; Mismatches 4;
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A;Reference number: A61328; MUID:75146765
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80.0%;
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36.8%;
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Best Local Similarity 36.84
Matches 7; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 50.0
Matches 4; Conservative
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2 PIDDD 6
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homo sapien
calliphora
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felis silve
pyrrhocoris
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canis famil
conus episc
conus penna
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glycine max
tachypleus
                                                                              February 21, 2002, 16:43:41; Search time 20.15 Seconds (Without alignments) 38.211 Million cell updates/sec
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thunnus obe
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conus ermin
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alteromonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               snuid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
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P80241
P80263
P22691
P22691
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P81071
P810688
P81667
P81683
P
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P28355
P18651
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P15986
P23684
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                  100059 seqs, 36664827 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TKNA_RANRI
TKYD_RANCA
TRYP_EELCA
UPA2_HUMAN
PRAIL_CALVO
UNO2_PINRS
UNO2_PINRS
UP51_UPEIN
CM51_UPEIN
CM51_UPEIN
                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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COXB_THUOB
RRPL_CHAV
NUO3_SOLTU
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CXA3_CONAL
A2M_OCTVU
CXA1_CONER
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MARI_ALTSP
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CXAB_CONPE
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ACT6_SOYBN
TAC1_TACGI

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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120
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Match Length DB
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Perfect score:
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                                                        OM protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Result
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P1825 tachypleus P82694 periplaneta P14215 limulus pol P14216 limulus pol P80704 comamonas t P14466 bison bonas P14467 bubalus bub P80410 palomena pr P23210 herpes simp P42993 cyprinus ca P42994 raja clavat	ALIGNMENTS  RT; 15 AA.  Hence update)  Lation update)  Lastropoda; Caenogastropoda;  Le; Conus.  Ly blocks alpha3 beta4 nicotinic  Liy blocks alpha3 beta4 nicotinic  Cotine-evoked norepinephrine release.";  ACT ON POSTSYNAPTIC MEMBRANES, THEY  LICHOLINE RECEPTORS (NACHR) AND THUS  BLOCKS MAMMALIAN NICOTINIC  FROSED OF ALPHA-3/BETA-4 SUBUNITS.  S; METHOD-ELECTROSPRAY.  Choline receptor inhibitor; Amidation;  LIDATION.  EEEBSFEC700155 CRC64;	1; Length 15; 1; Indels 0; Gaps 0; (EC 2.7.1.112) (P56-LCK) tebrata; Euteleostomi; Muridae; Murinae; Rattus.
1 TAC3_TACGI PH1_PERAM 1 PPM7_LIMPO 1 DHAB_COMTE 1 FIBB_BISBO 1 FIBB_BUSBO 1 FIBB_BUSBO 1 FIBB_BUSBO 1 FIBB_BUSBO 1 FIBB_BUSBO 1 FIBB_BUSBO 1 FIBB_BUSBO 1 FIBB_BUSBO 1 FIBB_BUSBO 1 RYJS_HAVIR 1 WYJS_HAVIR 1 WYJS_HAVIR 1 WYJS_HAVIR 1 WYJS_HAVIR 1 WYJS_HAVIR 1 WYJS_HAVIR 1 WYJS_HAVIR		8%; Score 31; DB 1%; Pred. No. 62; 2; Mismatches;
17.5 17.5 18.1 17.5 18.1 17.5 18.1 17.5 21.1 17.5 21.1 17.5 21.1 17.5 21.1 17.5 21.1 17.5 21.1 17.5 21.1 17.5 21.1 17.5 21.1 17.5 21.1 17.5 21.1 17.5 21.1 17.5 21.1 17.5 21.1 17.5 21.1 17.5 21.1 21.1 21.1 21.1 21.1 21.1 21.1 21	T 1  CONAL  CONAL  STARL STANDARD; P56640. 15-DEC-1998 (Rel. 37, La ALPHA-CONOTOXIN AUIB.  CONUS aulicus (Court con ENARYOCAS, MOLIB.  CONUS aulicus (Court con ENARYOCAS, MOLIB.  CONUS aulicus (Court con RELAR-CONOTOXIN AUIB.  SEQUENCE, AND SYNTHESIS. TISSUE-Venom; MEDLINE-9900332; Pubmed ALBADA CONOTOXIN AUIB se acetylcholine receptors J. Neurosci. 18 857.857.  INHIBIT THEM. THEM. THIS PACETYLCHOLINE RECEPT  ACETYLCHOLINE RECEPT INHIBIT THEM. THIS PACETYLCHOLINE RECEPT  ACETYLCHOLINE RECEPT  INHIBIT THEM. THIS PACETYLUS INHIBIT THEM.  INHIBIT THEM. THIS PACETYLUS SECTROMETRY: M  POSESSYBAPLIC DEUROCOXIN; VOROUM.  DISULFID  BOISULFID  AND SESSYBAPLIC DEUROCOXIN; VOROUM.  SEQUENCE IS AA; 1578	TY Match 25.8%;  t Local Similarity 57.1%;  ches 4; Conservative 2  1 CYRTNPE 7                 8 CFATNPD 14  AT  LCK_RAT  601621.  101-JUN-1994 (Rel. 29, Last se 30-MAY-2000 (Rel. 29, Last se 30-MAY-2000 (Rel. 39, Last an FROTO-ONGGENE TYROSINE-PROTE CKK  SAT  AT  LCK_RAT  FARGMENT).  CONTROBERT 101-101-101-101-101-101-101-101-101-101
34 21 35 21 36 21 37 21 39 21 40 . 21 42 20 44 20 45 20	RESULT 1  CXA2_CONAL  CXA2_CONAL  AC P56640;  DT 15-DEC-1998 (Rel. 37, Last seq DT 15-DEC-1998 (Rel. 37, Last seq DT 15-DEC-1998 (Rel. 37, Last seq DT 15-DEC-1998 (Rel. 37, Last ann DE ALPHA-CONOTOXIN AUIB.  OS CONUS aulicus (Court cone).  OS EUKATYOTOXIN MACHESOS;  ON CBI_TAXID=89437;  RN SEQUENCE, AND SYNTHESIS.  RR SEQUENCE, AND SYNTHESIS.  RR SEQUENCE, AND SYNTHESIS.  RR SEQUENCE, AND SYNTHESIS.  RR MEDLINE=9900392; Pubmed=97869  RA LUO S., Kulak J.M., Cartier G.  RR MEDLINE=9900392; Pubmed=97869  RA LUO S., Kulak J.M., Cartier G.  RR ALON S., Kulak J.M., Cartier G.  RR ALON S., Rulak J.M., Cartier G.  RR ALD S., Rulak J.M., ALPHA-CONOTOXINS  CC -1- MASS SPECTROMETRY: WW-1572  KW Venom.  FT DISULFID 3 15  FT DISULFID 3 15  FT DISULFID 3 15  RR BODL RES 15 AA; 1578 MW; 8	Query Match Best Local Similar Matches 4; Con  2y 1 CYRTNPE 7 1:    :   Db 8 CFATNPD 14 ECK_RAT 1D LCK_RAT 1D
	R N N N N N N N N N N N N N N N N N N N	N

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type of hydrogenase without iron-sulfur clusters in methanogenic
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Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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| 7 PTDDE
                                                                                                                                                                                                                                                                                      COXB_THUOB
P80974;
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P13179;
                                                                                                              NON_TER
SEQUENCE
                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                   InterPro; IPR00719; Euk_pkinase.
InterPro; IPR001245; Tyr_kin.
PROSITE; PS00107; PROTEIN KINASE_ATP; PARTIAL.
PROSITE; PS500117; PROTEIN_KINASE_DOM; PARTIAL.
PROSITE; PS50011; PROTEIN_KINASE_DOM; PARTIAL.
Proto-oncogene; Tyrosine-protein kinase; Phosphorylation; Transferase;
ATP-binding; Myristate; Palmitate; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                {Zirngibl C., van Dongen W., Schwoerer B., von Buenau R.,
R*chter M., Klein A., Thauer R.K.;
"H2-forming methylenetetrahydromethanopterin dehydrogenase, a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P32441;
01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
H(2)-FORMING NS,NIO-METHYLENETETRAHYDROMETHANOPTERIN DEHYDROGENASE
(EC 1.5.99.11) (H2-DEPENDENT METHYLENE-H4MPT DEHYDROGENASE)
                                                                                                                                                         -!- DISEASE: PROVIRAL INSERTION UPSTREAM OF THE LCK GENE CAUSES OVEREXPRESSION, LEADING TO THE DEVELOPMENT OF THYMIC LYMPHOMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
Methanothermobacter.
NCBI_TaxID=145261;
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Pred. No. 2e+02;
0; Mismatches 1; Indels
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PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            29B848FB8F0EB776 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 AA.
                                                                                                                                                                                           DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                           MEDLINE=93141260; PubMed=8423992;
Shin S., Steffen D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE#92394151; PubMed=1521540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.3%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 AA; 1914 MW;
                                                                                                                                                                                                                                                                                                           EMBL; Z15029; CAA78748.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methanobacterium wolfei.
                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||| || SNPEDD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 SNPTDD 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT).
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SEQUENCE
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archaea.";
Eur. J. Blochem. 208:511-520(1992).
Eur. J. Blochem. 208:511-520(1992)
-!- CATALYTIC ACTIVITY: N(5),N(10)-METHYLENETETRAHYDROMETHANOPTERIN +
REDUCED COENZYME F(420) = 5-METHYL-5,6,7,8-TETRAHYDROMETHANOPTERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thunnus obesus (Bigeye tuna).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;

Scombridae; Thunnus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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-1- FUNCTION: THIS PROFIEN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The subunit structure of cytochrome-c oxidase from tuna heart and
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0
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-!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VB FAMILY.
InterPro; IPR02124; COX5B.
PROSITE; PS00848; COX5B; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97454291; PubMed-9310366;
Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CYTOCHROME C OXIDASE POLYPEPTIDE VB (EC 1.9.3.1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                   Score 27; DB 1; Length 19;
Pred. No. 3.2e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.7%; Score 26; DB 1; Length 20; 80.0%; Pred. No. 4.8e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                       OC17E9D7BF1F97C9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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                                                                                                                 + COENZYME F(420).
-!- COFACTOR: ZINIC (BY SIMILARITY).
-!- PATHWAY: INVOLVED IN METHANOGENESIS.
-!- SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                      Oxidoreductase; Methanogenesis; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                22.5%;
80.0%;
                                                                                                                                                                                                                                                                                             19 AA; 1911 MW;
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01-AUG-1991
01-AUG-1991
30-MAY-2000
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P22691;
                                                                                                                                                                                                                                                                                                                                       TKNA_RANRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
TKND_RANCA
                                                                                                                                                                                                                                                                                                                         TKNA_RANRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DA PT PT
    SSSSSSE
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                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                 VICTORY 171:285-290(1989).

-!- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPPING, AS WELL AS METHYLATION OF CAPS, AND POLY(A) SYNTHESIS.

-!- SUBUNIT: THOUGHT TO FORM A TRANSCRIPTION COMPLEX WITH THE NUCLEOCAPSID (N) PROTEIN.

-!- SIMILARITY: WITH THE L PROTEIN.
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RNA POLYMERASE BETA SUBUNIT (EC 2.7.7.48) (LARGE STRUCTURAL PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
01-FEB-1994 (Rel. 28, Last annotation update)
NADH-UBIQUINONE OXIDOREDUCTASE 20 KDA SUBUNIT (EC 1.6.5.3)
Solanum tuberosum (Potato).
Solanum tuberosum (Potato).
Subaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Purification of the NADH:ubiquinone oxidoreductase (complex I) of
the respiratory chain from the inner mitochondrial membrane of
Solanum tuberosum.";
                                                                                                                                                                                                            "Structure and expression of the glycoprotein gene of Chandipura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CV. BINTJE; TISSUE-Tuber;
MEDLINE-94124587; Pubmed-8294484;
Herz U., Schroeder W., Liddell A., Leaver C.J., Brennicke A.,
                                                                                                                                                                                 Masters P.S., Bhella R.S., Butcher M., Patel B., Ghosh H.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.8%; Score 25; DB 1; Length 11;
80.0%; Pred. No. 3.4e+02;
ive 0; Mismatches 1; Indels
                                                                                  Chandipura virus (strain 1653514).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Rhabdoviridae; Vesiculovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase; RNA-directed RNA polymerase.

NON_TER 11 11
SEQUENCE 11 AA; 1189 MW; 0335D6E3AAB2D764 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol. Chem. 269:2263-2269(1994)
                                                                                                                                                                    PubMed=2741347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; J04350; AAA42917.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                       (L PROTEIN) (FRAGMENT
                                                                                                                                                                                                                                                                                                                                      PARAMYXOVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                     MEDLINE=89299473;
                                                                                                                            NCBI_TaxID=11273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 NPTDD 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            œ
                                                                                                                                                                                               Banerjee A.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grohmann L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUO3_SOLTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
NUO3_SOLTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
  qq
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TISSUE-Brain;
MEDLINE-9204543; PubMed=1658233;
O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;
O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;
"Ranakinin: a novel NKI tachykinin receptor agonist isolated with neurokinin B from the brain of the frog Rana ridibunda.";
J. Neurochem. 57:2086-2291(1991).
- I. FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
                        CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RANAKININ (SÜBSTANCE-P-RELATED PEPTIDE).
Rana ridibunda (Laughing frog) (Marsh frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
                                                                   -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
-!- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS.
-!- SUBCELLULAR LOCATION: MATRIX SIDE OF THE MITOCHONDRIAL INNER
FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
                                                                                                                                                                                                                                                                                                                                                                                             4;
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                                                                                                                                                                                                                                                                                                                                       Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 11;
                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3A2460CC59D40B07 CRC64;
                                                                                                                                                                                                                                                              8C80B69EFA87AAC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
InterPro; IPR003580; Protachykinin.
InterPro; IPR002040; Tachykinin.
                                                                                                                                                                                                                                                                                                                                       Score 25; DB 1; 1
Pred. No. 4.9e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.0%; Score 24; DB 1; 50.0%; Pred. No. 4.8e+02;
                                                                                                                                                                             PIR; G49732; G49732.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
NON_TER
SEQUENCE 15 AA; 1571 MW; 8C80B69EFA87AAC9 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tachykinin; Neuropeptide; Amidation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02202; Tachykinin; 1.
SMART; SM00203; TK; 1.
PROSITE; PS00267; TACHYKININ; 1.
                                                                                                                                                                                                                                                                                                                                       20.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD_RES 11 11 11
SEQUENCE 11 AA; 1352 MW;
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 50...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 SNATDETXLKDVSA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 19, (Rel. 19, (Rel. 39, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                             12 SNPTDD----DVSS 21
                                                   TO BE UBIQUINONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 RTNPEDIY 10
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1 KPNPERFY 8
                                                                                                                                                       MEMBRANE.
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TRYPSIN.

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rissue=Plasma;
                                                                                                          14 PTDDD 18
                                                                                                                       PIDDD 6
                                                                                                                                                                                           UPA2_HUMAN
P30088;
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   CHAIN
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
SEQUENCE
                                                             Query Match
                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                         Best Local
Matches
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UNSURE
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                                                                                                                                                                                  UPA2_HUMAN
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                                                                                                                                                                                                                                                   FUNCTION: TACHYKININS ÅRE ACTIVE PEPTIDES WHICH EXCITE NEURONS, EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
RANATACHYKININ D (RTK D).
Rana catesbelana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rania.
                                                                                 TISSUE-Intestine;
MEDLINE-91254337; PubMed-2043143;
Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
"Isolation of four novel tachykinins from frog (Rana catesbeiana)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Felis silvestris catus (Cat).
Wakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
NCBL_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steiner J.M., Medinger T.L., Williams D.A.;
"Purification and partial characterization of feline trypsin.";
Comp. Biochem. Physiol. 116B:87-93(1997).
-!- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-, LYS-.
-!- SUBCELLULAR LOCATION: EXTRACELLULAR.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPERS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                              ő
                                                                                                                                                                             TISSUE-Intestine;
MEDLINE-94023216; PubMed-8210506;
Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
"Four novel tachykinins in frog (Rana catesbelana) brain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Serine protease; Digestion; Pancreas; Zymogen. PROPEP, 1 8 ACTIVATION PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 24; DB 1; Length 11; Pred. No. 4.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                  3A34256C59D40B07 CRC64;
                                                                                                                                                                                                                                                                                                   -! - SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
                                                                                                                                            Biochem. Blophys. Res. Commun. 177:588-595(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
TRYPSIN PRECURSOR (EC 3.4.21.4) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                     PIR: JE0429; JE0429.
PIR: D61033; D61033.
Interpro: IPR002040; Tachykinin.
PRSSITE: PS00267; TACHYKININ; FALSE_NEG.
Tachykinin; Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50240; TYYPSIN DOM; PARTIAL. PROSITE; PS00134; TRYPSIN HIS; PARTIAL. (PROSITE; PS00135; TRYPSIN_SER; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Pancreas;
MEDLINE=97235546; PubMed=9080665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                       20.0%;
50.0%;
                                                                                                                                                                                                                                         Pept. 46:81-88(1993).
                                                                                                                                                                                                                                                                                                                                                                       MOD_RES 11 11
SEQUENCE 11 AA; 1350 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                        SEQUENCE, AND SYNTHESIS.
                                                                                                                                 brain and intestine.
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 RTNPEDIY 10
                                                NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : ||| |
1 KPNPERFY 8
                                                                                                                                                                                                                            intestine.";
Regul. Pept. '-!- FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRYP_FELCA P81071;
                                                                                                                                                                                                                                                                                        MUSCLES
                                                                                                                                                                   SEQUENCE.
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Calliphora.
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Plasma protein map: an update by microsequencing.";
Electrophoresis 13:707-714(1992).
-!- MISCELANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 4.4, ITS MW IS: 49 KDA.
SWISS-2DPAGE; P30088; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                            .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1993 (Rel. 25, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF PLASMA (SPOT 10) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Thoracic ganglion;
MEDLINE-2919611; Pubmed-1549595;
Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I., Rehfeld J.F., Thorpe A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 23; DB 1; Length 10;
Pred. No. 6.1e+02;
1; Mismatches 2; Indels
                                                                                                                 Length 16;
                                                                                                                                                            Indels
                                                A6D751BB58760A86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1079 MW; 51AC54AAB77775B7 CRC64;
                                                                                            Score 24; DB 1; Len
Pred. No. 7.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CALLIMIRFAMIDE 1.
Calliphora vomitoria (Blue blowfly).
                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93092937; PubMed=1459097;
                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1993 (Rel. 25, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.2%;
57.1%;
                                                                                                                 20.0%;
80.0%;
                                                1825 MW;
                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1993 (Rel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
10 AA;
9
16
16 AA;
                                                                                                                                     Similarity
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :| || |
SPPDDQV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 NPTDDDV 19
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Gaps

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Uperoleia inundata (Floodplain toadlet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
                           -!- INDUCTION: BY WATER-STRESS.
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.4, ITS MM IS: 43 KDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-skin secretion;
Bradford A.M., Raffery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
Adams G.W., Severini C.;
"Novel uperin peptides from the dorsal glands of the australian
floodpian toadlet Uperoleia inundata.";
Aust. J. Chem. 49:475-484(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.-!- MASS SPECTROMETRY: MW=1426; METHOD=FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conus aulicus (Court cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                         Score 23; DB 1; Length 13;
Pred. No. 8.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 23; DB 1; Length 13;
Pred. No. 8.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                     2; Indels
                                                                                   NON_CONS 7 8
NON_TER 13 13
SEQUENCE 13 AA: 1559 MW; 966B5A43EF94B411 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 AA; 1457 MW; 290CA148C384B5A7 CRC64;
                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
UPERIN 5.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                   13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 AA.
                                                                                                                                                                                     1; Mismatches
  proteins.";
Electrophoresis 20:1098-1108(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                                                                        19.2%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.2%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 80.0.
                                                                                                                                                                      Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE, AND SYNTHESIS. TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALPHA-CONOTOXIN AUIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=104953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=89437;
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                                                                                                                                                                                                                                           3 SAPTRDNV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amphibian skin.
SEQUENCE 13 A
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                                                                                                                                                                                                                                                                                                   UP51_UPEIN
ID UP51_UPEIN
AC P82036;
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                                                                                                                                                           Query Match
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Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
Frigerio J.-M., Plomion C.;
"Separation and characterization of needle and xylem maritime pine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus
                                                                                                                                                                                                                                                                                                                                                                                                 Phyllomedusa rohdei (Rohde's leaf frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
                        Proc. Natl. Acad. Scl. U.S.A. 89:2326-2330(1992).
                                                                                                                                                                                    ;
0
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0
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neuropeptides (designated calliFMRFamides) from the blowfly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UN02_PINPS STANDARD, PRT, 13 AA.
P81667;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF NEEDLES (N55) (FRAGMENTS).
                                                                                                                                         Score 23; DB 1; Length 12;
Pred. No. 7.5e+02;
Treat-hes 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 23; DB 1; Length 13; Pred. No. 8.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                               AMIDATION.
2DDDB316914AB5A7 CRC64;
                                                                                                                                                                                                                                                                                                                                         01-NOV-1986 (Rel. 03, Created)
01-NOV-1986 (Rel. 03, Last sequence update)
01-APR-1988 (Rel. 07, Last annotation update)
                                                                                                                                                                                                                                                                                                                 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Int. J. Pept. Protein Res. 27:175-182(1986).
PIR; A05174; A05174.
Amphibian skin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pinus pinaster (Maritime pine).
Eukaryota; Viridiplantae; Strep
                                                                                                                                                      19.2%;
42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.2%;
66.7%;
                                                                                Neuropeptide; Amidation.
MOD_RES 12 12
SEQUENCE 12 AA; 1390 MW;
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SEQUENCE 13 AA; 1646 MW;
                                                                                                                                        Query Match
Best Local Similarity 42.9,
                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
             Calliphora vomitoria.";
Proc. Natl. Acad. Sci. U
                                                                 PIR; E44787; E44787
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                     TRYPTOPHYLLIN-13
                                                                                                                                                                                                              11 PSNPTDD 17
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2 PNQPSDN 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Phyllomedusa
                                                                                                                                                                                                                                                                                                                TP13_PHYRO P04096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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UN02_PINPS
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Gaps

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Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D., Olivera B.M., McIntosh J.M.;
"Alpha-conotoxin AulB selectively blocks alpha3 beta4 nicotinic acetylcholine receptors and nicotine-evoked norepinephrine release.";
J. Neurosci. 18:8571-8579 (1998).
-I- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-4 SUBUNITS.
-I- MASS SPECTROMETRY: WM=1725.6; METHOD=ELECTROSPRAY.
--- MASS SPECTROMETRY: MM=1725.6; METHOD=ELECTROSPRAY.
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 42.9%; Pred. No. 1e+03;
Matches 3; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                           AMIDATION.
1E310FEB8FDC7001 CRC64;
                                                                                                                                                                                             8
16
16
1731 MW;
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3
16
16 AA;
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8 CFATNSD 14
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                                                                                                                                                                            Venom.
DISULFID
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MOD_RES
    δý
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Search completed: February 21, 2002, 16:52:20 Job time: 519 sec

## GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

February 21, 2002, 16:43:01 ; Search time 60.03 Seconds
(without alignments)
51.170 Million cell updates/sec

US-08-753-851-5 120 1 CYRTNPEDIYPSNPTDDDVSS 21 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

473505 seqs, 146272329 residues

Searched:

5819 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 21

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SPTREMBL\_17:\* Database :

1: sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fungi:\*
4: sp\_human:\*
5: sp\_invertebrate:\*
6: sp\_mammal:\*
7: sp\_mhc:\* sp\_organelle:\* sp\_phage:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_plant:\*
sp\_rodent:\*
sp\_virus:\*
sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\*

## SUMMARIES

			Description	09i7f8 drosophila	Q9qv20 mus sp. per	016218 homo sapien	O9rlp2 neisseria q	018764 sus scrofa	Q28079 bos taurus		038573 bacteriopha	P70650 mus musculu	Q9xnq3 boophilus m	O9twi8 ceratitis c	Q9twi5 ceratitis c	Q9qux7 rattus sp.	Q9uc52 homo sapien	Q9uc15 homo sapien	Q9qvil rattus sp.	O9edr1 mus musculu	Q9r896 chlamydia t	Q9utt6 schizosacch
CHIMMINOC			ID	Q917F8	090020	016218	Q9RLP2	018764	028079	P82573	038573	P70650	69XNQ3	Q9TWI8	Q9TWI5	Q9QUX7	Q9UC52	Q9UCL5	09QVI1	Q9EQR1	Q9R896	Q9UTT6
			DB	. 2	11	4	7	9	9	7	δ	11	œ	Ŋ	'n	11	4	4	11	11	7	3
			Match Length DB	13	19	21	20	21	20	18	18	18	19	20	20	20	16	18	18	18	20	21
	æ	Query	Match	26.7	26.2	25.0	23.3	23.3	22.5	21.7	21.7	21.7	21.7	21.7	21.7	21.7	20.8	20.8	20.8	20.8	20.8	20.8
			Score	32	31.5	30	28	28	27	26	26	26	26	26	26	26	25	25	25	25	25	25
		Result	No.	-	7	m	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19

Q9ud48 homo sapien Q90609 gallus gall P82310 panulirus j Q9tr87 bos taurus Q9ct94 mus musculu Q40562 nicotiana t Q40563 nicotiana t Q9npq7 homo sapien Q40565 macropus ro P70649 mus musculu Q9uck0 homo sapien Q9uck0 homo sapien Q9uck0 homo sapien Q9tk0 calanum tub Q9tk1 rattus norv P82619 periplaneta Q9tk1 lambia anta Q9tk0 lambia anta Q9r565 chromatium Q9r569 haemophilus Q9r549 sus scrofa Q9uman homo sapien Q9r549 sus scrofa Q9uman homo sapien Q9r549 sus scrofa Q9uman homo sapien Q9r549 mus scrofa	Q92115 rattus sp. O50180 pseudomonas P82262 aspergillus
21 4 Q9UD48 21 13 Q90609 20 5 P82310 20 6 Q9TR87 12 11 Q9CT94 15 10 Q40563 16 4 Q9NPQ7 18 6 Q4665 18 10 Q9SR0 20 10 Q9SR0 21 11 Q9R1H1 12 5 P82619 13 8 Q9TKG6 15 1 Q9WM1 15 2 Q9R5D5 16 2 Q9R5D5 16 2 Q9R5D5 17 13 Q9UMN3 17 13 Q9UNN3 19 6 Q9TRP4	11 2 3
225 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	19. 19.
01000000000000000000000000000000000000	444 445 5

## ALIGNMENTS

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Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN'1998 (TrEMBLrel. 05, Created)
01-JAN'1998 (TrEMBLrel. 05, Last sequence update)
01-ON-1998 (TrEMBLrel. 06, Last annotation update)
NEURON-1998 (TREMBLR) 08, Last annotation update)
NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR, BETA 4 SUBUNIT (FRAGMENT).
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                             Eukaryota; Metázoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stein D.C., Gunn J.S.; "Use of a non-selective tansformation technique to construct a multiple restriction-modification deficient mutant of Neisseria
                                                                                                                                                                                                                                                                              .;
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                                                                            Reale M.A., Hu G., Zafar A.I., Getzenberg R.H., Levine S.M.,
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 28; DB 2; Length 20;
Pred. No. 1.3e+03;
1; Mismatches 7; Indels
                                                                                                                                                                                                                                              Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases. EMBL; U42459; AAD56589.1; -. NON TER SEQUENCE 20 AA: 2245 MW; 4C893C704879FFD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
PUTATIVE CYSTEINEYL T-RNA SYNTHETASE (FRAGMENT).
                                                                                                                                                                                                                                              Score 30; DB 4; Le
Pred. No. 6.8e+02;
; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                  20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                              SEQUENCE FROM N.A.
MEDLINE=94320088; Pubmed=8044801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.3%;
                                                                                                                                                                                                                                              25.0%;
62.5%;
                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                           4 TNPEDIYP 11
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                                                                                                                                                                                                                                                                                                                           |:| | ||
TDPVDYYP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-WR302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gonorrhoeae.
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Q9RLP2;
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Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Sanders R.D.C., Scheeler F., Shen H.,
Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
Sprakas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Pe J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stark A., Meijer J.; "Purification and characterization of multifunctional enzyme from mouse liver peroxisomes."; Comp. Biochem. Physiol. 108B:471-480(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryata; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                        26.7%; Score 32; DB 5; Length 13; 100.0%; Pred. No. 2.1e+02; rive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                              13 AA; 1554 MW; 5D52855A93735EB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                016218 PRELIMINARY; PRT; 21 AA. 016218; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-2096 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) DELETED IN COLORECTAL CANCER PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 AA.
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                                                                                                                                                                                                            EMBL; AE003818; AAG22274.1; -. FlyBase; FBgn0033836; CG18278.
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                        Query Match 26.7
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Best Local Similarity
Matches 8; Conserv
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SEQUENCE
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Lammen I.;

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Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,
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MEDIJNR=96207403; PubMed=8615017;
Groeneveld H., Oudot F., van Duin J.V.;
"RNA phage KUI has an insertion of 18 nucleotides in the start codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                  "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Pred. No. 2.2e+03;
                                                                                                                                                                                                                                                                                    Score 26; DB 2; Length 18;
Pred. No. 2.2e+03;
1; Mismatches 0; Indels
                                                                                -i- CATALYTIC ACTIVITY: ATP + URIDINE = ADP + UMP.
-i- CATALYTIC ACTIVITY: ATP + CYTIDINE = ADP + CMP.
-i- PATHWAY: PYRIMIDINE SALVAGE PATHWAY.
-i- MASS SPECTROMETRY: MW=24334.01; METHOD=ELECTROSPRAY.
-i- SIMILARITY: BELONGS TO THE URIDINE KINASE FAMILY.
Transferase; Kinase.
NON_TER
                                                                                                                                                                                                                                       BA532B372051EDC6 CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
SYNTAXIN 3 ISOFORM D-2 (FRAGMENT).
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Last annotation update)
                                                                   Submitted (MAY-2000) to the SWISS-PROT data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 AA.
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COAT GENE.
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1991 MW;
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55.6%;
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of its lysis gene.";
Virology 218:141-147(1996).
EMBL; S81763; AAD14371.1; -
HSSP; P07234; lUNA.
                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity هه..
معرف 4; Conservative
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Best Local Similarity
5; Conserv
                                                                                                                                                                                                                                     18 AA;
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                    VanBogelen R.A.;
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5 TDDDI 9
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SEQUENCE
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SEQUENCE
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P70650;
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Q38573
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                        "Genetic mapping of CHRNA3 and CHRNB4 to pig chromosome 7 extends the syntenic conservation with human chromosome 15 and mouse chromosome 9.";
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01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) (FRAGMENTS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID-9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE-LACTATING MAMMARY GLAND;
MEDLINE-96351712; PubMed-8747930;
Spicer A.P., Duhig T., Chilton B.S., Gendler S.J.;
"Analysis of mammalian MUCl genes reveals potential functionally important domains.";
Mamm. Genome 6:885-888(1995).
EMBL; L41553; AAB48100.1; -.
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Pred. No. 1.3e+03;
1; Mismatches 7; Indels
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Pred. No. 1.8e+03;
1; Mismatches 7; Indels
                                                                                                                                                     21 AA; 2196 MW; EA98A064013C0FFD CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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MEDLINE=98161940; PubMed=9501320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE, AND MASS SPECTROMETRY.
                                                                                 Mamm. Genome 9:263-264(1998).
EMBL; AF007797; AAC13376.1;
                                                                                                                                                                                                      23.3%;
38.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.5%;
42.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 AA; 2055 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 42.9
Matches 6; Conservative
                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Best Local Similarity
Matches 5; Conserv
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Query Match

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STRAIN-JRS4;

P82573; P82573

RESULT
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AC P88
AC P87
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MAJOR CUTICULAR PROTEIN (FRAGMENT).

Ceratitis capitata (Mediterranean fruit fly).

Ceratitis capitata (Mediterranean fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Tephritoidea; Tephritidae; Ceratitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              o. mai-2000 (TrEMBLrel. 13, Created)
Ol-MAY-2000 (TrEMBLrel. 14, Last sequence update)
Ol-JUN-2000 (TrEMBLrel. 14, Last annotation update)
MAJOR CUTICULAR PROTEIN (FRAGMENT)
Caratitis capitata (Mediterranean fruit fly).
Bukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Mooptera; Endopterryqta; Diptera; Brachycera; Muscomorpha;
Tephritoidea; Tephritidae; Ceratitis.
                                                                                                                                                                                                                                                                                                                                                                               Tsiliras A., Koromantzou E., Allen G., Dimitriadis G.; "Partial N-terminal sequences of larval cuticular proteins from the dipteran Ceratitis capitata."; Hereditas 122:79-83(1995). SEQUENCE 20 AA: 2408 MW; 2BC25E2F9EC15A80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95279142; PubMed=7759285;
Tsiliras A., Koromantzou E., Allen G., Dimitriadis G.;
"Partial N-terminal sequences of larval cuticular proteins from the
dipteran Ceratitis capitata.";
Hereditas 122:79-83(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 20;
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                                                                                                                                         01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
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(TrEMBLrel. 13, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95279142; PubMed=7759285;
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66.78;
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                      PRELIMINARY;
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 4; Conserv
      2 YSTNHKDI 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 NPEDIY 10
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01-MAY-2000
                                                                                                                                                                                                                                                                                                                                             SEQUENCE.
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                                                                                                                           O9TWI8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            090UX7;
                                                                                                    Q9TWI8
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                                                                RESULT 11
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                                                                                  Q9TWI8
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"The novel mitochondrial gene arrangement of the cattle tick,

"The novel mitochondrial gene arrangement of the cattle tick,

"The novel mitochondrial gene arrangement of the cattle tick,

Boophilus microplus: fivefold tandem repetition of a coding region.";

MOL. Biol. Evol. 16:732-74((1999).

-I- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY

CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-

3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE

CATALYTIC SUBUNIT OF THE ENZYME COMPLEX. COI IS THE

CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER FORMED BY HEME A3

AND COPPER B (BY SIMILARITY).

-I- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4

FERRICYTOCHROME C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -:- COPACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
-:- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
-:- SUBCELLOIAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
EMBL: AF110613; AAD28396.1; --
InterPro; IPR000883; COX1.
                                                                                                                                                                                                                                                                                                                      Gaps
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Parasitiformes; Ixodida; Ixodidae; Boophilus.
NCBI_TaxID=6941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
                                                                                              01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
                                                                                                                                                                                                                                                                                Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 26; DB 8; Length 19;
Pred. No. 2.4e+03;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                   18 AA; 2043 MW; 289FBCA184495155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C58C9C41FCAB0FE0 CRC64;
                                                                                                                                                                                                                                                                            Score 26; DB 11;
Pred. No. 2.2e+03;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=N;
MEDLINE=99297341; PubMed=10368952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boophilus microplus (Cattle tick).
                                                                              MEDLINE=95321968; PubMed=7598732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Respiratory chain; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.78;
62.58;
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55.6%;
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Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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SEQUENCE 19 AA;
                                                        TISSUE-FOREBRAIN;
                                                                                                                                                                                                                                                                                                                                                         PEDIYPSNP 14
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                               1 PEPKLPRNP 9
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09XN03; O9XNQ3 RESULT 10

09XNQ3

Matches

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OX RN RC RX RX RX RX BL BL SQ SQ SQ

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                                                  Rattus sp.
Bukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID-10118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Roghani M., Segovia B., Whitechurch O., Binoux M.;
"Purification from human cerebrospinal fluid of insulin-like growth
                                                                                                                                                                                                                          Satch T., Hosokawa M.; "Molecular aspects of carboxylesterase isoforms in comparison with other esterases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96170127; PubMed-8597091;
Satoh T., Hosokawa M.;
"Molecular aspects of carboxylesterase isoforms in comparison with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY 2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
11-SULIN-LIKE GROWTH FACTOR BINDING PROTEIN 22 KDA FORM (FRAGMENT).
11-MOULN-LIKE GROWTH FACTOR BINDING PROTEIN 22 KDA FORM (FRAGMENT).
11-MOULN-LIKE GROWTH FACTOR BINDING PROTEIN 22 KDA FORM (FRAGMENT).
11-MOULN-LIKE GROWTH FACTOR GROWTH FACTOR BINDING PROTEIN 22 KDA FORM (FRAGMENT).
11-MOULN-LIKE GROWTH FACTOR GROWTH FACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
CARBOXYLESTBRASE ISOZYME (FRAGMENT).
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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Pred. No. 2.8e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toxicol. Lett. 82:439-445(1995).
SEQUENCE 16 AA; 1599 MW; SDA6286D3C6BFFED CRC64;
                                                                                                                                                                                                                                                                                                                            2133 MW; 435160FFA80E086D CRC64;
01-MAY-2000 (TrEMBLrel. 13, Last annotation update) CARBOXYLESTERASE ISO2YME (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                           Score 26; DB 11; Le
Pred. No. 2.5e+03;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                  MEDLINE=96170127; PubMed=8597091;
                                                                                                                                                                                                                                                                                                       Toxicol. Lett. 82:439-445(1995)
SEQUENCE 20 AA; 2133 MW; 43
                                                                                                                                                                                                                                                                                                                                                                                                             21.7%;
80.0%;
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62.5%;
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Best Local Similarity 80.0.
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Best Local Similarity 62.5
Matches 5; Conservative
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| YPSSP 5
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Q9UC52
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RT factor binding proteins (IGFBPs). Isolation of IGFBP-2, an altered RT form of IGFBP-3 and a new IGFBP species.";

RL Growth Regul. 1:125-130(1991).

SQ SEQUENCE 18 AA; 1948 MW; AC3F4170E95081E3 CRC64;

Query Match

Query Match

20.8%; Score 25; DB 4; Length 18;

Best Local Similarity 26.7%; Pred. No. 3.1e+03;

Matches 4; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 7 EDIYPSNPTDDDVSS 21

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Db 1 DSFVPXEPSDEKALS 15

Search completed: February 21, 2002, 16:51:54

Job time: 533 sec
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Tue Feb 26 05:52:42 2002

4.

## GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

- protein search, using sw model OM protein

February 21, 2002, 16:39:06; Search time 64.88 Seconds Run on:

(without alignments)
23.976 Million cell updates/sec

US-08-753-851-5

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 522463 seqs, 74073290 residues Searched:

206698

Minimum DB seq length: 0 Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A\_Geneseq\_1101:\*

/SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:\*
/SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:\*
/SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:\*
/SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:\*
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/SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:\*
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/SIDS8/gcgdata/geneseg/genesegp/AA1989.DAT: /SIDS8/gcgdata/geneseg/genesegp/AA1990.DAT:

/SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:

/SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA1993.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA1994.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:\* /SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT:

/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:\* /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

					CHANGE	
Recult		8 0.00rg				
No.	Score	Match	Watch Length DB	DB	ID	Description
: :	120	!	21	15	AAR53477	CD44 peptide CD44-
7	36.5		21	19	AAW42092	BS106 synthetic po
e	36.5	30.4	21	20	AAY13470	BS106 polypeptide
4	36		16	18	AAW14606	Human antithrombin
5	35.5	29.6	16	20	AAY43350	GTF antiqenic epit
9	33	27.5	7	19	AAW54457	Human native angio
7	33	27.5	80	19	AAW54458	Human native angio
80	33	27.5	10	21	AAB06281	proSKI-1 putative
6	33	27.5	14	21	AAB08529	Amino acid sequenc
10	33	27.5	18	20	AAY05230	Human Stat6 antige
11	33	27.5	20	22	AAG64195	Protein sequence 2

	12	33	27.5	20	22	AAB99270 AAW34298	Peptide sequence Kringle 5 peptide
5 32 26.7 11 22 AAB92094 32 26.7 11 22 AAB92093 33 26.7 12 22 AAB92093 34 26.7 12 22 AAB92093 35 26.7 12 22 AAB92693 36 26.7 12 22 AAB96564 37 26.7 16 11 AAV17924 38 26.7 16 11 AAV17924 39 26.7 16 19 AAW77101 31 25.8 10 21 AAY90798 31 25.8 10 22 AAW99297 31 25.8 10 22 AAW99297 31 25.8 10 22 AAW99297 31 25.8 110 22 AAW99494 31 25.8 13 22 AAW86060 31 25.8 13 22 AAW86092 31 25.8 13 22 AAW89494 31 25.8 13 22 AAW86685 31 25.8 20 22 AAW858693 31 25.8 20 22 AAB86092	14	35	26.7	11	21	AAB01899	
5 32 26.7 11 22 AAB36569 3 2 26.7 12 22 AAB32089 3 2 26.7 12 22 AAB36564 1 2 2 AAB36564 1 3 2 26.7 12 22 AAB36568 1 3 2 26.7 16 11 AAR77924 3 2 26.7 16 11 AAR77924 3 2 26.7 16 19 AAW37101 5 3 2 26.7 16 19 AAW37101 5 3 2 26.7 16 19 AAW37101 5 3 2 26.7 16 19 AAW37101 6 3 2 26.7 16 20 AAW37105 6 3 2 26.7 16 19 AAW37105 7 3 2 26.7 19 18 AAW37105 8 3 1 25.8 10 22 AAW39297 9 3 1 25.8 10 22 AAW39297 1 25.8 10 22 AAW3960 1 25.8 13 22 AAW31006 1 25.8 13 22 AAW39494 1 25.8 13 22 AAW39159 1 25.8 13 22 AAW39159 1 25.8 15 20 AAW39159 1 25.8 20 19 AAW365356 2 2 AAB57671 2 3 1 25.8 20 22 AAB57661	15	32	26.7	11	22	AAB92094	Laminin fragment
7 32 26.7 12 22 AAB92089 32 26.7 12 22 AAB92089 32 26.7 12 22 AAB95089 13 2 26.7 12 22 AAB36568 13 2 26.7 16 11 AAR717924 32 26.7 16 11 AAR777924 32 26.7 16 19 AAW37101 4 32 26.7 16 19 AAW37101 5 32 26.7 16 21 AAW37101 5 32 26.7 16 21 AAW371054 31 25.8 10 22 AAW309237 5 31 25.8 10 22 AAW309237 6 31 25.8 10 22 AAW309237 6 31 25.8 13 22 AAB86092 6 31 25.8 13 22 AAB86092 6 31 25.8 13 22 AAB86092 7 31 25.8 13 22 AAB86092 8 31 25.8 20 22 AAB95889 9 31 25.8 20 22 AAB55809 9 31 25.8 20 22 AAB55809	16	32	26.7	11	22	AAB36569	Mammalian kringle
8 32 26.7 12 22 AAB92093 32 26.7 12 22 AAB92093 1 32 26.7 12 22 AAB956564 3 2 26.7 16 11 AAV17924 3 2 26.7 16 11 AAV17924 3 2 26.7 16 18 AAW97101 5 32 26.7 16 20 AAW97101 5 32 26.7 16 21 AAW97101 8 31 25.8 10 22 AAW9237 9 31 25.8 10 22 AAW9237 1 25.8 10 22 AAW9237 9 31 25.8 10 22 AAW9237 1 25.8 10 22 AAW99237 1 25.8 12 21 AAY53086 1 25.8 13 22 AAW96060 1 31 25.8 13 22 AAW86060 1 31 25.8 13 22 AAW86060 1 25.8 13 22 AAW86060 1 31 25.8 13 22 AAW86092 1 25.8 13 22 AAW86092 1 25.8 13 22 AAW86083 1 25.8 13 22 AAW86083 1 25.8 13 22 AAW86083 1 25.8 17 20 AAW89159 2 31 25.8 20 12 AAW86883 3 3 2 26.7 18 20 22 AAB85809	17	32	26.7	13	22	AAB92089 .	
32 26.7 12 22 AAB36564 32 26.7 12 22 AAB36564 32 26.7 16 11 AAY17924 33 26.7 16 11 AAY17924 33 26.7 16 11 AAY17924 32 26.7 16 19 AAW37101 32 26.7 16 19 AAW37101 31 25.8 10 21 AAY4586 31 25.8 10 22 AAW3376 31 25.8 10 22 AAW3377 31 25.8 10 22 AAW3927 31 25.8 11 22 AAW3927 31 25.8 12 21 AAY33086 31 25.8 13 22 AAW39494 31 25.8 13 22 AAW39494 31 25.8 13 22 AAW39159 31 25.8 17 20 AAW39159 31 25.8 20 19 AAW36585 31 25.8 20 22 AAW365895 31 25.8 20 22 AAW365895 31 25.8 20 22 AAW365895	18	32	26.7	12	22	AAB92093	Laminin fragment 8
12 2 AAB15668  13 2 26.7 12 22 AAB36568  13 2 26.7 16 11 AAR(77924  13 2 26.7 16 19 AAR(77924  13 2 26.7 16 19 AAR(77924  13 2 26.7 16 20 AAR(70798  13 2 26.7 16 21 AAR(79101  13 2 26.7 19 18 AAR(731054  13 2 2 8 10 22 AAR(731054  13 2 2 8 10 22 AAR(7310566  13 2 2 8 10 22 AAR(73105666000000000000000000000000000000000	19	32	26.7	12	22	AAB36564	Mammalian kringle
1 32 26.7 16 11 AAN17924 32 26.7 16 11 AAN17924 32 26.7 16 11 AAN97101 5 32 26.7 16 19 AAN97101 5 32 26.7 16 21 AAN97101 6 32 26.7 16 21 AAN94586 7 12 5.8 10 21 AAN9376 9 31 25.8 10 22 AAN9237 1 25.8 10 22 AAN9237 1 25.8 10 22 AAN9237 1 25.8 10 22 AAN93286 3 1 25.8 13 22 AAN86092 4 31 25.8 13 22 AAN86092 6 31 25.8 13 22 AAN86092 6 31 25.8 13 22 AAN86092 9 31 25.8 13 22 AAN86092 1 25.8 13 22 AAN89159 1 25.8 17 20 AAN89159 1 25.8 20 22 AAN85685 1 25.8 20 22 AAN86585	20	32	26.7	12	22	AAB36568	Mammalian kringle
2 32 26.7 16 11 AARO7527 3 2 26.7 16 18 AAW09992 3 2 26.7 16 20 AAV07101 5 32 26.7 16 21 AAV94586 3 2 26.7 16 21 AAV94586 3 1 25.8 10 22 AAW3376 3 1 25.8 10 22 AAW0327 2 3 1 25.8 10 22 AAW03297 3 1 25.8 10 22 AAW03297 4 31 25.8 10 22 AAW03297 5 8 12 2 AAW09297 5 8 13 22 AAW09494 5 3 1 25.8 13 22 AAB66060 6 3 1 25.8 13 22 AAW09494 6 3 1 25.8 15 20 AAW09494 7 3 1 25.8 17 20 AAW094594 8 3 1 25.8 20 19 AAW09585 8 2 2 2 AAB5809 8 3 2 5.8 20 22 AAB5809 8 3 2 5.8 20 22 AAB5809	21	32	26.7	16	11	AAY17924	ic
3 3 2 26.7 16 18 AAW09992 3 2 26.7 16 20 AAW07101 5 3 2 26.7 16 20 AAW37101 7 3 2 26.7 19 18 AAW33054 9 3 1 25.8 10 21 AAW33057 0 3 1 25.8 10 22 AAW09237 1 25.8 10 22 AAW09237 2 3 1 25.8 10 22 AAW09237 3 1 25.8 10 22 AAW09237 4 3 1 25.8 13 21 AAW53086 5 3 1 25.8 13 22 AAW86060 6 3 1 25.8 13 22 AAW86092 6 3 1 25.8 13 22 AAW86092 1 25.8 15 22 AAW89159 1 25.8 17 20 AAW89159 2 3 1 25.8 17 20 AAW89159 3 1 25.8 20 19 4 AAR568585 3 2 2 8 20 22 AAW568585 3 3 2 2.8 20 22 AAW568585 3 3 2 2.8 20 22 AAW568585	22	32	26.7	16	11	AAR07527	ebi
4 32 26.7 16 19 AAN37101 5 32 26.7 16 20 AAY00798 32 26.7 16 21 AAY94586 6 31 25.8 10 21 AAV3376 9 31 25.8 10 22 AAM09237 1 25.8 10 22 AAM09237 1 25.8 10 22 AAM09237 3 1 25.8 10 22 AAM09237 4 31 25.8 10 22 AAM0924 5 31 25.8 13 22 AAB86060 6 31 25.8 13 22 AAB86092 6 31 25.8 13 22 AAB86092 6 31 25.8 13 22 AAB86092 6 31 25.8 17 20 AAW89494 9 31 25.8 17 20 AAW89494 1 25.8 20 19 AAW56585 2 2 AAB58093 3 1 25.8 20 22 AAB58093 3 1 25.8 20 22 AAB58093 3 25.8 20 22 AAB58093	23	32	26.7	16	18	AAW09992	HTLV-1 envelope pr
5 32 26.7 16 20 AAVO0798 5 32 26.7 16 21 AAV94586 8 31 25.8 10 18 AAW3376 9 31 25.8 10 22 AAW92377 1 25.8 10 22 AAW9237 2 31 25.8 10 22 AAW9297 3 1 25.8 10 22 AAW9297 3 1 25.8 10 22 AAW9397 5 31 25.8 13 21 AAF93086 6 31 25.8 13 21 AAF93086 6 31 25.8 13 22 AAB86060 7 31 25.8 13 22 AAB86060 8 31 25.8 15 20 AAW89494 9 31 25.8 15 20 AAW89159 9 31 25.8 17 20 AAW89159 1 25.8 20 12 AAF9586 9 31 25.8 20 22 AAB5809 1 25.8 20 22 AAB5809 1 25.8 20 22 AAB5809	24	32	26.7	16	19	AAW37101	envelope
5 32 26.7 16 21 AAV94586 31 25.8 10 21 AAV93305 31 25.8 10 22 AAM9337 31 25.8 10 22 AAM9237 31 25.8 10 22 AAM9237 31 25.8 10 22 AAM9237 31 25.8 10 22 AAM13407 31 25.8 13 21 AAY53086 31 25.8 13 21 AAY53086 31 25.8 13 22 AAB66060 31 25.8 13 22 AAB66092 4 31 25.8 15 22 AAB66092 6 31 25.8 15 22 AAB66092 1 25.8 17 20 AAW99159 3 3 25.8 17 20 AAW99159 3 3 25.8 20 19 4 AAR5685 3 3 25.8 20 22 AAB5809	25	32	26.7	16	20	AAY00798	HTLV1 envelope per
32 26.7 19 18 AAW31054 31 25.8 10 21 AAW3376 31 25.8 10 22 AAW3376 31 25.8 10 22 AAW3237 31 25.8 10 22 AAW3237 31 25.8 10 22 AAW32087 4 31 25.8 10 22 AAW3407 5 31 25.8 12 21 AAW3407 6 31 25.8 13 22 AAW36060 7 31 25.8 13 22 AAW36060 7 31 25.8 13 22 AAW36060 8 31 25.8 15 22 AAW36060 9 31 25.8 17 20 AAW36159 9 31 25.8 20 22 AAW36585 9 31 25.8 20 22 AAW56895	. 26	32	26.7	16	21	AAY94586	Two tandem copies
31 25.8 10 18 AAM43376 31 25.8 10 21 AAM93376 31 25.8 10 22 AAM9297 2 31 25.8 10 22 AAM9297 3 125.8 10 22 AAM13407 3 1 25.8 10 22 AAM13407 4 31 25.8 12 21 AAM13407 5 31 25.8 13 21 AAB6666 5 31 25.8 13 22 AAB6660 6 31 25.8 13 22 AAB6660 7 31 25.8 15 20 AAM99194 9 31 25.8 15 20 AAM99159 1 25.8 17 20 AAM99159 2 31 25.8 20 19 AAM56585 3 31 25.8 20 22 AAB5809 3 31 25.8 20 22 AAB5809	27	32	26.7	19	18	AAW31054	Mugwort pollen all
9 31 25.8 10 21 AAV53097 13 25.8 10 22 AAM09237 2 31 25.8 10 22 AAM09237 3 1 25.8 10 22 AAM13407 3 1 25.8 10 22 AAM13407 5 31 25.8 13 21 AAV53086 5 31 25.8 13 21 AAV53086 6 31 25.8 13 22 AAB86060 7 31 25.8 15 20 AAW89494 9 31 25.8 15 20 AAW89159 1 25.8 17 20 AAW89159 2 3 25.8 20 19 AAW56858 3 3 25.8 20 22 AAB55809 3 3 25.8 20 22 AAB55809 3 3 25.8 20 22 AAB57081	28	31		10	18	AAW43376	Immunogenic HLA-A
0 31 25.8 10 22 AAM09237 2 31 25.8 10 22 AAM09297 3 31 25.8 10 22 AAM13407 4 31 25.8 10 22 AAM13407 4 31 25.8 12 21 AAM53086 5 31 25.8 13 21 AAM53086 6 31 25.8 13 22 AAB86092 7 31 25.8 13 22 AAB86092 8 31 25.8 15 22 AAM89159 9 31 25.8 15 20 AAM89159 1 25.8 20 19 AAM55809 3 3 25.8 20 22 AAB55809 4 31 25.8 20 22 AAB55809 5 31 25.8 20 22 AAB55809	59	31		10	21	AAY53097	Anticoagulant pept
1 31 25.8 10 22 AAM09297 2 31 25.8 10 22 AAM10474 3 11 25.8 10 22 AAM10474 3 11 25.8 12 21 AAY53086 5 31 25.8 13 22 AAB86060 6 31 25.8 13 22 AAB86060 8 31 25.8 13 22 AAB86092 9 31 25.8 15 20 AAW89199 1 25.8 15 20 AAW89159 1 25.8 19 14 AAR4356 2 2 2 AAB55809 3 1 25.8 20 22 AAB5809 4 31 25.8 20 22 AAB5809 5 20 22 AAB57671	30	31		10	22	AAM09237	HLA-Al decamer #10
2 31 25.8 10 22 AAM10474 31 25.8 10 22 AAM13407 5 31 25.8 12 21 AAY53086 5 31 25.8 13 22 AAB86060 6 31 25.8 13 22 AAB86060 8 13 25.8 15 22 AAB86092 8 31 25.8 15 20 AAW89494 9 31 25.8 15 20 AAW89159 1 25.8 17 20 AAW89159 2 31 25.8 20 19 AAW56585 3 31 25.8 20 22 AAB55809 4 31 25.8 20 22 AAB57671 5 31 25.8 20 22 AAB57671	31	31		10	22	AAM09297	HLA-B *0702 decame
3 31 25.8 10 22 AAM3407 4 31 25.8 12 21 AAY53086 5 31 25.8 13 22 AAB6000 7 31 25.8 13 22 AAB6000 8 31 25.8 13 22 AAB6009 9 31 25.8 15 22 AAG8614 9 31 25.8 15 22 AAG88514 1 31 25.8 17 20 AAW89159 2 3 25.8 20 19 AAW56585 3 31 25.8 20 22 AAB55809 4 31 25.8 20 22 AAB57601 5 32 28 20 22 AAB57601	32	31		10	22	AAM10474	HLA-A *0201 decame
4 31 25.8 12 21 AAY 3086 5 31 25.8 13 22 AAB86060 7 31 25.8 13 22 AAB86092 8 31 25.8 15 20 AAW 8949 9 31 25.8 15 20 AAW 8945 1 25.8 15 20 AAW 8915 1 31 25.8 19 14 AAW 3556 2 31 25.8 20 19 AAW 35695 3 31 25.8 20 19 AAW 35695 3 31 25.8 20 22 AAB 55809 4 31 25.8 20 22 AAB 55809 5 32 22 AAB 5609	33	31		10	22	AAM13407	HLA-A26 decamer #4
5 31 25.8 13 21 AAB10012 5 31 25.8 13 22 AAB86060 8 31 25.8 13 22 AAB86092 8 31 25.8 15 20 AAW89494 9 31 25.8 15 22 AAG88514 10 31 25.8 17 20 AAW89159 2 31 25.8 20 19 AAR56585 3 31 25.8 20 22 AAB55809 4 31 25.8 20 22 AAB57671 5 31 25.8 20 22 AAB57671	34	31		12	21	AAY53086	Anticoagulant pept
31 25.8 13 22 AAB86060 31 25.8 13 22 AAB86092 31 25.8 15 20 AAW89494 31 25.8 15 22 AAG88514 31 25.8 17 20 AAW89159 31 25.8 20 19 AAW86585 31 25.8 20 19 AAW568585 31 25.8 20 22 AAB5809 31 25.8 20 22 AAB5809 31 25.8 20 22 AAB5809	32	31		13	21	AAB10012	pylori
31 25.8 13 22 AAB86092 31 25.8 15 20 AAW89494 31 25.8 15 20 AAW89159 31 25.8 17 20 AAW89159 31 25.8 20 19 AAW564356 31 25.8 20 19 AAW56585 31 25.8 20 22 AAB55809 31 25.8 20 22 AAB571 31 25.8 20 22 AAB571	36	31		. 13	22	AAB86060	pylori
31 25.8 15 20 AAW89494 31 25.8 17 20 AAR89159 31 25.8 17 20 AAR89159 31 25.8 19 14 AAR54356 31 25.8 20 19 AAW56585 31 25.8 20 22 AAB5809 31 25.8 20 22 AAB571 31 25.8 20 22 AAB571	37	31		13	22	AAB86092	H. pylori beta-ure
31 25.8 15 22 AAG88514 31 25.8 17 20 AAM89159 31 25.8 19 14 AAR54356 31 25.8 20 19 AAM56885 31 25.8 20 22 AAB5809 31 25.8 20 22 AAB5809 31 25.8 20 22 AAB58081	38	31		15	20	AAW89494	Conopeptide AuIB.
31 25.8 .17 20 AAW89159 31 25.8 19 14 AAR54356 31 25.8 20 19 AAW56885 31 25.8 20 22 AAB55809 31 25.8 20 22 AAB571 31 25.8 20 22 AAB571	39			15	23	AAG88514	HER2/NEU DR supern
31 25.8 19 14 AAR54356 31 25.8 20 19 AAW56585 31 25.8 20 22 AAB55809 31 25.8 20 22 AAB57671 31 25.8 20 22 AAB58081	40	31		. 17	20	AAW89159	Anti-p53 monoclona
31 25.8 20 19 AAW56585 31 25.8 20 22 AAB55809 31 25.8 20 22 AAB57671 31 25.8 20 22 AAB58081	41	31		19	14	AAR54356	Ambr
31 25.8 20 22 AAB55809 31 25.8 20 22 AAB571 31 25.8 20 22 AAB58081	42	31		20	19	AAW56585	Synthetic TcaAii p
31 25.8 20 22 AAB57671 31 25.8 20 22 AAB58081	43	31		20	22	AAB55809	PL peptide #20. 3
.8 20 22 AAB58081 DNAM	44			50	22	AAB57671	DNAM-1 PL peptide
	45	31	25.8	20	22	AAB58081	DNAM-1 PL peptide

## ALIGNMENTS

AAR53477 standard; peptide; 21 AA AAR53477

AAR53477;

(first entry) 01-DEC-1994

CD44 peptide CD44-5

Cell adhesion molecule; CD44; antiinflammatory; rheumatoid; arthritis; tumor cell metastasis; autoimmune disease; immunosuppressive. 

Homo sapiens

WO9409811-A.

11-MAY-1994

93WO-US10412. 29-OCT-1993; 92US-0973339. 30-OCT-1992;

(UYDU-) UNIV DUKE.

Telen MJ; Patton KL, Liao H, Hale LP, Haynes BF,

WPI; 1994-167121/20.

Use of CD44 protein and new peptide.derivs - for developing prods for inflammation, immune-mediated tissue damage and tumour cell metastasis ~

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6 PEDIYP-SNPTDDD 18
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                                                                                                                                                                                                                                                                                         31-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                  Gordon J,
                                                                                                      AAY13470;
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                                                                   AAY13470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BS106 is a breast tissue gene with which breast cancer and related diseases are associated. The BS106 polypeptides AAW42089-W42092 can be utilized in a variety of of assays for the detection of antibodies to breast tissue. They can also be used as immunogens for the detection of antibodies to breast tissue. The products and methods discussed in this invention can be used for detecting, diagnosing, stading, preventing or treating, or detecting predisposition to diseases or conditions of the breast such as breast cancer.
                                                                                                                                                              Gaps
                                 mediated tissue damage such as occurs in the course of autoimmune diseases. e.g. rheumatoid arthritis. It can also be used for determining metastatic potential or treat or prevent tumor cell metastasis. This peptide corresponds to AA 161-180 of the CD44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting BS106 gene products - useful for developing products for detecting, staging, preventing, treating or determining predisposition to e.g. breast cancer
                                                                                                                                                                                                                                                                                                                                                           Human; BS106; breast tissue gene; breast cancer; detection marker.
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0
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Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
Roberts-Rapp L, Russell JC, Stroupe SD;
                      The peptide can be used for treating inflammation and immune-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 21;
                                                                                                                                        Length 21;
                                                                                                                                                              Indels
                                                                                                                                    100.0%; Score 120; DB 15;
100.0%; Pred. No. 2.4e-11;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                AAW42092 standard; Peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 17; Page 93; 114pp; English.
Claim 4; Page 14; 83pp; English.
                                                                                                                                                                                  1 CYRTNPEDIYPSNPTDDDVSS 21
                                                                                                                                                                                             1 cyrtnpediypsnptdddvss 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.4%;
50.0%;
                                                                                                                                                                                                                                                                                                                                    BS106 synthetic polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0742067
                                                                                                                                                                                                                                                                                                             25-SEP-1998 (first entry)
                                                                                                                                    Ouery Match
Best Local Similarity 100.
Matches 21; Conservative
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Best Local Similarity 50.0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ABBO ) ABBOTT LAB
                                                                                                    21 AA;
                                                                              protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                        AAW42092;
                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                      AAW42092
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The invention provides BS106 polynucleotides (AAX55578-82) and polypeptides (AAX13466-470). The BS106 nucleic acids correspond to a breast tissue gene and can be used as markers for breast tissue disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The products can be used for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining diseases or conditions associated with BS106, especially breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; antithrombin III; mutant; carboxy-terminal; extension; sulphated tyrosine; prevention; treatment; thrombosis; disease.
                                                                                                                                                                                                                                                         BS106; breast; marker; detection; diagnosis; breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kratochvil JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human antithrombin III carboxy-terminal extension.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Colpitts TL, Fr
SC, Klass MR,
Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36.5;
Pred. No. 61
                                                                                                      AAY13470 standard; Protein; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Page 93; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW14606 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated BS106 nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dose, Hodges
Russell JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.4%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0962094.
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                                                                                                                                                                                                                    BS106 polypeptide sequence
                                                                                                                                                                             26-JUL-1999 (first entry)
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Best Local Similarity
'-hag 7; Conserve
| | || : | || :
padtypatgpadde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-326991/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Billiing-Medel PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roberts-rapp L,
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Gaps

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Indels

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W09815574-A1
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                                                                                                                                                                                                              Query Match
Best Local Si
Matches 10;
                                                                                                                                                                                                                                                                                                              AAW54457;
                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                          GTF; antigenic epitope; glucosyltransferase; immunogenic epitope; teeth;
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                    Human antithrombin III mutant with C-terminal peptide containing a sulphated tyrosine - useful for treatment and prevention of thrombic
                                                                                                                                                                                                                                                                                                                                                                                                 immunogenic composition; streptococcal glucan; antibody response; cariogenic bacteria; mutans streptococci; colonisation; caries; dental caries; immunisation; therapy.
                                                                                                                                                                              A human antithrombin III (AT III) mutant, comprising a carboxy-terminal sulphated tyrosine peptide extension, i.e. the present peptide, can be used to prevent and/or treat thrombotic
                                                                                                                                                                                                                                                            ;
       Location/Qualifiers
1..3
/note= "carboxy-terminus of wild type human antithrombin III"
                                                                                                                                                                                                                                            Score 36; DB 18; Length 16;
Pred. No. 53;
3; Mismatches 7; Indels
                                                                                                                                                                  Disclosure; Page 6; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                             AAY43350 standard; peptide; 16 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith DJ;
                                                                                                                                                                                                                                            Query Match 30.0%;
Best Local Similarity 37.5%;
Matches 6; Conservative
                                                                          95JP-0228694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US07828
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| cvktdlydyypeedte 16
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                                                                                                                                                                                                                                                                                                                                                                           GTF antigenic epitope.
                                                                                                       (EISA ) EISAI CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LEES/) LEES A.
(TAUB/) TAUBMAN M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Taubman MA,
                                                                                                                     WPI; 1997-231188/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-620289/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SMIT/) SMITH D J.
                                                                                                                                                                                                                       16 AA;
                                            JP09071600-A.
                                                                          06-SEP-1995;
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                                                            18-MAR-1997
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                                                                                                                                                                                                                       Sequence
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                                                                                                                                                     disease
Key
Region
                                                                                                                                                                                                                                                                                                                      AAY43350
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This sequence represents a glucosyltransferase (GTF) immunogenic epitope, and can be used in the immunogenic composition of the invention. The immunogenic composition (A) comprises at least one streptococcal glucan (SG) and at least one component (I) covalently coupled, (in)directly, to SG. (A) elicits antibodies (Ab) to both SG and (I). (A), and related compositions, are used to induce an antibody response to cariogenic acceptation compositions, are used to induce an antibody response to cariogenic streptococcus mutans, S. rattus, S. cricetus or S. sobrinus), especially to prevent colonisation, to reduce numbers of bacteria or to reduce incidence of caries, in humans or other animals. The composition can therefore be used for the treatment or prevention of caries (particularly dental caries). Abs raised against (A) can be used: (a) to detect SG, and (b) for passive immunisation, e.g. applied directly to the surface of theth. The produces a conjugate which induces significant immunity to both components, resulting in immunological memory and children.
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Immunogenic compositions for control of dental caries, based on Streptococcus mutans components, particularly for vaccination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
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Pred. No. 63;
2; Mismatches
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                                                                                                                                                 Claim 11; Page 44; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW54457 standard; protein; 7 AA
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58.8%;
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2 ped--ptdptdpgdpss 16
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nes 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 AA;
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used to for the treatment of anglogenic disease. The generated anglostatin is a protein that is a fragment of plasminogen having the same N-terminal amino acid sequence as plasmin and a C-terminus in damino acid sequence as plasmin and a C-terminus in thingle 5. The generated anglostatins are used to treat anglogenic disease, e.g. tumours and their metastases, rheumatoid arthritis, atherosclerosis, eye, cardiovascular, cerebral vascular or diabetes associated disorders, or immune diseases such as chronic inflammation. A DNA that encodes the protein optionally linked to expression control elements can be used in gene therapy to treat the same diseases. Antibodies that bind selectively to the native anglostatin are used in standard immunoassays for detection or determination of anglostatin for diagnosis or monitoring of anglogenesis, and affinity purification. These methods allow anglostatin to be produced on a large scale.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Angiostatin; plasminogen; human; thiol donor; activator; tumour; anglogenic disease; rheumatoid arthritis; atherosclerosis; eye disorder; cardiovascular; cerebral vascular; diabetes; immune disease; plasmin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This represents the human native angiostatin C-terminal sequence. This was deduced to be a plasminogen fragment. The invention provides a method for in vitro generation of angiostatin which comprises treating plasminogen with a plasminogen activator and a sulphydryl (thiol) donor. The thiol donor converts the plasmin to angiostatin which can be
                                                              plasminogen with a plasminogen activator and a sulphydryl (thiol) donor. The thiol donor converts the plasmin to angiostatin which can be
This represents the human native angiostatin C-terminal sequence. This was deduced to be a plasminogen fragment. The invention provides a method for in vitro generation of angiostatin which comprises treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Generating angiostatin in vitro or in vivo - by treating plasminogen with activator and thiol donor, for treatment of angiogenic disease, e.g. tumours, arthritis, eye disease etc.
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Pred. No. 4.3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 42; Page 79; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW54458 standard; protein; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chronic inflammation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                    elements can be used in gene therapy to treat the same diseases. Antibodies that bind selectively to the native angiostatin are used in standard immunoassays for detection or determination of angiostatin for diagnosis or monitoring of angiogenesis, and affinity purification. These methods allow angiostatin to be produced on a large scale.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a possible cleavage site in proSKI-1 which may be targeted by a zymogen to form mature subtilisin-kexin isoenzyme 1 (SKI-1). The conserved site was identified by alignment of SKI-1 with other subtilases. SKI-1 is a type-1 membrane-bound proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel soluble proteic fragment of subtilisin-kexin isoenzyme for producing a polypeptide useful for treating hypercholesterolemia, liver steatosis and amyloidosis, comprises a specific amino acid sequence -
                                                               disease, e.g. tumours and their metastases, rheumatoid arthritis, atherosclerosis, eye, cardiovascular, cerebral vascular or diabetes associated disorders, or immune diseases such as chronic inflammation. A DNA that encodes the protein optionally linked to expression control
used to for the treatment of angiogenic disease. The generated angiostatin is a protein that is a fragment of plasminogen having the same N-terminal amino acid sequence as plasmin and a C-terminus in
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Davignon J;
                                                     kringle 5. The generated angiostatins are used to treat angiogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; pro-brain-derived neurotrophic factor; proBDNF; subtilisin-kexin isoenzyme 1; SKI-1; proSKI-1 zymogen processing; antilipaemic; cytostatic; vasotropic; SKI-1 inhibitor; hypercholesterolaemia; liver steatosis; Ras-dependent cancer; restenosis; amyloid protein formation.
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                                                                                                                                                                                                                                                                              Score 33; DB 19; Length v; Pred. No. 4.3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marcinkiewicz M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proSKI-1 putative zymogen cleavage site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 6..7
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                                                                                                                                                                                                                                                                                              27.5%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-365601/31.
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                             8 AA;
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| cyttnp 6
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Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB06281;
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which cleaves pro-brain-derived neurotrophic factor. Peptides which bind to and are cleaved by SKI-1 may be used for monitoring SKI-1 activity, for screening enhancers of SKI-1 activity, or for screening enhancers of SKI-1 activity. Proteic fragments of SKI-1 which bind to the SKI-1 catalytic site may be used as inhibitors of SKI-1 activity. They may be used to treat diseases involving overexpression of SKI-1 or SKI-1 substrate. Such diseases include hypercholesterolaemia, high levels of fatty acids, lipids or farnesyl pyrophosphate, liver steatosis, Ras-dependent cancer, restenosis and amyloid protein formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The specification describes a method for determining the conformational state of a protein. The method uses at least one labelled binding partner capable of binding to the protein in a manner dependent on the conformational state of the protein. The method is for detecting the conformational state of a protein, for detecting post-translational modifications of proteins, and for determining the activity of an enzyme. The present sequence represents a binding partner of human p47-phox. p47-phox is a substrate of protein kinase C Detection of the conformational changes in p47-phox is used to measure protein kinase C activity, using the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                 Conformational state; post-translational modification; enzyme activity;
                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of a binding partner peptide of p47-phox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Determining the conformational state of a protein, comprises the protein with a labeled binding protein and assessing the
                                                                                                                                                       Length 10;
                                                                                                                                                                               4; Indels
                                                                                                                                                        DB 21;
                                                                                                                                                                               Mismatches
                                                                                                                                                                  87
                                                                                                                                                       Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                      AAB08529 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 30; 56pp; English.
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                                                                                                                                                       27.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-2000; 2000WO-GB00668
                                                                                                                                                                                                                                                                                                                                                                                             p47-phox; protein kinase C
                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FLUO-) FLUORESCIENCE LTD.
                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Colyer J, Craig RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-565475/52
                                                                                                                                                      Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                     3 RINPEDIYPS 12
                                                                                                                                                                                                                           1 rnnpssdyps 10
                                                                                                                      10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200050901-A1
                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-FEB-1999;
                                                                                                                                                                                                                                                                                                                                    20-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-AUG-2000.
                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                          AAB08529
                                                                                                                                                                                                                                                                           AAB08529
                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                      SSSSSSSX8
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Score 33; DB 21; Pred. No. 1.3e+02;

27.5%; 35.7%;

Query Match Best Local Similarity

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times sequence is an antigenic Iraqment of an isologim, of the human Stat6 (signal transducers and activators of transcription), of the invention. The detection and/or quantitation of DNA or anticons of Stat6 and/or Stat6 and/or Stat6 can be used to detect differential expression of Stat6 isoforms in numerous diseases, including myeloid cancer, asthma, sarcoma, scleroderma, bone marrow fibrosis, fibrotic diseases and AIDS: The nucleic acids can be used to screen genomic or CDNA libraries or to identify complementary sequences. The identification of the genetic locus of the Stat6 gene can be used to screen detection of chromosomal aberrations of the Stat6 gene can be used for detection of chromosomal aberrations and translocations involving the Stat6 gene. Antibodies against the isoforms can be used to detect the statescription the isolated and/or Stat6c in a sample. Because of the transcription the isolated and purified forms can be used to study gene transcription the isolated and purified forms can be used to study gene can be used as agonists or antagonists. The two polypeptides may also be used in gene therapy protocols. In particular, stat6b and/or Stat6c can therapeutically modulate the development and differentiation of B and CT cells and can enhance IL-4 immunological function in immunocompromised individuals, Stat6 activation correlates with function of gene correlated regulator of gene correlated regulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stat6; Stat6b; human; signal transducers and activators of transcription; isoform; myeloid cancer; asthma; sarcoma; scleroderma; fibrotic disease; bone marrow fibrosis; AIDS; Stat6c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isoforms of Stat6 - having differential effects on the modulation of Stat6 activity in cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is an antigenic fragment of an isoform of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33; DB 20;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pierce JH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 20; 88pp; English.
                                                                                                                                                                                                                                                                                                     AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Stat6 antigenic fragment.
                                                                                                                                                                                                                                                                                                 AAY05230 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US17821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0070397
97US-0056075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patel B,
1 CYRTNPEDIYPSNP 14
                                                                           1 cgrskpgpavpprp 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-214517/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Larochelle WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcription.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9910493-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JAN-1998;
27-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                      AAY05230;
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AAG64195;

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AAG64195

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Matches

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The present invention relates to a set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of plant genomes e.g. from Arabidopsis thaliana (see AAG83361-AAG84504). The peptides of the present invention are useful in an assay to identify a peptide, especially a peptide pesticide or herbicide. The peptides are also useful for tools for agricultural research and development. The present peptide was used to illustrate the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasminogen; human; Kringle 5 peptide; anti-angiogenesis agent; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metastatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma; psoriasis; arthritis; macular degeneration; diabetic retinopathy; autoimmune disease; ocular disease; capillary proliferation; therapy;
                                                                                                                                                           Plant; peptide pesticide; peptide herbicide; agricultural research.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 22; Length 20;
Pred. No. 1.9e+02;
Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A set of peptide ligands for agricultural research therapeutic agents comprise specific complementary encoded by genes of plant genomes .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 10; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
     AAB99270 standard; Peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW34298 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.5%;
                                                                                                                                                                                                                                                                                                            13-DEC-2000; 2000WO-GB04781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kringle 5 peptide fragment.
                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 frtsredstysgdtdfd 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 YRTNPEDIYPSNPTDDD 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              Roberts GW, Heal JR;
                                                                                                                                                                                                                                                                                                                                                                                         (PROT-) PROTEOM LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-381629/40.
                                                                                                                     Peptide sequence 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kringle 5 receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 AA;
                                                                                                                                                                                                                                   WO200142279-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Modified-site
                                                                                11-SEP-2001
                                                                                                                                                                                                                                                                                                                                                   13-DEC-1999;
                                                                                                                                                                                                                                                                         14-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW34298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW34298
       δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a set of complementary peptide ligands
generated from Mycoplasma genitalium genome sequences. These
specific complementary peptides interact with their relevant target
proteins encoded by the microbial genome. They are capable of
another protein or receptor and are thus useful as reagents and drugs,
another protein or receptor and are thus useful as reagents and drugs,
and as lead ligands to facilitate drug design and development. They
are useful as tools for functional genomic studies, reagents for the
configuration of high-throughput screens, as a starting point for
therapeutic agents. The analysis and acquisition of peptide sequences
facilitates understanding of protein-protein interactions. The method
allows for analysis of an entire database at a time, thus overcoming
sampling problems. The present sequence is provided as an example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complementary peptide ligands as reagents and drugs for drug discovery programs and as lead ligands to facilitate drug design and development, are generated from microbial genome sequences
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
     5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB 22; Length 20
Pred. No. 1.9e+02;
2; Mismatches 7; Indels
     Indels
                                                                                                                                                                                                                                                                                                                              complementary peptide; ligand;
   3;
   Mismatches
                                                                                                                                                                                                                                                                                                                          Mycoplasma genitalium; complementary pept protein-protein interaction; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 12; 161pp; English.
                                                                                                                                                                      AAG64195 standard; Peptide; 20 AA.
   4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .3-DEC-2000; 2000WO-GB04778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99GB-0029466
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                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 frtsredstysgdtdfd 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 YRTNPEDIYPSNPTDDD 18
 Conservative
                                     7 EDIYPS--NPTDDDVS 20
                                                          |||:| ||:| |::
edifppllppteqdlt 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roberts GW, Heal JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PROT-) PROTEOM LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-514238/56.
                                                                                                                                                                                                                                                                                        Protein sequence 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200142278-A2
                                                                                                                                                                                                                                                 22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-JUN-2001.
7;
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and development of peptides to proteins

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Gaps

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/note= "N-Ac-Tyr"

Seguence

Matches

ŏ g RESULT 12 AAB99270

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Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XEXAX
                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is synthetic a kringle 5 (K5) peptide homologous to human plasminogen. K5 peptide fragments homologous to this sequence, are anti-analyogenesis agents, specifically for treating or preventing cancer, particularly primary or metastatic solid tumours, carcinomas, sarcomas, lymphomas, haemanglomas. They can also be used for treating or preventing comparists, arthritis, macular degeneration and diabetic retinopathy. The fragments can also be used to treat autoimmune or coular diseases, capillary proliferation within atherosclerotic plaque, haemophiliac conjubit ovulation and establishment of the placenta. K5 antiscra or inhibit ovulation and establishment of the placenta. K5 antiscra or can any be used to induce angiogenesis, e.g. for wound challing. The K5 peptides are also used to raise specific antibodies (Ab), for diagnosis and for affinity purification of K5 receptors. The K5 peptides are also used to raise specific antibodies (Ab), for diagnosis. The Ab are used to indentification of smaller cresponse to the peptides or used for detect/quantify the peptides in antibodies and confidential capillation of smaller confidential capillation of endothelial cells with low toxicity against inhibit proliferation of endothelial cells with low toxicity against commal cells. Typically they have 800-times greater inhibitory activity commal cells. Typically they have 800-times greater inhibitory activity commal cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                       plasminogen - useful as anti-angiogenesis agents for treating cancer, psoriasis, arthritis etc., including gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.7%; Score 32; DB 18; Length 11; 55.6%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                  New kringle 5 peptide(s) and fusion proteins derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiangiogenic; cancer; tumour; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32; DB 10. Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human plasminogen kringle 5 peptide fragment #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
11
/note= "C-terminal amide"
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                                                                                                                                                                                                                                                                                                                                                                                                             Example 5; Page 43; 78pp; English.
                                                                                                                                                                                                                                                               Wang
                                                                                                                              97WO-US07700
                                                                                                                                                                 97US-0832087
96US-0643219
                                                                                                                                                                                                                                                             EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
                                                                                                                                                                                                                                                             Gubbins
                                                                                                                                                                                                                                                                                               WPI; 1997-558670/51.
                                                                                                                                                                                                                        (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 YRTNPEDIY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ||| :|
| yttnprkly 9
Modified-site
                                                                                                                                                                                                                                                             Davidson DJ,
                                                     WO9741824-A2
                                                                                                                              05-MAY-1997;
                                                                                                                                                                 03-APR-1997;
03-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-SEP-2000
                                                                                          13-NOV-1997
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The invention relates to a method of preparing plasminogen kringle 5
c peptide fragments. The method comprises mixing mammalian plasminogen and
c elastase in the ratio 1:100-1:300, followed by incubating and isolating
the fragment. The kringle 5 peptides are inhibitors of anglogenesis and
cendothelial cell proliferation and migration. The peptides are useful
c endothelial cell proliferation and migration. The peptides are useful
c for treating anglogenic diseases, primary and metastatic solid tumours
c and carcinomas of various organs such as breast, genital tract,
cendocrine glands, skin, tumours of the brain and eyes and solid tumours
arising from haematopoietic malignancies such as leukaemias and
cliseases (e.g., rheumatold arthritis), ocular diseases, skin diseases
(e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Webber
CS yndrome), diseases caused by excessive or abnormal stimulation of
condothelial cells (e.g., crohn's disease, atherosclerosis), diseases
which have anglogenesis as a pathologic consequence (e.g., cat scratch
disease and ulcers). The peptides are also useful as a birth control
agent which inhibits ovulation and establishment of the placenta.
Sequences Aab01888, AAB01889 and AAB01895-B01905 represent human
c plasminogen kringle 5-derived peptides synthesised and used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Preparation of Kringle five peptide fragment for treating various slackers such as anglogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by incubation and isolation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                 'note= "N-terminal acetyl moiety"
                                                                                                                                  "C-terminal amide moiety"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 5; Column 36; 48pp; English.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB92094 standard; Peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laminin fragment SEQ ID NO:1270.
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55.6%;
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97US-0832087.
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Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                     /note=
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   Key
Modified-site
                                                                                               Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Davidson DJ:
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The present invention describes a modified therapeutic peptide (I)

comprising a therapeutically active amino acid region (III) and a
reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
a less therapeutically active amino acid region (IV), which covalently
bonds with amino/Mydroxyl/thiol groups on blood components to form a
peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

(I) are useful for modifying therapeutic peptides e.g. hormones, growth
factors and neurotransmitters, to protect them from peptidase activity
in vivo for the treatment of various disorders. Endogenous therapeutic
peptides are not suitable as drug candidates as they require frequent
administration due to rapid degradation by peptidases in the body.
Modifying and attaching therapeutic peptides to albumin prevents or
reduces the action of peptidases to increase length of activity (half
ilfe) and specificity as bonding to large molecules decreases
intracellular uptake and interference with physiological processes.

AAB90829 to AAB92441 represent peptides which can be used in the
exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                                                                                                                            Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 611; 733pp; English.
                                                                                                                                                                                                                                                                 99US-0134406.
99US-0153406.
99US-0159783.
                                                                                                                                                                                                                          17-MAY-2000; 2000WO-US13576.
                                                                                                                                                                                                                                                                                                                                                     (CONJ-) CONJUCHEM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-112059/12
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                                                                                                                                           WO200069900-A2.
                                                                                                                                                                                                                                                                 17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                   Homo sapiens.
Synthetic.
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Gaps
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Ouery Match 26.7%; Score 32; DB 22; Length 11; Best Local Similarity 55.6%; Pred. No. 1.4e+02; Matches 5; Conservative 1; Mismatches 3; Indels
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2 YRTNPEDIY 10 | ||| :| | yttnprkly 9

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Search completed: February 21, 2002, 16:42:57 Job time: 231 sec

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Appl Appl Appl Appl

Sequence

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us-08-753-851-5.rai

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SOFTWARES PATENTIAL POST NEEDS 1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/143,311B FILING DATE: 29-OCT-1993
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,339
FILING DATE: 30-OCT-1992
CLASSIFICATION: 436
APPLICATION NUMBER: 07/669,730
                  US-09-231-797-25
US-08-934-224-25
US-08-934-223-25
US-09-413-492-25
US-09-413-492-25
US-08-055-530-21
US-08-055-530-21
US-08-055-530-21
US-08-044-50
US-08-944-50
US-08-944-50
US-08-944-50
US-08-944-868A-50
US-08-944-423A-50
US-08-944-423A-50
US-08-944-433-85
US-08-944-433-85
US-08-444-733-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HALE, LAURA P.
APPLICANT: PATTON, KAREN L.
APPLICANT: TELEN, MARILYN J.
APPLICANT: LIAO, HUA-XIN.
APPLICANT: LIAO, HUA-XIN.
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 15-MAY 1991
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J. 32,955
REGISTRATION UNMER: 32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08143311B Patent No. 5863540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: NIXON & VANDERHYE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HAYNES, BARTON F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 703-010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-143-311B-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: ARLINGTON STATE: VIRGINIA
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44444444444444444
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STREET: 11
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Left No. 5378805
Sequence 28, April Sequence 28, April Sequence 28, April 28
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14.969 Million cell updates/sec
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Sequence 5, Appli
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Sequence 4, Appli
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Sequence 3, P
Sequence 53,
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                                                                                                                                                                        February 21, 2002, 16:40:46; Search time 31.57 Seconds
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Sequence 5,
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/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
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/cgn2_6/ptodata/2/jaa/PcTu5_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PcTu5_COMB.pep:*
                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-257-392-15
US-08-116-733-4
US-08-469-615-3
US-08-469-615-3
US-08-48-611-14.2A-3
US-08-311-42A-3
US-08-318-85-6A-53
US-08-857-068-3
US-08-938-55-4
US-08-938-55-4
US-08-620-977A-8
US-08-938-95-4
US-08-602-999A-115-4
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3-08-612-973-86
3-08-927-597-86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-934-222-25
US-08-933-402-25
US-09-207-621-25
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                    OM protein
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                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                        Run on:
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                                                                                                                                                                                                                                                                           Title:
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GENERAL INFORMATION:
APPLICANT: Cottingham, Ian R.
APPLICANT: Garner, Ian
TITLE OF INVENTION: Peptide Production as Fusion Protein in
TITLE OF INVENTION: Transgenic Mammal Milk
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                            ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 New York Avenue, Sulte 600 CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppd disk
MEDIUM TYPE: Floppd disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/727,153
FILING DATE: 08-0CT-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/718,523
FILING DATE: 06-0CT-1996
PRIOR APPLICATION NUMBER: WO PCT/GB95/00769
FILING DATE: 05-APR-1995
PRIOR APPLICATION NUMBER: WO PCT/GB95/00769
FILING DATE: 05-APR-1995
PRIOR APPLICATION NUMBER: GB 9406974.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: GB 9406974.7
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                            Sequence 5, Application US/08727153 Patent No. 6211427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                      US-08-727-153-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
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                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Cottingham, Ian R.
APPLICANT: Garner, Ian
TILLE OF INVENTION: Peptide Production as Fusion Protein in
TITLE OF INVENTION: Transgenic Mammal Milk
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
                      Length 21;
                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.2%; Score 35; DB 4; Length 12; 75.0%; Pred. No. 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: TENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEN PC COMPATIAL
COMPUTER: TEN PC COMPATIAL
COMPUTER: TEN PC COMPATIAL
COMPUTER: TEN PC COMPATIAL
COMPUTER: PatentIn Release #1.0, Version #1.30
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,595
FILING DATE: (Herewith)
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/727,153
FILING DATE: 08-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/718,523
FILING DATE: 08-OCT-1996
PRIOR APPLICATION NUMBER: WO PCT/GB95/00769
FILING DATE: 05-APR-1995
PRIOR APPLICATION NUMBER: WO PCT/GB95/00769
FILING DATE: 05-APR-1995
PRIOR APPLICATION NUMBER: WO PCT/GB95/00769
FILING DATE: 08-APR-1995
PRIOR APPLICATION NUMBER: WO PCT/GB95/00769
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INPORMATION:
ANAME: DEATER DATA:
ANAME: DEA
                      100.0%; Score 120; DB 2;
100.0%; Pred. No. 1.5e-11;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08938595 Patent No. 6197946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                  1 CYRTNPEDIYPSNPTDDDVSS 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34,333
                                                                                                                                                   1 CYRTNPEDIYPSNPTDDDVSS 21
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Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: not relevant; MOLECULE TYPE: peptide US-08-938-595-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Fleshner, Raz E. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 PSNPTDDD 18
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COUNTRY:
                                                                                                                                                                                                                                                                                                                            US-08-938-595-5
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Gaps
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                                                                                                                                                                                                                                                                                      DB 4;
20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15, Application US/07729099
Patent No. 5403581
GENERAL INFORMATION:
APPLICANT: Binger, Mary-Helen
APPLICANT: Pasamontes, Luis
TITLE OF INFORTION: Coccidiosis Vaccines
CORRESPONDENCE ADDRESS:
                                    0623.0460001
                                                                                                                                                                                                                                                                                      Score 35;
Pred. No.
NAME: Fleshner, Raz E.
REGISTRATION NUMBER: 34,331
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                    29.2%;
75.0%;
                                                                                                                                                                            TOPOLOGY: not relevant
                                                                                                                                             LENGTH: 12 amino acids
                                                                                     TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                             , MOLECULE TYPE: peptide US-08-727-153-5
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|: ||||| PAFPTDDD 10

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28.3%; Score 34; DB 1; Length 18; 40.0%; Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,035
                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 45;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Binger, Mary-Helen
APPLICANT: Pasamontes, Luis
TITLE OF INVENTION: Coccidiosis Vaccines
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: Hoffmann-La Roche Inc
340 Kingsland Street
NAME: Roseman, Catherine R
REGISTRATION NUMBER: 34,240
REFERENCE/DOCKET NUMBER: 8514
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6208
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/08770035
Patent No. 6008342
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/729,099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Roseman, Catherine R
REGISTRATION NUMBER: 34,240
REFERENCE/DOCKET NUMBER: 8514
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (201) 235-6208
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 15
                                                                                                                                                                                                                                                                                                                ; ORGANISM: Eimeria tenella US-08-257-392-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Eimeria tenella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide HYPOTHETICAL: YES FRAGMENT TYPE: C-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 18 amino acids
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Matches 6; Conservative
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                                                                                                                                                                                                                              MOLECULE TYPE: peptide
HYPOTHETICAL: YES
FRAGMENT TYPE: C-termin
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 TNPEDIYPSNPTDDD 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | |: : | | ||:
1 TQPDTEFRSGPGDDE 15
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: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U. ZIP: 07110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-770-035-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.3%; Score 34; DB 1; Length 18; 40.0%; Pred. No. 45; 6; Indels Live 3; Mismatches 6; Indels
                                                                                                                                                                                   OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/729,099
FILING DATE: 19910712
CLEASIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ROSEMAN, Catherine R
REGISTRATION NUMBER: 34,240
REFERENCE/DOCKET NUMBER: 8514
TELEPONE: (201) 235-6208
TELEPONE: (201) 235-5208
TELEPONE: (201) 235-53500
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: Binger, Mary-Helen
APPLICANT: Pasamontes, Luis
TITLE OF INVENTION: Coccidiosis Vaccines
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/729,099 FILING DATE: 12-JUL-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/257,392
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
    ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/08257392
Patent No. 5688513
                                                                                                     ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eimeria tenella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide HYPOTHETICAL: YES FRAGMENT TYPE: C-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 18 amino acids
AMINO ACID
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 TNPEDIYPSNPTDDD 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | |: : | ||:
1 TQPDTEFRSGPGDDE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREEL.
CITY: Nutley
STATE: New Jersey
                              STREEL.
CITY: Nutley
STATE: New Jersey
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Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-729-099-15
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US-08-257-392-15
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Gaps

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APPLICANT: Kurata, Akihiko
TITLE OF INVENTION: Immunodominant Sites of HTLV-I Envelope
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                          ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,615
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP STREET: P.O. Box 747 CITY: Falls Church STATE: Virginia
                       ADDRESSEE: Birch, Stewart, Kolasch & Birch, STREET: P.O. Box 747
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.7%; Score 32; DB 1; 35.7%; Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: 1.16
; OTHER INFORMATION: /label= peptide_sp3
US-08-469-615-3
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION 1973.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,118
FILING DATE: 16-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30330
REFERENCE/DOCKET NUMBER: 1173-500P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08466763
Patent No. 5695762
GENERAL INFORMATION:
APPLICANT: Berzofsky, Jay A.
APPLICANT: Kurata, Akihiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8050
TELEFAX: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SS: not relevant
not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 703-205-8050 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CYRTNPEDIYPSNP 14
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1 CLNTEPSQLPPTAP 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: htlv-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: pe
HYPOTHETICAL: NO
FRAGMENT TYPE: if
ORIGINAL SOURCE:
                                                                                                           COUNTRY:
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US-08-466-763-3
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APPLICANT: Berzofsky, Jay A.
APPLICANT: Kurata, Akihiko
APPLICANT: Kurata, Akihiko
TITLE OF INVENTION: Immunodominant Sites of HTLV-I Envelope
TITLE OF SEQUENCES: 19
                                                              Score 34; DB 3; Length 18;
Pred. No. 45;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 32; DB 1; Length 16; Pred. No. 77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
FILING DATE: US/08/116,733
FILING DATE: 07-SEP-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08116733
Patent No. 5516632
GENERAL INFORMATION:
APPLICANT: PALKER, Thomas J.
APPLICANT: HAYNES, Barton F.
TITLE OF INVENTION: SYNTHETIC PEPTIDES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08469615 Patent No. 5622703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                              28.3%;
40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 35.7
Matches 5; Conservative
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                                                                                                         6; Conservative
                                                                                                                                                4 TNPEDIYPSNPTDDD 18
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1 TQPDTEFRSGPGDDE 15
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                                                            Query Match
Best Local Similarity
Matches 6; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 22201-4714
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US-08-770-035-15
                                                                                                                                                                                                                                                                           US-08-116-733-4
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Length 16;

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40,949
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         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 35.,
                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                    internal
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                                                                                                                                                                                                                           MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Lee Cheng
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CYRTNPEDIYPSNP 14
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1 CLNTEPSQLPPTAP 14
                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
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COUNTRY: U.S.A.
ZIP: 20006
                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
CLONE: HTLV-I
                                                                                                                                                                                                                                                                     2
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                                                                                                                                                                                                                                                                     ANTI-SENSE:
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APPLICANT: Berzofsky, Jay A.
APPLICANT: Berzofsky, Jay A.
APPLICANT: RUATLA: Akiliko
APPLICANT: KURATLA: AKILIKO
TITLE OF INVENTION: TCELL RESPONSES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.7%; Score 32; DB 1; Length 16; 35.7%; Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: Windows95
SOFRWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME. TEST : Peptide LOCATION: 1..16 OTHER INFORMATION: /label= peptide_sp3
                                                                                                                                                                                    NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30330
REFRENCE/DOCKET NUMBER: 1173-497P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 702-205-8000
TELEPHONE: 703-205-8050
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/411,142A FILING DATE: 27-MAR-1995 PRICATION DATA:
                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,118
FILING DATE: 16-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                        APPLICATION NUMBER: US/08/466,763
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08411142A Patent No. 5882853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 16-MAY-1994
APPLICATION NUMBER: 07/401,411
FILING DATE: 01-SEP-1989
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                                                                                                                                                                                                                                                                                                                                       16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 26.7
Best Local Similarity 35.7
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CYRTNPEDIYPSNP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: htlv-I
                                                                         FILING DATE: 06 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ns
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                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-466-763-3
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STATE:
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APPLICANT: Garner, Ian
APPLICANT: Garner, Ian
TITLE OF INVENTION: Peptide Production as Fusion Protein in
TITLE OF INVENTION: Transgenic Mammal Milk
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
                                                                                                                                                                                                                                                                             MOCARHAGIN, A NOVEL COBRA VENOM PROTEASE, AND THERAPEUTIC USES THEREOF: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,977A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 31; DB 1;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Brown, Scott A. REGISTRATION NUMBER: 32,724 REFERENCE/POCKET NUMBER: G15239 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Berndt, Michael C.
APPLICANT: Bunlop, Lindsay
APPLICANT: Andrews, Robert
APPLICANT: Deluca, Mariagrazia
TITLE OF INVENTION: MCARRAGIN, FITLE OF INVENTION: PROTEASE, ANI
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                Sequence 8, Application US/08520977A Patent No. 5659018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08938595 Patent No. 6197946 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 25.8
Best Local Similarity 40.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-520-977A-8
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5 TDLYDYYPEEDTEGD 19
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8 CFATNPD 14
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                   1 CYRTNPE 7
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TELEFAX: (
                                                                                                           RESULT 13
US-08-520-977A-8
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US-08-938-595-4
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                                                                                                                                                  Length 9;
                                                                                                                                                                                                                                                                                                                                                                            Patent No. Docuve...
GENERAL INFORMATION:
APPLICANT: Cartier, G. Edward
APPLICANT: Yoshikami, Doju
APPLICANT: Toshikami, Doju
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: CONOPEPTIDES AUIA, AUIB AND AUIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Venable, Baetjer, Howard & Civiletti
1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/857,068
                                                                                                                                                Score 31; DB 2; 1 Pred. No. 1.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31; DB 2;
Pred. No. 1e+02;
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                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08857068 Patent No. 5866682
LENGIH: 9 amino acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 2426/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEPHONE: 202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.8%;
                                                                                                                                              25.8%; 71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disulfide-bond 2..8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disulfide-bond 3..15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Conus aulicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 57.14
نامع 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 15 amino acids TYPE: amino acid
                                                                                                                                              Query Match 25.8
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein ORIGINAL SOURCE:
                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-318-856A-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1201 New CITY: Washington STATE: D.C.
                                                                                                                                                                                                                       11 PSNPTDD 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20002
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LOCATION:
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US-08-857-068-3
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US-08-857-068-3
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25.0%; Score 30; DB 4; Length 8; 100.0%; Pred. No. 1.6e+05;
                                                    CLASSIFICATION: 800
PRIOR APPLICATION B00
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/718,523
FILING DATE: 08-0CT-1996
PRIOR APPLICATION NUMBER: WP PCT/GB95/00769
FILING DATE: 05-APR-1995
PRIOR APPLICATION NUMBER: GB 9406974.7
FILING DATE: 108-APR-1994
APPLICATION NUMBER: GB 9406974.7
FILING DATE: 08-APR-1994
ATTORNEY AGENT INFORMATION:
NAME: Fleshner, Raz E.
REGISTRATION NUMBER: 34,331
REFERENCE/DOCKET NUMBER: 0623.046001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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100.0%; Pic
                                       08-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: not relevant; MOLECULE TYPE: peptide US-08-727-153-4
                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.C
Best Local Similarity 100.
Matches 5; Conservative
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STRANDEDNESS: sir
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2 PTDDD 6
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Patent No. 6211427
GENERAL INFORMATION:
APPLICANT: Cottingham, Ian R.
APPLICANT: Garner, Ian
TITLE OF INVENTION: Peptide Production as Fusion Protein in
TITLE OF INVENTION: Transgenic Mammal Milk
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 New York Avenue, Suite 600 STATE: Washington STATE: DC.
                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,595 FILING DATE: (Herewith)
CLASSIFICATION: 800
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 08/727,153

PRILING DATE: 08-0CT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/718,523

FILING DATE: 08-0CT-1996

PRIOR APPLICATION NUMBER: WO PCT/GB95/00769

FILING DATE: 05-APR-1995

PRIOR APPLICATION NUMBER: GB 9406974.7

FILING DATE: 08-APR-1994

ATTORREY/AGENT INFORMATION:

NAME: Fleshner, Raz E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34,331
FP 0623.0460003
                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TELEPHONE: 202-371-2600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Fleshner, Raz E.
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SS: single
not relevant
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LENGTH: 8 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: peptide US-08-938-595-4
                                                                                                                                          OPERATING SYSTEM:
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Best Local Similarity
Matches 5; Conserva
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                  COUNTRY: US
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2 PTDDD 6
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 21, 2002, 16:44:15 ; Search time 33.6 Seconds
(without alignments)
47.609 Million cell updates/sec Run on:

US-08-753-851-6

123 1 CTVHPIPDEDSPWITDSTPRI 21 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

4046 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR\_68:\* Database :

pir1:\* pir2:\* pir3:\* pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description		hypothetical prote	$\mathbf{z}$	protein p12E - Fri	hypodermin B - ear	alpha-conotoxin EI	H+-transporting AT	transcription fact	hypothetical prote		avenin gamma-4 - o	calsequestrin, car	NADH dehydrogenase	pollen allergen I	trypsin (EC 3.4.21	39K protein 3225 -	_	mixed lymphocyte r	pyrogenic exotoxin	ermG leader peptid	dissimilatory sulf	lactase-phlorizin	cytochrome-c oxida	dissimilatory sulf	fatty acid ethyl e	xenopsin-related p	xenopsin-related p	ಥ	protein QF200051 -	multicatalytic end
SUMMARIES	ID	:	A35678	S32883	S66613	A20190	A58589	860633	B23692	S10876	JQ2307	S29207	A39040	808590	A44773	A61328	PS0259	A60856	PX0031	A44799	B26930	S63489	B46592	S77981	S63490	A42920	JS0302	A60320	A56863	90	PC2326
	DB	,																7													
	Query Match Length		18	21	16	16	18	19	16	20	11	15	18	21	20	<b>ω</b>	11	13	. 15	17	19	19	19	20	20	17	σ	6	15	15	19
оP	Query		24.4	22.8	22.0	22.0	22.0	22.0	21.1	21.1	20.3	20.3	20.3	20.3		6	ó,	19.5		•		•	6		•	19.1	18.7	18.7	18.7	18.7	18.7
	Score		30	28	27	27	27	27	56	56	25	25	25	25		. 24		24		24			24	24	Ň		23	23	23	23	23
	Result No.		1	7	m	4	ស	9	7	89	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

RESULT

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cytotoxic T-lympho	pev-kinin 1 - pena	leucopyrokinin - M	substance P-like p	kassinin-like pept	kassinin-like pept	amine oxidase (cop	acidic proline-ric	Ig heavy chain CDR	neural cell adhesi	hypothetical prote	collecting duct wa	Ig heavy chain CRD	protein kinase (EC	agrin - electric r
149423	PD0029	A23967	E60409	B60409	C60409	S71304	A29806	PT0228	D39690	809395	151905	PT0294	S20410	150503
2.0	1 73	7	7	7	7	7	7	7	7	~	7	7	7	7
20	7	œ	11	11	11	11	11	12	13	13	13	14	15	15
18.7	17.9	17.9	17.9	17.9	17.9	17.9	17.9	17.9	17.9	17.9	17.9	17.9	17.9	17.9
23	22	22	22	22	22	22	22	22	22	22	22	22	22	22
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1  A35(Date: 28-Sep-1990 fisequence_revision 5 region) - mouse C:Species: Mus musculus (house mouse) C:Species: Mus musculus (house mouse) C:Apcession: A35(A) C:Date: 28-Sep-1990 fisequence_revision 28-Sep-1990 fitext_change 05-Nov-1999 C:Accession: A35(A) A7:Interrick, D.L.; Ainn, S.A.; Fitzgerald, M.; Higuchi, H.; Sabol, S.L.; Meyerhardt, Mol. Cell. Biol. 10, 3717-3726, 1990 A7:Rilpatrick, D.L.; A35(A) A7:Rilpatrick, D.L.; A35(A) A7:Rilpatrick, D.L.; A35(A) A7:Rilpatrick, D.L.; A35(B) A7:Rilp
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560633
H+-transporting ATP synthase (EC 3.6.1.34) protein 8 - brine shrimp mitochondrion (st C;Species: mitochondrion Artemia sp. (brine shrimp)
A;Variety: strain La Mata
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 07-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the "A" chain of a rat heteromeric CCA
                                                                                                                                                                                                                                                  A;Genetic code: SGC4
C;Superfamily: H+-transporting ATP synthase protein β
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X67263; NID:911210; PIDN:CAA47685.1; PID:911211
A;Experimental source: strain La Mata
A;Note: the source is designated as Artemia parthenogenetica
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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C;Date: 04-Oct.1991 #sequence_revision 04-Oct.1991 #text_change 30-Sep-1993
C;Accession: B23692.
J; Biol. Chem. 265, 22480-22486, 1990
A;Tille: Purification and molecular cloning of the "A" chain of a rat hetero A;Reference number: A23692; MUID:91093096
A;Reference number: B23692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein - human
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 18-Nov-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 8.8e+02;
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Pred. No. 7.7e+02;
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v 100.0%; Pred. No.
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80.0%;
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A;Molecule type: mRNA
A;Residues: 1-16 <VUO>
A;Cross-references: GB:J05701
      14
                                              4 CCYHPTCNMSNPQI 17
      1 CTVHPIPDEDSPWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Genome: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-19 <PER>
                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S60633
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EPSPW 13
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                                         C; Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C; Accession: $66613 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
E; Hensel, J.; Hintz, M.; Karas, M.; Linder, D.; Stahl, B.; Geyer, R.
Eur. J. Blochem. 232, 373-380, 1995
A; Title: Localization of the palmitoylation site in the transmembrane protein pl2E of Fr
A; Reference number: $66613; MUID:96035869
A; Accession: $66613
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A;Reference number: A58589; MUID:96062516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Note: sequence confirmed by chemical synthesis
C;Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynapt
C;Superfamily: alpha-conotoxin
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R. Lecroisey, A.; Tong, N.T.; Keil, B.
Eur. J. Blochem. 134, 261-267, 1981
A.; Title: Hypodermin B, a trypsin-related enzyme from the insect Hypoderma lineatum. A; Reference number: A20190; MUID:83261874
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C;Species: Conus ermineus (ermine cone)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: AS8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypodermin B - early cattle grub (fragment)
C;Species: Hypoderma lineatum (early cattle grub)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 18-Jun-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 27; DB 1; Length 18;
Pred. No. 7.2e+02;
2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                         Length 16;
                                                                                                                                                                                                                                                                                                                                                                   1; Indels
protein p12E - Friend murine leukemia virus (fragments)
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6.3e+02;
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Pred. No. 6.3e+
0; Mismatches
                           C; Species: Friend murine leukemia virus
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A;Molecule type: protein
A;Residues: 1-9;10-16 <HEN>
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A; Molecule type: protein
A; Residues: 1-16 <LEC>
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C;Accession: A39040
R;Cala, S.E.; Jones, L.R.
J. Biol. Chem. 266, 391-398, 1991
A;Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by cas A;Reference number: A39040; MUID:91093153
A;Accession: A39040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Hayashida, N.; Matsubayashi, T.; Shinozaki, K.; Sugiura, M.; Inoue, K.; Hiyama, T. Curr. Genet. 12, 247-250, 1987
A;Title: The gene for the 9 kd polypeptide, a possible apoprotein for the iron-sulfur A;Reference number: S07170; MUID:88210537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Cryptomeria japonica (Japanese cedar)
C; Species: Cryptomeria japonica (Japanese cedar)
C; Species: O: Mar-1993 #sequence_revision 03-Mar-1993 #text_change 11-Jan-2000
C; Accession: A44773
R; Taniai, M.; Ando, S.; Usui, M.; Kurimoto, M.; Sakaguchi, M.; Inouye, S.; Matuhasi, FEBS Lett. 239, 329-332, 1988
A; Title: N-re-reminal amino acid sequence of a major allergen of Japanese cedar pollen A; Reference number: A44773
A; Sccssion: A44773
A; Status: preliminary
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                                                                                                                                                                                                calsequestrin, cardiac muscle - dog (fragments)
C;Species: Canis lupus familiaris (dog)
C;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 23-Feb-1997
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C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase
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Pred. No. 1.7e+03;
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A;Molecule type: protein
A;Residues: 1-18 <CAL>
C;Keywords: cardiac muscle; heart; phosphoprotein
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Best Local Similarity 75.0
Matches 3; Conservative
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-21 <HAY>
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7 PYPEQQOPF 15
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avenin gamma-4 - oat (fragment)
N.Alternate names: CIP-1; coeliac immunoreactive protein 1
N.Alternate names: CIP-1; coeliac immunoreactive protein 1
C.Speciles: Avena sativa (oat)
C.Speciles: Toolilla, F.; Ortiz, M.L.; Mendez, E.
R.Rocher, A.; Collilla, F.; Ortiz, M.L.; Mendez, E.
R.Reference number: S29207
A.Title: Identification of the three major coeliac immunoreactive proteins and one alpha
A.Rocession: S29207
A
C; Accession: S10876
R; Assouline, Z.; Kerbiriou-Nabias, D.M.; Pietu, G.; Thomas, N.; Bahnak, B.R.; Meyer, D. Babchem. Biophys. Res. Commun. 153, 1159-1166, 1988
A; Title: The human gene for von Willebrand factor. Identification of repetitive Alu sequivalence number: S10876; WUID: 88268889
A; Reference number: S10876; WUID: 88268889
A; Accession: S10876
A; Accession: Ltanslation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-20 <ASS>
A; Cross-references: EMBL: X07258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical 1.5K protein - tomato chloroplast (strain Toko)
C:Species: chloroplast Lycopersicon esculentum (tomato)
C:Species: chloroplast Lycopersicon esculentum (tomato)
C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 23-Mar-1995
C;Accession: JQ2307
R;Kawagoe, Y.; Kikuta, Y.
Theor. Appl. Genet. 81, 13-20, 1991
A;Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.).
A;Reference number: JQ2306
A;Molecule type: DNA
A;Residues: 1-11 < KAW>
A;Experimental source: strain Toko
C;Genetics:
A;Genome: chloroplast
C;Keywords: chloroplast
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Pred. No. 1.1e+03;
3; Mismatches 3; Indels
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Pred. No. 1.1e+03;
0; Mismatches 1;
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trypsin (EC 3.4.21.4) precursor - minke whale (fragment)
C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
C;Accession: A61328
R;Bricteux-Gregoire, S.; Schyns, R.; Florkin, M.; Emmens, M.; Welling, G.W.; Beintema, J Biochim. Biophys. Acta 386, 244-255, 1975
A;Title: N·terminal amino acid sequence of trypsinogen from the lesser rorqual, Balaenop
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C;Species: Oryza sativa (rice)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C;Accession. PS0259
C;Accession. A.; Kamo, M.
submitted to JIPID, April 1993
A;Reference number: PS0209
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A.Molecule type: protein
A.Residues: 1-8 <BRL
C.Keywords: hydrolase; protein digestion; serine proteinase; zymogen
F:1-8/Domain: activation peptide #status experimental <APT>
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Pred. No. 1.9e+03;
1; Mismatches 3; Indels
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A,Molecule type: protein
A,Residues: 1-11 cTSU>
A,Experimental source: callus
C,Comment: molecular weight 39K, pI 5.7.
A;Molecule type: protein
A;Residues: 1-20 <TAN>
C;Superfamily: pectate lyase LAT59
C;Keywords: pOllen
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Copyright (c) 1993 - 2000 Compugen Ltd
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10 10 10 10 10 10 10 10 10		STANDARD; 1.40, Cr 1.40, La	tigerinus zoa; Chor chia; Anu 73;	MASS	R., S antim	ACTER ACTER EUS, ATION ITY:	Antibiotic; 10 11 11 A; 1344 MW;	24. 71. ative		STANDARD;	` ` `	oldes ss; Ac repto
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TRPB KLEAE SRTD_ATREN EOR2 MYRGU MGMT_BOVIN ANG1_BOVIN ANG1_BOVIN ANG1_CLICK LPK2_LOCMI TOP1_SALTY ANG7_CRIGE	ALIG	RD; PRT; Created) Last sequence	TIGERININ-1. Hoplobatrachus tigerinus (Rana tigerina). Eukaryota; Metazoa; Chordata; Craniata; Ve Amphibia: Batrachia; Anura; Neobatrachia; Hoplobatrachus. NCBL_TaxID=103373;	SPECTROMETRY, M.V., Vairamar	R., Sitaram N.; antimicrobial pe		Amidation. AMIDATION	Score Pred. 1; Mis		PRT;	ed) sequence annotati 99.1.3)	obacteri ineae; S
LSTAAU LATEAE ATREA MYRGU BOUIN BOUIN LOUICK LCHICK LSALTY CRIGE	ALIGNMENTS	PRT; 11 AA. ed) sequence update)	rtebrata; Ranoidea;	OMETRY, AND DISULFIDE   Vairamani M., Raju N.P	tides from the	11). VITY AGAINST B.SUBTILIS, AND S.CEREVISIAE. ED. METHOD=MAIDI.	midation. AMIDATION. A2087DC960476056 CRC64;	30; DB 1; Len No. 82; matches 1;		21 AA.	ted) sequence update) annotation update) .99.1.3) (FRAGMENT).	Streptomyces sphaeroides.  Streptomyces sphaeroides.  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; St
P145553 K P145553 K P14511 a P1417 B P1417 B P10117 B P10118 G P41688 B P40686 S P09037 C			Euteleostomi; Ranidae;	BONDS.	Indian frog	LIS, E.COLI		gth 11; Indels 0;				ae; Streptomyces
stapnylococ klebsiella atractaspis myrmecia gu bos taurus bothrops ja bos taurus gallus gall locusta mig salmonella crinia geor kassina mac			omi;		g Rana	, i.		Gaps				res.
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COXA_THUOB
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                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                          CATALYTIC ACTIVITY: ATP-EEPENDENT BREAKAGE, PASSAGE AND REJOINING OF DOUBLE-STRANDED DNA.
SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE BNZYME FORMS AN A2B2 TETRAMER.
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"Alpha-conotoxin EI, a new nictinic acetylcholine receptor antagonist with novel selectivity.";
Biochemistry 34:14519-14526(1995).
-!-FOWCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THES
           STRAIN-NCIB 11891;
MEDLINE-93316846; PubMed-8392138;
Thiara A.S., Cundliffe E.;
"Expression and analysis of two gyrB genes from the novobiocin
                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conus ermineus (Atlantic fish-hunting cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
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Pred. No. 3.2e+02;
5; Mismatches 5; Indels
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60A61A6C427A6B5E CRC64;
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
ALPHA-CONOTOXIN EI.
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MEDLINE-96062516; PubMed-7578057;
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28.6%;
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
Scombridae; Thunnus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                          "The subunit structure of cytochrome-c oxidase from tuna heart and
                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
TRYPSIN PRECURSOR (EC 3.4-21.4) (FRAGMENT).
Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
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01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CYTCCHROME C OXIDASE POLYPEPTIDE VA-1 (EC 1.9.3.1) (FRAGMENT).
Thunnus obesus (Bigeye tuna).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F., Kadenbach B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Serine protease; Digestion; Pancreas; Zymogen. PROPEP 1 8 ACTIVATION PEPTIDE.
             Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A6D751BB58760A86 CRC64;
Score 27; DB 1; Ler
Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 24; DB 1;
Pred. No. 9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 AA.
                                                                                                                                                                                               16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR001254; Trypsin.
PROSITE: PS50240; TRYPSIN.DOM: PARTIAL.
PROSITE: PS00134; TRYPSIN.HIS; PARTIAL.
PROSITE; PS00135; TRYPSIN.SER; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRYPSIN.
                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Heart, and Liver;
MEDLINE-97454291; PubMed-9310366;
           22.0%;
35.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.5%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1825 MW;
                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                            1 CTVHPIPDEDSPWI 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              >16
                                                                                                        4 CCYHPTCNMSNPQI 17
             Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 PIPDED 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 PIDDDD 7
                                                                                                                                                                                             TRYP_FELCA P81071;
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8 ¥ ¥ C C C C C C C R T

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Hollman G.M., Cook B.J., Nachman R.J.;
Hollman G.M., Cook B.J., Nachman R.J.;
Primary structure and synthesis of a blocked myotropic
neuropeptide isolated from the cockroach, Leucophaea maderae.";
Comp. Blochem. Physiol. 85c:219-224(1986).
-!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).
-!- MISCELLANBOUS: AN ANALOG WITHOUT THE N-TERMINAL PCA RESIDUE WAS
SYNTHESIZED AND FOUND TO EXHIBIT GREATER ACTIVITY (144%) THAN THE
PARENT NEUROPEPTIDE. THE PORTION OF THE SEQUENCE OF LPK MOST
CRITICAL FOR THE MYOTROPIC PROPERTIES IS LIMITED TO THE
PENTAPEPTIDE FRAGMENT FTPRL.
                                                                                                       01-13AN-1990 (Rel. 13, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
01-FEB-1994 (Rel. 28, Last annotation update)
LEUKOPYROKININ (LPK) (LEM-PK).
Leucophaea maderae (Madelra cockroach).
Eukaryotta: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygotta; Meoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nachman R.J., Holman G.M., Cook B.J.,
"Active fragments and analogs of the insect neuropeptide leucopyrokinin: structure-function studies.";
Biochem. Biophys. Res. Commun. 137:936-942(1986).
                                                                                                                                                                                                                                                                                                                  16 AA; 1828 MW; 3C0E6735D98B38A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMIDATION.
92341771A9D5A1B6 CRC64;
Bacteria, Firmicutes, Bacillus/Clostridium group, Bacillus/Staphylococcus group, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                    Score 23; DB 1; 1
Pred. No. 1.2e+03;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neuropeptide; Amidation; Pyrokinin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Head;
MEDLINE=87052651; PubMed=2877794;
                                                                                           MEDLINE=98455825; PubMed=9782505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=86269041; PubMed=3015140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIK; AZ396/; AZ396/.
InterPro; IPR001484; Pyrokinin.
PROSITE; PS00539; PYROKININ; 1.
                                                                                                                                                                                                                                                                                                                                                                      18.7%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     949 MW;
                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE, AND SYNTHESIS.
                                                                                                                                                                                                                                                                                Hydrolase; Manganese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A23967; A23967
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 HPIPDEDS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 HKNPDTDT 15
                                  NCBI_TaxID=1404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPK_LEUMA
P13049;
                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                   NON TER
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LPK_LEUMA
                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                              -:- FUNCTION: THIS THE HERE A-CONTAINING CHAIN OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
-: CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.
-: SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
-: SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
OXIGOTEGUCIASE; HEME: Mitochondrion; Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.; "Isolation, identification and synthesis of locustamyotropin Il additional neuropeptide of Locusta migratoria. Member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-306.1991 (Rel. 19, Created)
01-406-1991 (Rel. 19, Last sequence update)
01-406-1991 (Rel. 19, Last sequence update)
01-406-1991 (Rel. 19, Last annotation update)
LCCUSTAMYOTROPIN 2 (LLOW-MT-2).
Locusta migratoria (Migratory locust).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
NCBI_TaxID=7004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cephalomyotropic peptide family.";
Insect Biochem. 20:479-484(1990).
-!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MOS-2001 (Rel. 40, Last annotation update)
MANGANESE-DEPENDENT INORGANIC PYROPHOXPHAYDES (EC 3.6.1.1)
(PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) (FRAGMENT).
                                                                                                                                                                                                                                       19.5%; Score 24; DB 1; Length 20; 50.0%; Pred. No. 1.18+03; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.7%; Score 23; DB 1; Length 8;
                                                                                                                                                                                    20 AA; 2404 MW; 7E82E43B7157355E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD_RES 8 8 AMIDATION.
SEQUENCE 8 AA; 934 MW; 26341771A9CAA87B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MYOTROPIC ACTIVITY).
-!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
InterPro; IPRO01484; Pyrokinin.
PROSTIF; PSO0539; PYROKININ; 1.
Neuropeptide; Amidation; Pyrokinin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1e+05;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                     Biochem. 248:99-103(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.78;
                                                                                                                                                                                                                                         Query Match 19.5
Best Local Similarity 50.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Corpora cardiaca;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPAC.
Bacillus megaterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                  10 DSPWIT 15
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12 DARWVT 17
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3 DFTPRL 8
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P56948;
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P22396;
                                                                                                                                                                  NON_TER
SEQUENCE
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 liver.";
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Matches

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Length 16;

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2 PHPDE 6
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P42987;
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MOD_RES
SEQUENCE
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MEDLINE=90287814; PubMed=2356157;
Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
Sommaco M., Severini C., de Biase D., Barra D., Bossa F.,
Roberts J.D., Melchiorri P., Erspamer V.;
"Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guntheri.";
Peptides 11:299-304(1990).
-!- FUNCŢION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudophryne guentheri (Fróg).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
Pseudophryne.
                                                                                                                                                                                                                                                                                TISSUE-Corpora cardiaca;

Predel R., Kellner R., Gaede G.;

"Myotropic neuropeptides from the retrocerebral complex of the stick insect, Carausius morcosus (Phasmatodea: Lonchodidae).";

Eur. J. Entomol. 96:275-278(1999).

-!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).

-!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).

-!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.

InterPro: IRRO01484; Pyrokinin.

MOD RES 11 11 AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                  Gaps
                                                                                                                                                                                                     Carausius morosus (Indian stick insect).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Phasmatodea; Heteronemiidae;
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Pred. No. 1.2e+03;
1; Mismatches 2; Indels
                               2; Indels
          DB 1; Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                      11 11 AMIDATION.
11 AA; 1236 MW; 2BFA5225BB46C1A8 CRC64;
         Score 22; DB 1;
Pred. No. 1e+05;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
KASSININ-LIKE PEPTIDE K-I (PG-KI).
                                                                                                                                                        20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PYROKININ-1 (CAM-PK-1) (FXPRL-AMIDE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 AA.
                                                                                                                                     11 AA.
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                                                                                                                                                                                                                                                                        SEQUENCE, FUNCTION, AND MASS SPECTROMETRY
                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.9%;
57.1%;
         Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                     15 TDSTPRI 21
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                                                                    ( |||:
2 TSFTPRL 8
                                                                                                                                   PKC1_CARMO
P82684;
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P42986;
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TKN1_PSEGU
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PKC1_CARMO
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MEDLINE-90287814; PubMed=2356157;
Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
Roberts J.D., Melchiorri P., Erspamer V.;
Six novel tachykinin- and bombesin-related peptides from the skin of
the Australian frog Pseudophryne guntheri.";
Peptides 11:299-304(1990).
-!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 22; DB 1; Length 11; Pred. No. 1.2e+03; 0; Mismatches 1; Indels
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Pred. No. 1.2e+03;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                 PROSTIE: PSOUCE, TACHYRININ: 1.

Tachykinin: Neuropeptide: Amidation.

MOD_RES 1 PYRROLIDONE CARBOXYLIC ACID.

MOD_RES 11 11 AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMIDATION.
3A247C37C9CB1AB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          3DBA7C37C9CBIAB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY
                                                                                  -! - SIMILARITY: BELONGS TO THE TACHYKININ FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Last Sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
KASSININ-LIKE PEPTIDE K-II (PG-KII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fachykinin; Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; C60409; C60409.
InterPro; IPR003580; Protachykinin.
InterPro; IPR002040; Tachykinin.
Fam; PF02202; Tachykinin; 1.
SMART; SM00203; TK; 1.
PROSITE; PS00267; TACHYKININ; 1.
                                                                                                          PIR; B60409; B60409.
InterPro; IPR003580; Protachykinin.
InterPro; IPR0020040; Tachykinin.
Pfam; PF02202; Tachykinin; 1.
SMART; SM00203; TK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudophryne guentheri (Frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.9%;
80.0%;
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80.0%;
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 11 AA; 1269 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 AA; 1246 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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19 AA; 2200 MW;
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Best Local Similarity 60.0
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                 FIBRINOPEPTIDE B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGREGATION.
                                                                                                                                                                                                                  | :||
2 HSLPD 6
                                                                                                                                                                                                      4 HPIPD 8
                         FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
NON_TER
SEQUENCE
                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                       FIBB_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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ECD1_LYMDI
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   QC 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DESCRIPTION DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.

-: CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).

-: SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
                                                                                                                                                                                     MEDLINE-90287814; PubMed=2356157; Simmaco M., Severini C., de Biase D., Barra D., Bossa F., Simmaco M., Severini C., de Biase D., Barra D., Bossa F., Roberts J.D., Melchiorri P., Erspamer V.; Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guntheri."; Peptides 11:299-304(1990).
-:- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                         EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dunn M.J., Corbett J.M., Wheeler C.H.; "HSC-2DPAGE and the two-dimensional gel electrophoresis database of dog heart proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
SUPEROXIDE DISMUTASE [MN], MITOCHONDRIAL (EC 1.15.1.1) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 22; DB 1; Length 11; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                         PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   AMIDATION.
3A247C2CC9CB1AB7 CRC64;
                                                                                                                                                                                                                                                                                                            -! - SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
SUBSTANCE P-LIKE PEPTIDE I (PG-SPI).
                      11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            Tachykinin; Neuropeptide; Amidation.
MOD_RES 1 1 PYRROLI
                                                                                                                                                                                                                                                                                                                     PIR; E60409; E60409.
InterPro; IPR003580; Protachykinin.
InterPro; IPR002040; Tachykinin.
                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Heart;
MEDLINE=98163340; PubMed=9504812;
                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02202; Tachykinin; 1.
SMART; SM00203; TK; 1.
PROSITE; PS00267; TACHYKININ; 1.
                                                                                             Pseudophryne guentheri (Frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.9%;
80.0%;
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11 AA; 1294 MW;
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                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                           NCBI_TaxID-30349;
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                                                                                                                                Pseudophryne.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ||||
2 PNPDE 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 PIPDE 9
                                                                                                                                                                             TISSUE-Skin;
                                                                                                                                                                                                                                                                                                MUSCLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SODM_CANFA
P54712;
                      TKN4_PSEGU
                                                                                                                                                                                                                                                                                                                                                                                                                   MOD_RES
SEQUENCE
                                                                                                                                                                  SEQUENCE
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                                 P42989;
RESULT 12
TKN4_PSEGU
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Acta Chem. Scand. 19:1789-1791 (1965).
-!- FUNCTION: FIBRINGEN HAS A DOUBLE FUNCTION: XIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS. MISCELLANGOUS: CONVERSION OF FIBRINGEN TO FIBRIN IS TRIGGERED BY THROMEIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
-i- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
-i- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartlodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
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                                                                                                                                                                                                                                                                                                                                                                                             Score 22; DB 1; Length 13;
Pred. No. 1.4e+03;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.9%; Score 22; DB 1; Length 19; 35.7%; Pred. No. 2.1e+03;
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                                                                                                                                                                                                                                                                                                         13 AA; 1476 MW; 9C9651DE8BE0672A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09F87E44F4F3863D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002181; Fibrinogen_C.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
Blood coagulation; Plasma; Sulfation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 21 AA. P80936; P55898; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 11-NOV-1997 (Rel. 35, Last annotation update) TESTIS ECDYSIOTROPIN PEPTIDE 1 (TE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-JAN-1990 (Rel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                             Oxidoreductase; Manganese; Mitochondrion. NoN_TER 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blomback B., Blomback M., Grondahl N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SULFATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                    HSSP; P04179; 1MSD.
HSC-ZDPAGE; P54712; DOG.
HTGFPPO; IPR001189; SOD_MI.
Pfam; PF00081; sodfe; 1.
PROSITE; PS00088; SOD_MN; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                   17.9%;
60.0%;
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OS Lymantria dispar (Gypsy moth).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pteryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pteryota; Neoptera; Endopteryota; Lepidoptera; Glossata; Ditrysia;

OC Noctuoidea; Lymantriidae; Lymantria.

OX NUBI_TaxID=13123;

RN [1]

RP SEQUENCE.

RC TISSUE-Brain;

RA Magner R.M., Loeb M.J., Kochansky J.P., Gelman D.B., Lusby W.R.,

RA Magner R.M., Loeb M.J., Kochansky J.P., Gelman D.B., Lusby W.R.,

RA Magner R.M., Loeb M.J., Kochansky J.P., Gelman D.B., Lusby W.R.,

RA Magner R.M., Loeb M.J., Kochansky J.P., Gelman D.B., Lusby W.R.,

RA Magner R.M., Loeb M.J., Kochansky J.P., Gelman D.B., Lusby W.R.,

RA Tadentification and characterization of an ecdysiotropic peptide from

RT Tadentification and characterization of an ecdysiotropic peptide from

RT Arch. Insect Biochem. Physiol. 34:175-189(1997).

CC -1- FUNUTION: START OR BOOST ECDYSTEROID SYNTHESIS IN TESTIS OF LARVAE

CC AND PUPAE.

OUETY MAtch

OUETY MAtch

Arch. Insect Biochem. Physiol. 34:175-189(1997).

AND PUPAE.

AND PUPAE.
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Search completed: February 21, 2002, 16:52:21 Job time: 520 sec

OM protein

Run on:

Sequence:

Minimum DB Maximum DB

Database

Result

Searched:

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099409 rattus sp. 097599 micrococcus 04558 bacillus sp 09ev48 staphylococ 09ev70 rattus sp. 094710 rattus sp. 056132 porcine cir 09f444 desulfovibr
                                            Q9urc7 saccharomyc
Q91188 equus cabal
Q9551 lampetra fl
Q95915 triticum tu
Q58817 oryza sativ
Q46747 escherichia
Q9har9 homo sapien
Q9y6d8 homo sapien
P70649 mus musculu
                           Q9twh2 oxytricha g
O91329 human immun
                                                                                                                                                                                            Q9s929 glycinė max
O62645 saguinus oe
                                                                                                                                                                                                              Q9prn1 petromyzon
Q62546 mus spretus
                                                                                                                                                                         Q9qv03 rattus sp.
Q9udd6 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENVELOPE PROTEIN (FRAGMENT).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE.

MEDLINE-5028770; PubMed=7524281;

Schroder J.M. Kameyoshi Y., Christophers E.;

Platelets secrete an eosinophil-chemotactic cytokine which is member of the C-C-chemokine family."

Adv. Exp. Med. Biol. 351:119-128(1993).

SEQUENCE I 6 AA; 1786 MW; 8B041B46AEACC2A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31; DB 4; Length 16;
Pred. No. 3.6e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
EOCP-1-EOSINOPHIL-CHEMOTACTIC CYTOKINE.
                          09TWH2
091329
091329
09U8C7
09N186
09PS51
09S817
046747
09CV9
09ES99
09ES99
09ES99
09EYH3
09QV73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.2%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 55.6'
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11 SPWITDSTP 19
Q61871
Q61871;
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RESULT
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Q9tr87 bos taurus
Q9twx8 manduca sex
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P82258 aspergillus
Q9tri3 bos taurus
                                                                       (without alignments)
51.170 Million cell updates/sec
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                                                              February 21, 2002, 16:51:54; Search time 60.03 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
          GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                 473505 segs, 146272329 residues
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Maximum Match 100%
Listing first 45 summaries
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sp_human:*
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sp_mammal:*
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sp_vertebrate:*
sp_unclassified:*
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Gaps

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STRAIN=SR1;
MEDLINE=95078947; PubMed=7987414;
MEDLINE=95078947; PubMed=7987414;
Merkle T., Haizel T., Matsumoto T., Harter K., Dallmann G., Nagy F.;
"Phenotype of the fission yeast cell cycle regulatory mutant piml-46
is suppressed by a tobacco cDNA encoding a small, Ran-like GTP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Mol. Kall Biol. 10:3717-3726(1990).
MGD; MGI:104628; Penk2.
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                 Nicotiana tabacum (Common tobacco).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta: eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-90287163; PubMed-2355920;
Kilpatrick D.L., Zinn S.A., FitzGerald M., Higuchi H., Sabol S.L.,
Meyerhardt J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 4.7e+02;
2; Mismatches 0; Indels
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
BETA-CRYSTALLIN ISOFORM A3 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
SPERMATGENIC-SPECIFIC PROENKEPHALIN.
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80.0%;
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EMBL; L16788; AAA73565.1; -.
Cell cycle; GTP-binding.
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66.78;
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Best Local Similarity
Matches 4; Conserv
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Matches 4; Conserv
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PLPDDD 10
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Merkle T., Haizel T., Matsumoto T., Harter K., Dallmann G., Nagy F.,
"Phenotype.of the fission yeast cell cycle regulatory mutant pim1-46
is suppressed by a tobacco cDNA encoding a small, Ran-like GTP-binding
                                             STRAIN-AKR; TISSUE-THYMUS;
MEDLINE-88091045; PubMed=2826802;
Laigret F., Repaske R., Boulukos K., Rabson A.B., Khan A.S.;
Laigret I F., Repaske R., Boulukos K., Rabson A.B., Khan A.S.;
murine leukemia progenitor sequences of mink cell focus-forming (MCF)
murine leukemia viruses: ecotropic, xenotropic, and MCF-related viral
RNAS are detected concurrently in thymus tissues of AKR mice.";
J. Virol. 62:376.386(1988).
EMBL: M19049; AAA18408.1;
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Eukaryota: Viridiplantae: Streptophyta; Embryophyta: Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; eussterids I; Solanales; Solanaceae; Nicotiana.

NCBI_TaxID=4097;
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Pred. No. 4.6e+02;
3; Mismatches 2; Indels
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Pred. No. 4.7e+02;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q40562 PRELIMINARY; PRT; 15 AA. Q40562; Ol.NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
                                                                                                                                                                                                       InterPro; IPR002050; Env_polyprotein.
Pfam; PF00429; ENV_polyprotein; 1.
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66.78;
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EMBL; L16786; AAA73564.1; -.
Cell cycle; GTP-binding.
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Best Local Similarity 44.4
Matches 4; Conservative
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Matches 4; Conserv
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SEQUENCE FROM N.A.
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9 PLKDKINPW 17
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2 PMPGSMGPW 10
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           Exp. Eye Res.
SEQUENCE 15
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Urbach E., Chisholm S.W.;
Urbach E., Chisholm S.W.;
"Genetic diversity in Prochlorococcus populations flow cytometrically sorted from the Sargasso Sea and Gulf Stream.";
Limnol. Oceanog. 43:1615-1630(1998).
EMBL; AF070208; AAD23258.1; -.
NON_TER 21 21.
       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
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                                                          MEDILINE-96030616; PubMed-7556477;
Shearer T.R., Shih M., Azuma M., David L.L.;
"Precipitation of crystallins from young rat lens by endogenous
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
                                                                                                                                                 Length 20;
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Pred. No. 6.8e+02;
2; Mismatches 6; Indels
                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC83509577BFF27F CRC64;
                                                                                                     EXP. EYE Res. 61:141-150(1995).
SEQUENCE 20 AA; 2147 MW; C5860A30C6220681 CRC64
                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYTOCHROME B6/F COMPLEX SUBUNIT IV (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                 Score 30; DB 11;
Pred. No. 6.4e+02;
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40.08;
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Best Local Similarity 42.9
Matches 6; Conservative
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Q9X3L7;
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Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matsura E., Igarashi M., Igarashi Y., Nagae H., Ichikawa K., Yasuda T., Koike T.;
"Molecular definition of human beta 2-glycoprotein I (beta 2-GPI) by conning and inter-species differences of beta 2-GPI in alternation of anticardiolipin binding.";
Int. Immunol. 3:1217-1221(1991)
SEQUENCE 10 As; 1100 MW; 94E681B767376EA1 CRC64;
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MEDLINE-86650639; PubMed-3933505;
Nagamine Y. Pearson D., Grattan M.;
Exon-intron boundary sliding in the generation of two mRNAs coding for porcine urokinase-like plasminogen activator.";
Blochen. Blochen. Res. Commun. 132:563-569(1985).
BISSP; P00749; 1URK.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1801 MW; 9989927EA849E253 CRC64;
61:141-150(1995).
AA; 1702 MW; 3F35688E1C5F233C CRC64;
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Last annotation update)
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Last annotation update)
                                                                                           Score 29; DB 11;
Pred. No. 6.6e+02;
1; Mismatches 4
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Pred. No. 8.3e+02;
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                                                                                           23.68; 44.48;
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80.0%;
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9 EDSPWITDS 17

us-08-753-851-6.rspt

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SEQUENCE FROM N.A. Roberts D.L., Dalgleish R., Cohen G.M., MacFarlane M.; "The mammalian CED4 homologue, APAF1, exists as two distinct forms in
                                                                                                                                                                                                                                                                 MEDLINE-20083971; Pubmed-10613847;
Caetano A.R., Shiue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
Bowling A.T., Murray J.D.;
Bowling A.T., Murray J.D.;
A comparative gene map of the horse (Equus caballus).";
Cenome Res. 9:1239-1249(1999).
EMBL; AF134056; AAF31299.1; -.
NON_TER 1 1
NON_TER 10 10
SEQUENCE 10 AA; 1144 MW; C4EA25676B02D6DD CRC64;
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Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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Pred. No. 2.2e+03;
2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human cells.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AJ133645; CAB65087.1; ...
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                                                                                                                   01-0cr-2000 (TrEMBLrel. 15, Created)
01-0cr-2000 (TrEMBLrel. 15, Last sequence update)
01-0cr-2000 (TrEMBLrel. 15, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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Pred. No. 1.2e+03;
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75.0%;
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Matches 3; Conserv
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MEDLINE-94223692; PubMed-8169960;
Perez M.L., Valverde J.R., Battesse R.;
Speciation in the Artemia genus: mitochondrial DNA analysis of bisexual and parthenogenetic brine shrimps.";
J. MOI. Evol. 38:156-168(1994).
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Hamel A.L., Nayar G.P.S.;
Hamel A.L., Nayar G.P.S.;
"Nucleotide sequence of four different isolates of circovirus detected in pigs with various clinical syndromes.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF109399; AAD03077.1: -FDOBES8BAFAA923 CRC64;
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Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;
Artemiidae; Artemia.
NCBL_TaxID=6663;
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           Score 27; DB 4; Length 17; 
Pred. No. 1.5e+03; 
0; Mismatches 7; Indels
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
0RF-7.
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Viruses; ssDNA viruses; Circoviridae; Circovirus.
NCBL_TaxID=85544;
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19 AA; 2246 MW;
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01-NOV-1996 (TrEMBLrel. 01,
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01-NOV-1998 (TrEMBLrel. 08,
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Matches 5; Conservative
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SEQUENCE
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RESULT 15
PR2258
PRELIMINARY; PRT; 20 AA.

AC PR2258
DT O1-MAX-2000 (TrEMBLrel. 13, Last sequence update)
DT O1-MAX-2000 (TrEMBLrel. 13, Last sequence update)
DT O1-MAX-2000 (TrEMBLrel. 13, Last sequence update)
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RN SEQUENCE.
OX NCB1_TAXID=5059;
RN [1]
RP SEQUENCE.
RC STRAIN-AFL-1505 / INDIAN ISOLATE;
RA Sarma P.U., Paliwal A., Fairwell T.;
RL Submitted (DEC-1999) to the SYRISS-FROT data bank.
CC -1-FUNCTION: BINDS TO IGG AND IGE.
CC -1-FUNCTION: BINDS TO IGG AND IGG-DING TO I
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Search completed: February 21, 2002, 16:51:54 Job time: 533 sec

Protein tyrosine p C3/C4/C5-derived c Src S43 domain bin Papilloma virus ty SRC SH3 domain-bin Protein tyrosine p

Artificial peptide Casein antimicrobi Casein antimicrobi Human secreted pro

Aspergillus niger Human secreted pro Protein tyrosine p Immunogenic peptid p53bp2 SH3 domain

Aspergillus niger Cladosporium herba Cladosporium herba

HLA-A2 restricted Neutral invertase Sequence of P85 po PL peptide #4. Sy CD3n PL peptide. CD3n PL peptide. Peptide containing Peptide binding in IL-IRII binding pe

Interleukin-1 type IL-1 antagonist pe Hepatitis B virus Human secreted pro Cytotoxic T-lympho

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Perfect

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Use of CD44 protein and new peptide derivs - for developing prods for inflammation, immune-mediated tissue damage and tumour cell
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                                               AAW17007
AAY67260
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AAB34527
AAB65576
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 93WO-US10412.
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 CD44 peptide CD44-6.
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Homo sapiens.
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Human bcl2 proto-o
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23.976 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                       522463 seqs, 74073290 residues
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                                                                February 21, 2002, 16:42:57
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Listing first 45 summaries
                                               protein search, using sw model
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AAM15658
AAM28159
AAM19218
AAM19218
AAM31875
AAM31875
AAR26224
AAR25776
AAR4521170
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Gapop 10.0 , Gapext 0.5
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                                                                                                     US-08-753-851-6
123
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118
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114
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118
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Match
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32.5
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Score

Result No.

123 39 40 39 5 39 5 36 36 36 37 38 38 38

110 110 110

us-08-753-851-6.rag

8 × C C C C C C X S

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(SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to human single exon nucleic acid probes
                                                                                                                                                                                                               Peptide #2092 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                    Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; SEQ ID No 20484; 487pp; English.
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Pred. No. 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank DR;
                                                                                                 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM28159 standard; Protein; 18 AA.
                                                                                               AAM15658 standard; Protein; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.1%;
42.1%;
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26-MAY-2000; 2000US-0207456.
30-UUN-2000; 2000US-0608408.
33-AUG-2000; 2000US-053386.
21-SEP-2000; 2000US-0234687.
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04-OCT-2000; 2000GB-0024263.
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ctt----ksspwcpnstp
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     pnpdapw----tprv 16
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                                                                                                                                                                                                                                                                        cervical cancer
                                                                                                                                                                                                                                                                                                                                                WO200157278-A2.
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                                                                                                                                     AAM15658;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
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                                                                              AAM15658
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                                                      mediated tissue damage such as occurs in the course of autoimmune diseases, e.g. rheumatoid arthritis. It can also be used for determining metastatic potential or to treat or prevent tumor cell metastasis. This peptide corresponds to AA 200-219 of the CD44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antiviral agent disrupting binding of VP22 to VP16 or gB -useful for treating infections caused by herpes simplex, e.g. cold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a herpes simplex virus (HSV) truncated tegument protein VP22 derived peptide. VP22 was used in the preparation of a novel antiviral agent, which inhibits the maturation and/or replication of HSV by disrupting association between VP22 and VP16 and/or gB. The agent can be used to treat, e.g. cold sores, genital herpes, chickenpox and shingles.
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                                         peptide can be used for treating inflammation and immune-
                                                                                                                                                                                                                               Length 21;
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                                                                                                                                                                                                                             100.0%; Score 123; DB 15;
100.0%; Pred. No. 1.5e-10;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 32.5%; Score 40; DB 19; Best Local Similarity 46.7%; Pred. No. 39; Matches 7; Conservative 3; Mismatches 1;
                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
Claim 4; Page 14; 83pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide; 20
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                                                                                                                                                                                                                                                                    21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Herpes simplex virus. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-130696/12
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW47198 standard;
                                                                                                                                                                                                                                                Best Local Similarity
Matches 21; Conserv
                                                                                                                                   protein sequence.
                                                                                                                                                                      21 AA;
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                                                                                                                                                                        Sequence
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AAW47198

Dp

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Gaps

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(see AA100010-AA110067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                     predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                              Novel single exon nucleic acid probe used to measuring gene expression
                                                                                                                                                                                                                                                                                                                                                    The present invention relates to novel single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide #5652 encoded by probe for measuring cervical gene expression.
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Pred. No. 41;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID No 12135; 322pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            breast disease and non-carcinoma tumours
                                                                                                                                                                                              Rank DR;
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                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                              Chen W,
                                  2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-023669.
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                   2000US-0180312
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                                                                                                                                                                                            Penn SG, Hanzel DK,
                                                                                                                                                                                                                            WPI; 2001-476286/51
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nes 8; Conserv
                                                                                                                                                                                                                                                                                a human breast
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                    21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                   04-FEB-2000;
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                                                     30-JUN-2000;
                                                                       03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                  Peptide #2196 encoded by probe for measuring placental gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta {\cdot}
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                                                                     Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 27; SEQ ID No 28428; 654pp; English.
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Pred. No. 41
                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank DR;
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30-JUN-2000; 2000US-0668408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GS-0024263.
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42.1%;
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                       genetic disorder
                                                                                                                                                        WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157270-A2
                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
17-0CT-2001
                                                                                                                                                                                                                                                            04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2001
                                                                                                                                                                                          09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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AAM03395 RESULT

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Gaps

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Gaps

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Pred. No. 1.2e+02; 1; Mismatches 3; Indels

Length 17;

Score 36; DB 22;

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The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
     analyzing gene expression in human placenta
                          SEQ ID No 32144; 654pp;
                                                                                                                                                                  29.3%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92WO-US00944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91US-0652531
91US-0745382
                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEMY ) GENETICS INST INC.
                                                                                                                                                                                        Conservative
                                                                                                          human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lavallie ER, McCoy J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-300041/36.
                                                                                                                                                                           Best_Local Similarity
Matches 5; Conser
                                                                                                                                                                                                             7 PDEDSPWIT 15
                                                                                                                                                                                                                                    psssspwlt 15
                                                                                                                                17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                         20-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-FEB-1991;
14-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9213955-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-AUG-1992
                           Claim 27;
                                                                                                                                                                                                                                                                                                                   AAR26224;
                                                                                                                                 Sequence
                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                   7
    qq
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                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                The present invention relates to human single exon nucleic acid probes (SENF: see AA110068-AA128459). The present sequence is a peptide encoded by one such probe. The SENPs are defived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical useful in grading and/or staging of diseases of the cervix, notably everyical cervical cancer.
                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide #5912 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                     .
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                                                                                          Human genome-derived single exon nucleic acid probes useful fanalyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                          29.3%; Score 36; DB 22; Length 17; 55.6%; Pred. No. 1.2e+02; 1ve 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 microarray; human; placenta; antenatal diagnosis;
                                                                                                                            Claim 27; SEQ ID No 24044; 487pp; English
                                               Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM31875 standard; Protein; 17 AA.
                       (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
                                              Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
04-OCT-2000; 2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US00663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                   Conservative
                                              Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanzel DK,
                                                                     WPI; 2001-488901/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                        7 PDEDSPWIT 15
                                                                                                                                                                                                                                                                                                                                                                                      | |||:|
psssspwlt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genetic disorder
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                                                                                                                                                                                                                                                                                          11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
04-OCT-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-0CT-2001
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                                                                                                                                                                                                                                                                                           Sequence
                                              Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM31875;
                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM31875
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protein. The protein encodes an enterokinase cleavage site and was inserted into the active site loop of thioredoxin between residues G34 and P35. The fusion protein containing this internal is enterchinase site was expressed at levels equivalent to native thioredoxin and was cleaved with an enterokinase treatment. The fusion protein was found to be as stable as native thioredoxin, being stable to a 10 minute incubation at 80C. It appears that the active-site loop of thioredoxin can tolerate a wide variety of peptide insertions resulting in soluble fusion proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                 thioredoxin; soluble; stable; stability; research; diagnosis; therapeutics; produce eukaryotic in prokaryotic; improved solubility; enhanced heat stability; enhanced protease stability; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA sequence encoding a fusion protein - comprises thioredoxin and a heterologous protein sequence; used to produce stable soluble proteins e.g. IL-11
                                                                                                                                                                                                                                                                                                           Peptide #7 inserted into active site loop of thioredoxin.
     AA.
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AAR26224 standard; Protein; 14
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AAR45927;

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AAR45927 RESULT

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diabetes mellitus type microtubule associated protein, Tau, Big Tau, ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M; neurofilament-F; presenilin I; presenilin II; cellular tumour antigen; glial fibrillary acidic protein; GRAP; p53; semaphorin III; HUPF-I; bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A; high mobility group protein-C; neuroendocrine specific protein A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteins and peptide(s) fused to thioredoxin or thioredoxin-like molecules – useful for prodn. of large amts. of heterologous proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer; frameshift mutation; age-related disease; neurodegenerative disorder; Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal; Huntington's disease; multiple sclerosis; alcoholic liver disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Small peptides (AAR75770-81) of random composition and hydrophilic, hydrophobic or neutral character were inserted into the active site loop (G34-P35) of E. coll thioredoxin (AAR75769). The resulting flusion proteins were expressed in the soluble cellular fraction of E. coll G1724 hosts at levels comparable to native thioredoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human bcl2 proto-oncogene mutant protein fragment 18.
                                                                                                                                                                                                                                                                                                                                                                                       Mccoy J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 16; L
Pred. No. 1.8e+02;
1; Mismatches 2;
                                                                                       Thioredoxin active site loop insert peptide.
                                                                                                                                                                                                                                                                                                                                                                                       Lavallie ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY21170 standard; Protein; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Page 39; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                         Thioredoxin; fusion protein.
                                                                                                                                                                                                                                                                           94WO-US14179
                                                                                                                                                                                                                                                                                                                                                                                       Grant K,
                                                                                                                                                                                                                                                                                                               93US-0165301
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                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                   (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-224326/29.
                                                                                                                                                                                                                                                                                                                                                                                     Diblasio-Smith E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 PWITDSTP 19
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| pwingatp
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                                                                                                                                                                                                                                                                           08-DEC-1994;
                                                                                                                                                                                                                                                                                                               10-DEC-1993;
                                                   20-NOV-1995
                                                                                                                                                                                                 WO9516044-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JUL-1999
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                                                                                                                                                             Synthetic
                 AAR75776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           random insertions of 14 amino acids were made at levels comparable to native thioredoxin. All of them were found in the soluble cellular fraction. The inserted sequences (ARM45921-R45932) include examples that were both hydrophobic and hydrophilic, and examples which contained Cys residues. It appears that the active site loop of thioredoxin can tolerate a wide variety of peptide insertions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Twelve randomly generated peptide insertions were made into the active site loop of E.coli thioredoxin, between residues Gly34 and Pro35. Each of the thioredoxin fusion proteins containing these
                                                                                                                                                                                                                                                                                                                              Randomly generated peptide 7 for insertion in E.coli thioredoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fusion proteins with a thioredoxin-like protein for high stability and solubility
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                                                                                                                                                                                                                                                                                                                                                                fusion gene; fusion protein; randomly generated peptide; bacterial thioredoxin; E.coli; trxA gene; active site loop; stability; increase; heterologous protein production; protein folding.
               Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 14;
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                                                   Indels
             Score 34; DB 13; L. Pred. No. 1.8e+02; 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 15; L. Pred. No. 1.8e+02; 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3 and Example 12; Page 32; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         resulting in soluble fusion proteins
                                                                                                                                                                                                                  AAR45927 standard; peptide; 14 AA.
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62.5%;
               27.6%;
62.5%;
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                                                                                                                                                                                                                                                                                          (first entry)
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             Query Match 27.6
Best Local Similarity 62.5
Matches 5; Conservative
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Best Local Similarity
                                                                                     PWITDSTP 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 AA;
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| pwingatp 8
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| pwingatp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUL-1992;
                                                                                                                                                                                                                                                                                          27-JUL-1994
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Gaps

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WO9845322-A2

AAR75776 standard; Peptide; 14 AA.

RESULT 10

AAR75776 ID AAR7

Sequence

Matches

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Length 14; Indels 9

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14-JAN-1997;
                                                  14-JAN-1997;
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11-DEC-1998;
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                                                                                                    Marsden HS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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                                                                                                                                                                                                                                                                                             This invention describes a novel method for the diagnosis of a disease caused by, or associated with, an RNA molecule that has a frameshift mutation. The method is used to diagnose age-related diseases, especially cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's disease, Down's syndrome, myotonic dystrophy, Huntington's disease, multiple sclerosis; alcoholic liver disease, diabetes mellitus type II and many others listed) or susceptibility to these disorders. The method allows a definitive diagnosis of Alzheimer's disease in living partients, at an early stage. It is based on the observation that disease may be caused by mutations in RNA rather than DNA. The invention describes the used of neuronal system RNA molecules, specifically proteins including
                                                                                                                                                                                                                                                                                                                                                                                                                         used of neuronal system RNA molecules, specifically proteins including beta-amyloid precursor protein (beta-APP), the microtubule associated proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule associated protein 2 (MAP2), neurofilament-L, neurofilament-E, presentlin I, presentlin II, glial fibrillary acidic protein (GRAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma 2 (bcl-2) prote-oncogene, semaphorin III, HUPF-1, high mobility group protein-C (HMGP-C) and neuroendocrine specific protein A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                Diagnosing disease by detecting frameshift mutations in RNA or corresponding protein mutations - used to diagnose cancer and neurological diseases, particularly Alzheimer's disease, and also for treatment and prevention with specific ribozymes or wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herpes simplex virus type 2; HSV-2 antibody; detection; HSV-1; multiply displayed peptide structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 19; Length 18
Pred. No. 2.3e+02;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSV-2 glycoprotein G partial sequence (residues 451-468).
                                                                                                                                       Van Leeuwen FW
                                                                                    RIJKSUNIV UTRECHT.
ROYAL NETHERLANDS ACAD ARTS & SCI.
UNIV ROTTERDAM ERASMUS.
                                                                                                                                                                                                                                                                         Disclosure; Figure 15; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW66667 standard; peptide; 18 AA.
                                   98WO-IB00705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.68;
                                                           97US-0043163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Herpes simplex virus type 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.98;
                                                                                                                                       Grosveld FG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
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3 csvwpwwelaspwv 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CTVHPIPDEDSPWI 14
                                                                                                                                                           WPI; 1998-609901/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 AA;
                                                                                                                                                                          N-PSDB; AAX75766
                                                                                                                                     Burbach JPH,
                                   02-APR-1998;
                                                           .0-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-NOV-1998
           15-0CT-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW66667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                    UYUT-)
                                                                                                              UYRO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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The invention relates to a multiply displayed peptide structure of formula [(X1)p-A-(X2)q-Spln-Core. X1, X2 = 1-6 non-interfering amino acid residues; A = Glu Glu Phe Glu Gly Ala Gly Asp Gly Glu Pro Pro Glu acid residues; A = Glu Glu Phe Glu Gly Ala Gly Asp Gly Glu Pro Pro Glu least 4; and p, q = 0 or 1. The linkage between the core and the spacer may be chemical or physical. Peptides of this formula are used in the diagnosis of herpes simplex virus type 2 (HSV-2). The peptides can distinguish HSV-2 from HSV-1. A series of 67 peptides (AAW66624-W66690), mostly 18 amino acids long, that spanned amino acids 21-699 of the predicted open reading frame of HSV qG2 structures of the invention and were made as multiply displayed peptide structures of the invention and were made against sera from HSV-1, HSV-2 antibody-positive individuals and from individuals having no laboratory evidence of HSV inflection. From the results, peptide 55 (AAW66678) was considered a likely candidate for type specific serodiagnosis of HSV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein tyrosine phosphatase; PTP; PEST; paxillin binding; adhesion; cell migration; division; cytostatic; antiinflammatory; angiogenesis; cancer; enzyme substrate identification; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                        New peptide compounds useful for detecting herpes simplex virus type 2\, - can differentiate between herpes simplex virus type 1 and type 2\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Wild type Pro been replaced by Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.6%; Score 34; DB 19; Length 18; 43.8%; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY67265 standard; protein; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 10; 25pp; English.
97GB-0000660
                                                                    97GB-0000660
                                                                                                                                                     (MEDI-) MEDICAL RES COUNCIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98CA-2238654
98US-0111993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 PIPDEDSPWITDSTPR 20
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| papttppptsthatpr 16
                                                                                                                                                                                                                                                                                                               WPI; 1998-459516/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 AA;
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therapeutically, e.g to prevent or treat tissue rejection, ischaemia, aneurysm, chronic inflammation, autoimmune diseases, etc. This peptide is derived from the C3/C4/C5 family of proteins in a region proximal to
                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequences. Indels are peptide sequences corresponding to insertion or deletion sequences in members of a family of proteins when their sequences are aligned and compared. The peptides often correspond to sites of interaction between proteins or proteins and their ligands. The invention relates to a method for identifying regions of contact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (interface peptides) in protein protein binding complexes and for the preparation of modulators of this interaction. The peptides presented here are modulators of the complement system (including peptides that act as vaccines by inducing modulating antibodies) which are useful
                                                                                                                                                                                                                                                                                     Modulatory cpds. identified by screening peptide(s) derived from indels - esp. from regions involved in protein-protein interaction, useful as inhibitors or activators of the complement system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cortactin; SH3 domain; binding peptide; Src homology region 3; tyrosine kinase; immune response; lymphokine; interleukin 1; NCk; Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
                                                                                                                                                                                                                                                                                                                                                                                                                                     The peptides AAW24940-69 represent peptides derived from "indel"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB 18;
Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Src SH3 domain binding peptide SEQ ID NO:157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW25373 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                      Claim 30; Page 23; 161pp; English.
                                                                                                                                          (MEDI-) MEDICAL BIOLOGY INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.8%;
71.4%;
                                                                  96US-0663617.
95US-0000674.
                      96WO-US10958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                      WPI; 1997-100166/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 SPWITDS 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||: ||
8 spwlkds 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
Unidentified.
                      27-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-FEB-1996;
                                                                     14-JUN-1996;
                                                                                         29-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-AUG-1997
                                                                                                                                                                                         Ogata RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW25373;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                            mutent protein sequence. The tragment corresponds to amino acus
355-374, and has the wild type proline residue corresponding to position
369 replaced by an alanine residue. PrP-PEST is a soluble PTP that is
ubsquitously expressed throughout embryonic development and in murine
adult tissues. The N-terminal portion of the encodes for the
catalytic domain, while the C-terminal portion is composed of 5 proline
catalytic domains, and a binding site for the adaptor protein Shc. The pro 2
domain is required for paxillin binding, and the synthesis of mutant
PPP-PEST proteins (e.g represented by this sequence) have shown that
proline 362 is important for paxillin binding activity. The invention
crelates to a compound that is capable of interfering with the binding of
PTP-PEST to signalling molecules that are involved in cell migration,
adhesion or division. The compound can be derived from minimal sequences
found in binding sites of PTP-PEST. The invention also relates to a
method for finding a genuine substrate for an enzyme in a cell that
compounds have expostatic and antiinflammatory activity. The compounds
are used for making medicaments for treating a disease related with cell
concern.
Concerned to the compound antiinflammatory activity. The compounds
career used for making medicaments for treating a disease related with cell
concerned.
Concerned to the compound and anglogenesis, especially
concerned.
Concerned to the movel method is used for identifying a genuine substrate for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ij
                                                                                                                                                                                                                                                                                                           This is a fragment of the protein tyrosine phosphatase (PTP) PEST, P369A mutant protein sequence. The fragment corresponds to amino acids
                                                                                                                                                            Novel therapeutic agents for treating diseases which are related to cell proliferation, migration, inflammation and angiogenesis especially cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indel; insertion; deletion; protein family; sequence alignment; interaction site; ligand; interface peptide; binding complex; modulation; complement; vaccine; antibody; tissue rejection; ischaemia; aneurysm; chronic inflammation; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 21; Length 20;
Pred. No. 2.6e+02;
2; Mismatches 3; Indels
                                                                     Angers-Lousteau A, Charest A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C3/C4/C5-derived complement inhibitory peptide C4-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "acylated N-terminus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW24962 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                            Example 4; Fig 18; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 27.6
Best Local Similarity 43.8
Matches 7; Conservative
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5 hpvp----piltpsap 16
                                                                     Cote J,
                 (UYMC-) UNIV MCGILL.
                                                                                                               WPI; 2000-097104/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Modified-site
                                                                  Tremblay ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-OCT-1997
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14

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AAW24962 RESULT

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Gaps

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Length 14; 1; Indels

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Kay BK, Quilliam LA, Rider JE;
Der CJ, Fowlkes DM,
Sparks AB, Thorn JM;
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WPI; 1997-424972/39.

Src homology region 3 binding peptide - used to activate Src tyrosine kinase(s) and to stimulate immune response by increasing production of certain lymphokine(s), e.g. interleukin-1

Claim 16; Page 99; 131pp; English

The present sequence represents a Src homology region 3 (SH3) binding peptide. SH3 binding peptides are selected from: (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which bind the MH3 domain of Abl; (d) peptides which bind the SH3 domain of Abl; (d) peptides which bind the SH3 domain of Abl; (d) peptides which bind the SH3 domain of Crk; (e) peptides which bind the SH3 domain of Crk; (f) peptides which bind the SH3 domain of Crk; (h) peptides which bind the MH3 domain of Yes; and (i) peptides which bind the maino-terminal SH3 domain of Yes; and (i) peptides which bind the method to identify inhibitors of their binding to their respective SH3 domains, which could be used to modulate the pharmacological activity of proteins or polypeptide containing the SH3 domain. The peptides can also be used to activate ST or STC-related protein tyrosine kinases, to stimulate the immune cresponse by increasing the production of certain lymphokines, e.g. conjugated molecule to certain cellular compartments containing STC or 

Seguence

Gaps .. 26.8%; Score 33; DB 18; Length 16; 44.4%; Pred. No. 2.8e+02; ive 4; Mismatches 1; Indels Query Match Best Local Similarity 44.4\* For 4; Conservative

.; 0

5 PIPDEDSPW 13 ò

|:|: |:|: plpetdtpy 16 Q

Search completed: February 21, 2002, 16:42:58 Job time: 232 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

protein - protein search, using sw model Θ

February 21, 2002, 16:43:35; Search time 31.57 Seconds (without alignments) 14.969 Million cell updates/sec Run on:

US-08-753-851-6 123 1 CTVHPIPDEDSPWITDSTPRI 21 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

212252 seqs, 22503292 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 21

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

Issued\_Patents\_AA:\* Database :

/cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*/cgn2\_6/ptodata/2/iaa/backfiles1.pep:\* /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\* /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\* /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\* /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	ID Description	US-08-143-311B-6 Sequence 6, Appli	US-08-143-311B-7 Sequence 7, Appli	6 Sequence 6,	-745-382-7 Sequence 7,	7 Sequence 7,	7 Sequence 7,	7	7 Sequence 7,	44,	18,	D-31 Sequence 31,	Sequence	181,	36, 4	57 Sequence 157,	Sequence 174,	38 . Sequence 188,	0 Sequence 10, 1	10,	US-08-522-269B-5 Sequence 5, Appli	2		251	-254 Sequence 254,	251,	_	
	h DB	 	20 2	20 4	.4	.4	.4 1	4 4		8	12 5							-6								21 1		
	Query Match Length DB				_	_	-		-	_								_	_	_	_							
ф	Query Match	100.0	48.8	32.5	27.6			27.6	27.6	27.6	26.8	26.8	26.8	26.8	26.8	26.8	26.8	26.0	26.0	26.0	26.0	26.0	25.2	25.2	25.2	25.2	25.2	
	Score	123	09	40	34	34	34	34	34	34	33	33	33	33	33	33	33	32	32	32	32	32	31	31	31	31	31	
	Result No.	-	7	m	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	

Sequence 3, Appli Sequence 1, Appli Sequence 163, App	16, 1 16, 1 16, 1	Patent No. 5217891 Sequence 16, Appl Sequence 16, Appl	Sequence 11, Appl Sequence 11, Appl Sequence 21, Appl	Sequence 13, Appl Sequence 13, Appl Sequence 32, Appl	Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl
US-08-617-929-3 PCT-US92-07218-1 US-07-942-245-163	US-08-370-567-16 US-08-438-759-16 PCT-US94-05684-16	5217891-8 US-08-555-394-16 US-08-745-892-16	US-08-854-222-11 US-09-188-039-11 US-08-277-660A-21	US-08-424-957-13 US-09-035-686-13 PCT-US93-06751-32	US-08-451-947-32 US-08-424-826A-32 US-08-928-694-32
122	2 1 1 1	3 1 6	3 8 1	H 4 D	3 2 1
20	17 17 17	901	14 14 15	15 15 15	17 17 17
24.8 24.8	24.4 24.4 24.4	23.6 23.6 23.6	23.6 23.6 23.6	23.6 23.6 23.6	23.6 23.6 23.6
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28 29 30	33	34 35 36	37 38 39	4 4 4 4 2 1	44 45

### ALIGNMENTS

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COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                     APPLICANT: PATTON, KAREN L.
ARPLICANT: TELEN, MARILYN J.
APPLICANT: LAGO, HUA-XIN
TITLE OF INVENTION: AN ADHESION MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/143,311B
FILING DATE: 29-OCT-1993
CLASSIFICATION: 436
                                                                                                                                                                                                                                              1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1579-50
                  Sequence 6, Application US/08143311B Patent No. 5863540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,339
FILING DATE: 30-0CT-1992
CLASSIFICATION: 436
APPLICATION NUMBER: 07/669,730
FILING DATE: 15-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: WILSON, MARY J. SP55 REGISTRATION NUMBER: 32,955 REFERENCE/DOCKET NUMBER: 157 TELECOMMUNICATION INFORMATION:
                                                                                  BARTON F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
                                                                             APPLICANT: HAYNES, BARTON APPLICANT: HALE, LAURA P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: /US CT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 703-816-4100 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: peptide US-08-143-3118-6
                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                        Patent No. 5863540
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                               VIRGINIA
                                                                                                                                                                                                                                                                                          CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 15 CLASSIFICATION:
                                                                                                                                                                                                                                                  ADDRESSEE:
US-08-143-311B-6
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                                                                                                                                                                                                                                                                     STREET:
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Sequence 7, Application US/07745382
Patent No. 5270181
GENERAL INFORMATION:
APPLICANT: MCCOY, John
APPLICANT: LaVallie, Edward
TITLE OF INVENTION: Peptide and Protein Fusions To
TITLE OF INVENTION: Thioredoxin and Thioredoxin-Like Molecules
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
OTHER INFORMATION: SYNTHETIC PEPTIDES DERIVED FROM THE VP22TRUNC
US-09-230-421-6
US-09-231-421-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 4; Length 20;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                   GENERAL INFORMATION:
APPLICANT: Medical Research Council
TITLE OF INVENTION: ANTI-HERPESVIRAL ALENTS AND ASSAYS
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: P18189C
CURRENT APPLICATION NUMBER: US/09/230,421
CURRENT FILING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/745,382
FILING DATE: 19910814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/652,531
Sequence 6, Application US/09230421
Patent No. 6200577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GII
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.5%;
46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 06-FEB-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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6 PNPDAPW----TPRV 16
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US-07-745-382-7
                                                                                                                                                                                                                                                                       SEQ ID NO 6
LENGTH: 20
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0
                             Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITI: ARLINGION
STATE: VIRGINIA
COUNTRY: U.S.A.
21201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OOMPUTER: IBM PC Compatible
OOMPUTER: Patentin Release #1.0, Version #1.25
SOFTWANTS: Patentin Release #1.0, Version MIL25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/143,311B
FILING DATE: 29-OCT 1993
CLASSIFICATION: 436
PRIOR APPLICATION NUMBER: 07/973,339
FILING DATE: 30-OCT-1992
CLASSIFICATION NUMBER: 07/69,730
FILING DATE: 13-MAR-1991
CLASSIFICATION: WAS APPLICATION NUMBER: 07/669,730
FILING DATE: 15-MAR-1991
CLASSIFICATION: WAS APPLICATION NUMBER: US/08/1401
CLASSIFICATION NUMBER: US/08/1401
APPLICATION NUMBER: US/08/1401
                           Query Match 100.0%; Score 123; DB 2; Best Local Similarity 100.0%; Pred. No. 2.8e-11; Matches 21; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 60; DB 2;
Pred. No. 0.018;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: HAYNES, BARTON F.
APPLICANT: HALLE, LAURA P.
APPLICANT: PATTON, KAREN L.
APPLICANT: TELEN, MARILIN J.
APPLICANT: LIAO, HOA-XIN
TITLE OF INVERTION: AN ADHESION MOLECULE
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIXON & VANDERHYE P.C
                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08143311B Patent No. 5863540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
                                                                                                                                                   1 CTVHPIPDEDSPWITDSTPRI 21
                                                                                                                        1 CTVHPIPDEDSPWITDSTPRI 21
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.8%;
91.7%;
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TELEFAX: 703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 48.8
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 DSPWITDSTPRI 21
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                                                                                                                                                                                                                                                RESULT 2
US-08-143-311B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-143-311B-7
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MOLECULE TYPE: peptide

RESULT

unknown

TOPOLOGY:

1;

Gaps

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.6%;
62.5%;
                                                           APPLICANT: Grant, Kathleen APPLICANT: LaVallie, Edward TITLE OF INVENTION: PEPTIDI TITLE OF INVENTION: THIOREI TITLE OF INVENTION: THIOREI
                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                        Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Massachusetts
                                                                                                                                                  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                        CITY: Cambridge STATE: Maser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
            SENERAL INFORMATION:
                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 PWITDSTP 19
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1 PWINGATP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                         02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-165-301A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                      STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QΩ
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                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: LaVallie, Edward
TITLE OF INVENTION: Peptide and Protein Fusions To
TITLE OF INVENTION: Thioredoxin and Thioredoxin-Like Molecules
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                           Score 34; DB 1; Length 14;
Pred. No. 53;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTY.

ZIP: 02140
COMPUTER: PLOPPY disk
MEDIUM TYPE: FlopPy disk
COMPUTER: IBM PC COMPATIBLE
OOPFATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/921,848
FTIING DATE: 19920728
FTIING DATE: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19920728
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/652,531
FILING DATE: 06-FEB-1991
PRIOR APPLICATION NUMBER: US 07/745,382
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: G15188A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-1170
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
10S-08-165-301A-7
: Sequence 7, Application US/08165301A
: Patent No. 5646016
                                                                                                                                                                                                                                                         Sequence 7, Application US/07921848
Patent No. 5292646
                                                         27.68;
62.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 62.50,
                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 87 CambridgePa
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-07-921-848-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMINO ACID
                                                                             Best Local Similarity
Matches 5; Conserv
                                                                                                                                12 PWITDSTP 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 PWITDSTP 19
                                                                                                                                                         1 PWINGATP 8
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                                                                                                                                                                                                                      RESULT 5
US-07-921-848-7
US-07-745-382-7
                                                               Query Match
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PAPLICANT: MCOV, John
HAPLICANT: MCOV, John
HAPLICANT: OBLISAS-Smith, Elizabeth
APPLICANT: GATA, KATHORE
ADDIANCES: CORRESPONDENCES: SO
CORPETED FOR COMPANIES
COMPANIES: TO POPT ALL
COMPANIES:
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 44, Application US/09017205
Patent No. 5965357
GENERAL INFORMATION:
APPLICANT: Marsden, Howard S
TITLE OF INVENTION: PEPTIDE STRUCTURES AND THEIR USE IN
TITLE OF INVENTION: DIAGNOSIS OF HERPES SIMPLEX VIRUS TYPE 2
                                                                                                                                                                   DB 5; Length 14;
53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 5965357th Glebe Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide from HSV-2 glycoprotein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34; DB
Pred. No. 70;
                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                     Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/017,205
FILING DATE: 02-FEB-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 604-436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
PGT-1059-05905-18
Sequence 18, Application PC/TUS9405905
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703)816-4100 INFORMATION FOR SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.6%;
                                                                                                                                                                     27.6%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (703)816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 45.0.
Best Local 7; Conservative
                                                                                                                                                                     Query Match 27.6
Best Local Similarity 62.5
Matches 5; Conservative
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                                              double
                                                                 ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US94-14179-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                         TYPE: amino acid
STRANDEDNESS: dou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                      12 PWITDSTP 19
                                                                                                                                                                                                                                                                              1 PWINGATP 8
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                                                                                                                                                                                                                                                                                                                                                        RESULT 9
US-09-017-205-44
      LENGIH:
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APPLICANT: Grant, Kathleen
APPLICANT: Grant, Kathleen
APPLICANT: LaVallie, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
CORRESPONDENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 14;
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,436
FILING DATE: 04-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 4
Pred. No. 53;
1; Mismatches
                                                                                                                                                                                                                        NAME: Melnert, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Genetics Institute, Inc.
87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US94/14179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Meinert, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELECOMMUNICATION INFORMATION:
**PELEPHONE: (617) 876-1170
TELEFAX: (617) 876-581
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application PC/TUS9414179
GENERAL INFORMATION
APPLICANT: MCCOY, John
APPLICANT: DiBlasio-Smith, Elizab
                                                                                                                                          PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/165,301
FILLING DATE: 10-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.6%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 62.3,
"That 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: peptide US-08-810-436-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Genet
STREET: 87 Cambr
CITY: Cambridge
                                                                                                      FILING DATE: 04 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 PWITDSTP 19
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| PWINGATP 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
PCT-US94-14179-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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Length 20;
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0; Mismatches 5; Indels
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APPLICANT: DILLNER, LENA
APPLICANT: DILLNER, LENA
APPLICANT: CHENC, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: DISECUL IN KMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: MASON & ASSOCIATES, P.A. STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500 CITY: CLEARWATER
                                                                                                                                                                                                                                                                                                                                                         Score 33; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
                                        REGISTRATION NUMBER: 19,007
REFERENCE/DOCKET NUMBER: SG19171
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-293-1404
TELEFAX: 202-872-0493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 176, Application US/08934915 Patent No. 5932412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: LOUISE A. Foutch 37,13 REGISTRATION NUMBER: 37,13 REFERENCE/DOCKET NUMBER: 19 FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         26.8%;
50.0%;
                           AISENBERG, Irwin M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
                                                                                                                               TELEFAX: 202-872-0493
TELEX: 440 069 ALS UI
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                          20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 50.(
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A. COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide US-08-934-915-176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CTVH--PIPDEDSP 12
                                                                                                                                                                                                                                              ; TYPE: amino acid
; TOPOLOGY: linear
US-07-678-974D-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-934-915-176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                           Query Match
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trna binding-dependent inhibition of microbial Pathogen Growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METHOD FOR DETECTION OF HUMAN PAPILLOMAVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.8%; Score 33; DB 5; Length 12; 57.1%; Pred. No. 61; 1; Indels ive 2; Mismatches 1; Indels
                                                                                    ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C STREET: Two Militia Drive CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/678,974D
FILING DATE: 25-JUN-1991
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 67
CORRESPONDER SADARESS:
CORRESPONDER BERMAN 6. ALSENBERG
STREET: 1730 RHODE ISLAND AVENUE, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIT-6299A PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036-3186
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/068,382
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Brock, David E.
REGISTRATION NUMBER: 22,592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 31, Application US/07678974D Patent No. 5629146 GENERAL INFORMATION:
                                                                                                                                                               COUNTRY: USA
2IP: 02173-4799
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUG SYSTEM: PC-DOS/MS-DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: M
TELECOMMUNICATION INFORMATION
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 951794
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: DILLNER, JOAKIM APPLICANT: DILLNER, LENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 12 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 26.8
Best Local Similarity 57.1
Matches 4; Conservative
                                           NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 DEDSPWI 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | | :||:
| DEQAPWV 11
                                                                                                                                 CITY: Lexi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US94-05905-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
US-07-678-974D-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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PEPTIDE-BASED VACCINE AGAINST PAPILLOMA
                                                                                              ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT. ADDRESSEE: P.C. STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 2; Length 20;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILLOATION NUMBER: US/08/945 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7752-0002-0 PCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SE96/00533
FILLING DATE: 23-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9501512-9
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/945,168 FILING DATE: 18-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 157, Application US/08602999A Patent No. 6184205 GENERAL INFORMATION:
                                                                                                                                                                                                                                  COMPOUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: QUILLIAM, Lawrence A. APPLICANT: DER, Channing J. APPLICANT: FOWLKES, Dana M. APPLICANT: RIDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEC ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPARKS, Andrew B. KAY, Brian K. THORN, Judith M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 24-APR-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: OBLON, NORMAN F. REGISTRATION NUMBER: 24, (REFERENCE/DOCKET NUMBER:
                                      VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 26.8
Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JEECURES: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-945-168-36
                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
APPLICANT: DILLNER, JI TITLE OF INVENTION: PI TITLE OF INVENTION: V: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CTVH--PIPDEDSP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 COKHTPPAPKEDDP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                          CITY: ARLINGTON
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US-08-602-999A-157
                                                                                                                                                                            STATE: V, COUNTRY:
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                                                            Gaps
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                                                          5;
                Score 33; DB 2; Length 20;
Pred. No. 1.1e+02;
0; Mismatches 5; Indels
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Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                     SYNTHETIC PEPTIDES OF HUMAN PAPTILLOMAVIRUS 1, 5, 6, 8, 11, 16, 18, 31, 33 AND 56, USEPUL IN IMMUNOASSAY FOR DIAGNOSTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
                                                                                                                                                                                                                              Sequence 181, Application US/08934915
Patent No. 5932412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
US-08-945-168-36
US-08-945-168-36
Sequence 36, Application US/08945168
Patent No. 5989548
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37,133
                                                                                                                                                                                                                                                                                       APPLICANT: DILLMER, JOAKIM
APPLICANT: DILLMER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC
TITLE OF INVENTION: PAPILLOMAN
TITLE OF INVENTION: USEFUL IN
TITLE OF INVENTION: USEFUL IN
TITLE OF INVENTION: USEFUL IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 19.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.8%;
50.0%;
                  26.8%;
50.0%;
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NAME: LOUISE A. FOULCH
REGISTRATION NUMBER: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 20 amino acids
amino acid
                                    Best_Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 50.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: peptide US-08-934-915-181
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                            1 CTVH--PIPDEDSP 12
                                                                                                                                    2 COKHTPPAPKEDDP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CTVH--PIPDEDSP 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: CLEARWATER
STATE: FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                US-08-934-915-181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                  Query Match
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COUNTRY: U.S.A.

ZUNHTRY: U.S.A.

ZUNHTRY: BO36-271.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IDMP C compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURREWT APPLICATION DATA:

APPLICATION NUMBER: US/08/602,999A

FILING DATE: 16-FEB-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie

REGISTRATION NUMBER: 18,872

REGISTRATION NUMBER: 1101-202

TELECHONE: (212) 790-9090

TELECHONE: (212) 790-9090

TELECHONE: (212) 790-9090

TELECHORATION FOR SEQ ID NO: 157:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STYPE: amino acid

SCOURCE TYPE: peptide

US-08-602-999A-157
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0;

Ouery Match 26.8%; Score 33; DB 4; Length 20; Best Local Similarity 44.4%; Pred. No. 1.1e+02; Matches 4; Conservative 4; Mismatches 1; Indels

5 PIPDEDSPW 13 |:|: |:|: 10 PLPETDTPY 18

Qy Dp Search completed: February 21, 2002, 16:43:36 Job time: 170 sec

us-08-753-851-7.rpr

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

February 21, 2002, 16:44:16 ; Search time 33.6 Seconds
(without alignments)
47.609 Million cell updates/sec

US-08-753-851-7 113 1 DSPWITDSTDRIFATRDQDTI 21

Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

4046 Total number of hits satisfying chosen parameters:

219241 seqs, 76174552 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 21

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ani	hypothetical prote		qlutamate-1-semial	protein p12E - Fri	H+-transporting AT	ribosomal protein	hypothetical prote		NADH dehydrogenase	mixed lymphocyte r	capsid protein VP2		pollen allergen I	hypothetical prote	_	calsequestrin, fas	pev-kinin 1 - pena	xenopsin-related p	xenopsin-related p	amine oxidase (cop	rase	collecting duct wa	hypodermin B - ear	transcription fact	gastrin - sheep	d(TTAGGG)n-binding	NADH dehydrogenase	serum heterodimer,
SUMMARIES	ID	S00492	A35678	S02473	A48301	S66613	860633	S78416	S10876	F28027	808590	PX0031	PQ0548	S77981	A44773	C85956	149423	A31049	PD0029	JS0302	A60320	S71304	PU0034	151905	A20190	B23692	GMSH	D48138	0	A56899
	DB	7	7	7	~	7	7	7	7	7	7	7	~	7	7	~	7	7	7	7	7	7	7	~	7	~	Н	7	7	7
	Length	20	18	16	16	16	19	21	20	21	21	15	19	20	20	17	20	20	7	თ	6	11	11	13	16	16	17	17	19	20
ф	Query Match	31.9	26.5	25.7	25.7	23.9	23.9	23.9	23.0	23.0	22.1	21.2	21.2	21.2	21.2	20.4	20.4	20.4	19.5	19.5	19.5	19.5	19.5	•	•		•	9.	٩.	•
	Score	36	30	29	29	27	27	27	26	26	25	24	24	24	24	23	23	23	22	22	22	22	22	22	22	22	22	22	22	22
	Result No.		7	e	4	Ŋ	Q	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

T-cell receptor be	seed protein ws-19	T-cell receptor be	Ig heavy chain CRD	NAD+ ADP-ribosyltr	unidentified 85K p	T-cell antigen rec	T-cell antigen rec	ubiquinolcytochr	T-cell receptor be	TcR C gamma 1 chai	urinary tract ston	T-cell receptor de	dystrophin - pig (	olfactomedin - bul	proteasome chain L
A38837	D61497	PH0895	PT0274	S21163	PC2369	S47356	S47385	S42741	PH1473	C49254	A56045	146652	PQ0119	A45781	G02018
7	7	7	7	7	7	7	7	7	7	~	7	7	7	7	7
21	21	10	12	12	13	13	13	15	16	18	20	50	21	21	18
19.5	19.5	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.1
22	22	21	21	21	21	21	21	21	21	21	21	21	21	21	20.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

rties.	0;
ug-1997 d prope	0; Gaps
01-A	0;
gment) bster) 8 #text_change in. 1. Isolatic	; Length 20; 4; Indels
spiny lobster (fra (Japanese spiny lo revision 31-Dec-198 1988 japonicus hemocyan ID:88196131	31.9%; Score 36; DB 2; Length 20; 46.2%; Pred. No. 18; ive 3; Mismatches 4; Indels
RESULT 1 S00492 hemocyanin chain Ia - Japanese spiny lobster (fragment) C:Species: Panulirus japonicus (Japanese spiny lobster) C:Species: Panulirus japonicus (Japanese spiny lobster) C:Species: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 01-Aug-1997 C:Accession: S00492 R;Makino, N.; Rimura, S. R;Makino, N.;	Query Match 31.9%; Best Local Similarity 46.2%; Matches 6; Conservative 3

7 DSTDRIFATRDQD 19 ||||::|:| DSTDKLLAQKQDD 19 δλ Dp

hypothetical protein (proenkephalin 5' region) - mouse C;Species: Mus musculus (house mouse) C;Date: 28-Sep-1990 #sequence\_revision 28-Sep-1990 #text\_change 05-Nov-1999 C;Accession: A35679 R;Kilpatrick, D.L.; Zinn, S.A.; Fitzgerald, M.; Higuchi, H.; Sabol, S.L.; Meyerhardt, Mol. Cell. Biol. 10, 3717-3726, 1990 A;Title: Transcription of the rat and mouse proenkephalin genes is initiated at distin A;Reference number: A35678; MuID:90287163 A;Accession: A35678 A;Accession: A35678 A;Accession: Brahmary A;Molecule type: mRNA A;References: GB:M55181; NID:9201032; PIDN:AAA40127.1; PID:9201033

Gaps 4; 26.5%; Score 30; DB 2; Length 18; 58.3%; Pred. No. 1.4e+02; Live 0; Mismatches 1; Indels Query Match
Best Local Similarity 58.3°
Matches 7; Conservative

1;

1 DSPWITDSTDRI 12 7 DSPW----EDRI 14 ΩŊ QQ

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C;Species: Homo sapiens (man)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 18-Nov-1994
C;Accession: S10876
C;Accession: S10876
R;Assouline, Z.; Kerbiriou-Nabias, D.M.; Pietu, G.; Thomas, N.; Bahnak, B.R.; Meyer, Biochem. Biophys. Res. Commun. 153, 1159-1166, 1988
A;Title: The human gene for von Willebrand factor. Identification of repetitive Alu s
                                                                                                                  H-transporting ATP synthase (EC 3.6.1.34) protein 8 - brine shrimp mitochondrion (st C; Species: mitochondrion Artemia sp. (brine shrimp)
A;Variety: strain La Mata
C; Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 07-Dec-1999
C; Accession: $60633
R; Perez, M.L.; Valverde, J.R.; Batuecas, B.; Amat, F.; Marco, R.; Garesse, R. J. Mol. Evol. 38, 156-168, 1994
A;Title: Speciation in the Artemia genus: mitochondrial DNA analysis of bisexual and A;Reference number: $60624; MuID: 94223692
A;Accession: $60633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Genome: mitochondrion
A;Genetic code: SGC4
C;Superfamily: H+-transporting ATP synthase protein 8
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Note: the source is designated as Artemia parthenogenetica A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 1-21 <GOL>
A; Note: the protein is designated as mitochondrial ribosomal protein L28
C; Keywords: mitochondrion; protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-19 <PER>
A;Cross-references: EMBL:X67263; NID:g11210; PIDN:CAA47685.1; PID:g11211
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                                                                                                                                                                                                                                                                                                                                                                                        A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 27; DB 2; Length 21;
Pred. No. 5.1e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 19;
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R:Goldschmidt-Reisin, S.; Graack, H.R.
submitted to the Protein Sequence Database, February 1998
A; Reference number: S78411
A; Accession: S78416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.9%; Score 27; DB 2; Le
100.0%; Pred. No. 4.5e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: strain La Mata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.9%;
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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DKVFQPRPED
                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
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| PWIT 11
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  SPWFT
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C;Species: Synechococcus sp.
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: A48301
R; Grimm, B.; Bull, A.; Welinder, K.G.; Gough, S.P.; Kannangara, C.G.
Carlsberg Res. Commun. 54, 67-79, 1989
A; Title: Purification and partial amino acid sequence of the glutamate 1-semialdehyde am A; Reference number: A48301; MUID:89374545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: S66613
R;Hensel, J.; Hintz, M.; Karas, M.; Linder, D.; Stahl, B.; Geyer, R.
R;Hensel, J.; Hintz, M.; Karas, M.; Linder, D.; Stahl, B.; Geyer, R.
Bur. J. Blochem. 232, 373-380, 1995
A;Title: Localization of the palmitoylation site in the transmembrane protein pl2E of Fr
A;Reference number: S66613; WUID:96035869
A;Accession: S66613
                                                                                                                                                                                                          ø
                                                                                                                                          Rimartin, A.; Wychowski, C.; Couderc, T.; Crainic, R.; Hogle, J.; Girard, M. EMBO J. 7, 2839-2847, 1988
A.;Title: Engineering a poliovirus type 2 antigenic site on a type 1 capsid results in A; Accession: S02473; MUID:89030650
A; Accession: S02473
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C;Species: Friend murine leukemia virus
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997
                                                                     C;Species: human poliovirus 1
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
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80.0%; Pred. No. 3.7e+02;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                Score 29; DB 2; I
Pred. No. 1.8e+02;
4; Mismatches 4;
                                                                                                                                                                                                                                                                             A;Status: not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-16 <MAR>
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A Molecule type: protein
A Residues: 1-16 <GRI>
C Keywords: intramolecular transferase; isomerase
                                             coat protein VP1 - human poliovirus 1 (fragment)
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38.5%;
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Best Local Similarity 80.0
Matches 4; Conservative
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A;Molecule type: protein
A;Residues: 1-9;10-16 <HEN>
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Best Local Similarity
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Matches 6; Conserv
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A; Reference number: S10876; MUID:88268889 A; Accession: S10876

A;Status: translation not shown A;Molecule type: DNA Residues: 1-20 <ASS> A;Cross-references: EMBL:X07258

23.0%; 80.0%;

Query Match 23.0 Best Local Similarity 80.0 Matches 4; Conservative

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Ribavison, M.D.; Rixon, F.J.; Davison, A.J.
J. Gen. Virol. 73, 2709-2713, 1992
A;Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of herp A;Reference number: PQ0544; MUID:93019027
A;Accession: PQ0548
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C; Superfamily: mammalian cytochrome-c oxidase chain Va
C; Keywords: electron transfer; membrane-associated complex; mitochondrial inner membr
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                        C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 24-Feb-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: human herpesvirus 1
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
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C;Species: Thunnus obesus (bigeye tuna)
C;Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 26-Feb-1998
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                                                                   C; Accession: PX0031
R; Shiromiya, T.; Ohara, T.; Wada, N.; Omori, A.; Kamada, N.
J. Blochem. 107, 435-439, 1990
A; Title: Rat liver arginase suppresses mixed lymphocyte reaction.
A; Reference number: PX0031; MUID:90256720
                                                                                                                                                                                                                                                                                                                                                           Length 15;
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Pred. No. 1.3e+03;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        capsid protein VP26 - human herpesvirus 1 (fragment)
mixed lymphocyte reaction inhibitor - rat (fragment)
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Pred. No. 1e+03;
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50.0%;
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33.3%;
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Best Local Similarity 33..
درد 3; Conservative
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A; Molecule type: protein
A; Residues: 1-20 <ARN>
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A; Residues: 1-19 <DAV>
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Best Local Similarity
Matches 4; Conserv
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4 VLATNNQD 11
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1 EEPWMSMSS
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Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987
A;Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid-A;Reference number: A94167
A;Accession: F280027
A;Accession: F280027
A;Residues: 1-21 < CAUSTANCE A;Residues: 1-21 < CAUSTANCE A;ACCESSION SEAUCS
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                                                                                                                                                                                                                                                                                                                                                                                                                          protein P9 - curled-leaved tobacco (fragment)
C;Species: Nicotiana plumbaginifolia (curled-leaved tobacco)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Jun-1993
C;Accession: F28027
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C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase
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A;Residues: 1-21 <HAY>
A;Cross-references: EMBL:X05881; NID:g11790; PIDN:CAA29305.1; PID:g11793
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Pred. No. 6.9e+02;
0; Mismatches 1; Indels
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Score 26; DB 2; Pred. No. 7.3e+02; 4; Mismatches 4

23.0%; 38.5%;

Best Local Similarity 38.5 Matches 5; Conservative

Query Match

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RESULT

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A; Gene: ndhD

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hypothetical protein 24327 [imported] - Escherichia coli (strain O157:H7)
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C;Accession: C85956
B;Perna, N.T.; Pluukett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Natile: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                           R;Taniai, M.; Ando, S.; Usui, M.; Kurimoto, M.; Sakaguchi, M.; Inouye, S.; Matuhasi, T.
PEBS Lett. 239, 329-332, 1988
A;Title: N-terminal amino acid sequence of a major allergen of Japanese cedar pollen (Cr
A;Reference number: A44773; MUID:89031257
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A Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-17 <STO>
A; Cross-references: GB:AE005174; NID:g12517535; PIDN:AAG58111.1; GSPDB:GN00145; UWGP:243
A; Experimental source: strain O157:H7, substrain EDL933
A; Genetics:
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                                                                                                                                                                                                                                                                                                                 C;Species: Cryptomeria japonica (Japanese cedar)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 11-Jan-2000
C;Accession: A44773
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21.2%; Score 24; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 3; Indels
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  Length 20;
                                                      1; Indels
Score 24; DB 2; I
Pred. No. 1.4e+03;
2; Mismatches 1;
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Job time: 190 sec
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A Status: preliminary
A Molecule type: protein
A Residues: 1-20 <TAN>
C; Superfamily: pectate lyase LAT59
C; Keywords: pollen
21.2%;
50.0%;
Query Match 21.2
Best Local Similarity 50.0
Matches 3; Conservative
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February 21, 2002, 16:52:21 ; Search time 20.15 Seconds
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US-08-753-851-7 113 1 DSPWITDSTDRIFATRDQDTI 21 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

1160 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 21

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	14482 vulp	thunnus	P19633 rattus norv	P21794 rattus norv	_	_	m	P18647 erythrocebu	macac	P12802 anas platyr	P40929 homo sapien	P40686 salmonella		P46980 pheretima v	P40951 rana margar	ς L	<u></u>	2		_		_		<u>~</u>	_	) palomena	1	5 theromyzc	P14539 tapirus ter	81422	7	8676	P18673 artocarpus
SUMMARIES	ID	FIBB_VULVU	COXA_THUOB	CAOS_RAT	HI70_RAT	PGKH_PHYPA	LE06_BIOGL	PPAC_BACME	APA1_ERYPA	GAST_MACMU	FIBB_ANAPL	UHA2_HUMAN	TOP1_SALTY	UHA3_CANFA	MY14_PHEVI	TKNM_RANMA	OBPA_MAMBR	ATPI_PAVLU	RL23_HALCU	ANGT_CRIGE	NO40_SOYBN	ULAL_MOUSE	LPAA_PORGI	CAT2_FASHE	MK2A_PALPR	BAIL_EUBSP	MK2B_PALPR	MK3_PALPR	HEMH_THETS	FIBB_TAPTE	CATA_ACIRA	ELAS_GADMO	LEC2_MACPO	LEC3_ARTIN
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LEC3_MACPO BTX_ATRBI	LEC1_MACPO LEC2_ARTIN	SKID_ATKEN TRYP_PROAT	YFLA_METVO ANG2_BOTJA	ANGT_BOVIN	ANGT_CHICK NUHM_CANFA
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# ALIGNMENTS

RESULT 1  ID FIBB_VULVU STANDARD; PRT; 19 AA.  ID FIBB_VULVU STANDARD; PRT; 19 AA.  PR 11482;  DT 01-JAN-1990 (Rel. 13, Created)  DT 01-JAN-1990 (Rel. 13, Last sequence update)  DF 01-JAN-1990 (Rel. 13, Last annotation update)  DE FIBRINOPEPTIDE B.  OS VULDES VULDES (Red fox).  C FIRET VOTA: Metazoa Chordata Craniata Vertebrata Entelegatomi.	metazog; Choluata; Cissipedia; Canidae; 19627; , Blomback M., Grondahl N.J.; , fibrinopeptides from mammals."; Scand. 19:1789-1791(1965). NN: FIBRINGEN HAS A DOUBLE FUNCTION: YIEL	-:- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISCLEDE BONDS:- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMEIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. INTERPRO, IPRO2181; FIDRINOGEN C. PROSITE; PSO0514; FIBRIN_AG_C_DOMAIN; PARTIAL. NON_TER 19 19 19 19 As; 2305 WW; 0B0D756C24A1F2CO CRC64;	Ouery Match 25.7%; Score 29; DB 1; Length 19; Best Local Similarity 50.0%; Pred. No. 86; Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 6 TDSTDRIFATRD 17	RESULT 2 COXA_THUOB COXA_THUOB COXA_THUOB COXA_THUOB COXA_THUOB STANDARD; PRT; 20 AA.  PR0972; DT 01-NOV-1997 (Rel. 35, Last sequence update) DT 01-NOV-1997 (Rel. 35, Last sequence update) DT 30-MAY-2000 (Rel. 39, Last annotation update) DT 30-MAY-2000 (Rel. 39, Last annotation update) DT 30-MAY-2000 (Rel. 39, Cast annotation update) DT 30-MAY-2000 (Rel. 39, Last annotation update) DT ACTOCHROME C OXIDASE POLYPETIDE VA-I (EC 1.9.3.1) (FRAGMENT). OC Arctinoptarygii; Neopterygii; Teleostei; Buteleostei; Scombroidei; OC Acathomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei; OC Scombridae; Thunnus. OC NOBI_TAXID=8241;
RESI FIB ID DT DT DE OS	CC C C R I B D C C C C C C C C C C C C C C C C C C	SO CC	M M M M M M M M M M M M M M M M M M M	RESS COXX AC DI DI DI DI OC OC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and chick muscle.";
J. Cell Biol. 107:667-697(1988).

-!- FUNCTION: CALSEQUESTRIN IS A HIGH-CAPACITY, MODERATE AFFINITY,
CALCIUM-BINDING PROTEIN AND THUS ACTS AS AN INTERNAL CALCIUM STORE
IN MUSCLE. THE RELEASE OF CALCIUM BOUND TO CALSEQUESTRIN THROUGH
A CALCIUM RELEASE CHANNEL TRIGGERS MUSCLE CONTRACTION. BINDS 40
TO 50 MOLES OF CALCIUM. ALSO BINDS LAMININ.
-!- SUBCELLULAR LOCATION: THIS ISOFORM OF CALSEQUESTRIN OCCURS IN THE
SARCOPLASMIC RETICULUM'S TERMINAL CISTERNAE LUMINAL SPACES OF
FAST SKELETAL MUSCLE CELLS. ASPARTACTIN IS FOUND IN THE BASAL
LAMINA SURROUNDING INDIVIDUAL MUSCLE
                                                                                             liver.";
Eur. J. Biochem. 248:99-103(1997).

Fur. J. Biochem. 248:99-103(1997).

-!- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME CONTOASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.

-!- CAPALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)0 + 4 FERRICYTOCHROME C.

4 FERRICYTOCHROME C.

A FERRICYTOCHROME C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
CALSEQUESTRIN, SKELETAL MUSCLE ISOFORM (ASPARTACTIN) (LAMININ-BINDING PROTEIN) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDILINE-88331073; PubMed-3417768;
Hall D.E., Frazer K.A., Hann B.C., Reichardt L.F.;
"Isolation and characterization of a laminin-binding protein from rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID*10116;
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                   "The subunit structure of cytochrome-c oxidase from tuna heart and
                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                    MEDLINE-97454291; PubMed-9310366;
Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
Kadenbach B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23; DB 1; Length 20;
Pred. No. 8.7e+02;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                   Score 24; DB 1; Length 20;
Pred. No. 6e+02;
                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- TISSUE SPECIFICITY: SKELETAL AND HEART MUSCLE.
-1- SIMILARITY: BELONGS TO THE CALSEQUESTRIN FAMILY.
PIR; A31049; A31049.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92ADE04FC2A69280 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       20 AA.
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PROSITE; PS00864; CALSEQUESTRIN_2; PARTIAL.
PROSITE; PS00863; CALSEQUESTRIN_1; 1.
                                                                                                                                                                                                                                                                                                              2; Mismatches
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                                                                                                                                                                                                                                                                                21.2%;
50.0%;
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                              TISSUE-Heart, and Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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PROSITE;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                            Mobbs C.V., Fink G., Pfaff D.W.; "HIP-70: a protein induced by estrogen in the brain and LH-RH in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kasten B., Buck F., Nuske J., Reski R.; "Cytokinin affects nuclear- and plastome-encoded energy-converting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΝÏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funarildae; Funariales; Funariaceae; Physcomitrella.
NCBI_TaxID*3218;
                                                                                                                                                                                                                                        Science 247:1477-1479(1990).
-!- INDUCTION: MOST PROMINENT PROTEIN INDUCED BY ESTROGEN IN
HYPOTHALAMUS AND MOST PROMINENT PROTEIN INDUCED BY LH-RH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OVY-1997 (Rel. 35, Last annotation update)
PHOSPHOGLYCERATE KINASE, CHLOROPLAST (EC 2.7.2.3) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                Length 19;
                                                                                                                                                                                                                                                                                                                                                               Score 21.5; DB 1; Length 1 Pred. No. 1.4e+03; 3; Mismatches 7; Indels
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                                           01-MAY-1991 (Rel. 18, Last sequence update)
01-AUG-1991 (Rel. 19, Last annotation update)
HORMONE-INDUCED PROTEIN 70 KDA (HIP-70) (FRAGMENT).
19 AA.
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 PRT;
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MEDLINE=97275459; PubMed=9129336;
                                                                                                                                                                                MEDLINE=90208308; PubMed=2181662;
                             (Rel. 18, Created)
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 STANDARD;
                                                                                        Rattus norvegicus (Rat).
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Best Local Similarity
'-has 6; Conserva
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01-FEB-1996
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P18647;
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"Bacillus subtilis ORF yybQ encodes a manganese-dependent inorganic
pyrophosphatase with distinctive properties: the first of a new class
of soluble pyrophosphatase?"
Microbiology 144.2563-2571(1998).
-!- CATALXTIC ACTIVITY: PYROPHOSPHATE + H(2)0 = 2 ORTHOPHOSPHATE.
                                  Gaps
                                                                                                                                                                                                                                                                                                                     Adema C.M., Hertel L.A., Miller R.D., Loker E.S.,
"A family of fibrinogen-related proteins that precipitates parasite-
derived molecules is produced by an invertebrate after infection.";
Proc. Natl. Acad. Sci. U.S.A. 94:8691-8656(1997).
-i- FUNCTION: BINDS AND PRECIPITATES ANTIGENS OF THE PARASITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
Planorbidae; Biomphalaria.
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        Score 21; DB 1; Length 15; Pred. No. 1.3e+03; 4; Mismatches 6; Indels
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16 16
16 AA; 1964 MW; A1665754589EF82C CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2010 (Rel. 40, Last annotation update)
MANGARESE-DEPENDENT INORGANIC PYROPHOSPHATASE (EC 3: (PYROPHOSPHATAE PHOSPHO-HYDROLASE) (PPASE) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: SECRETED IN THE HEMOLYMPH -!- INDUCTION: BY INFECTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                             20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMOLYMPH 65 KDA LECTIN BG06 (FRAGMENT).
                                                                                                                                          16 AA.
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                                4; Mismatches
                                                                                                                                                                                                                          Biomphalaria glabrata (Bloodfluke planorb)
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                                                                                                                                                                                                                                                                                                STRAIN=M-LINE; TISSUE-Hemolymph; MEDLINE=97385165; PubMed=9238039;
                   23.1%;
        18.68;
                                                                                                                                                                                                                                                                                                                                                                                   ECHINOSTOMA PARAENSEI.
                                3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                      5 ITDSTDRIFATRD 17
                                                                            2 LTEQASKVALTAD 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus megaterium.
      Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1404;
                                                                                                                                                                                                                                                              NCBI_TaxID=6526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 FATRDOD 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | | |:|
2 FTTFDKD 8
                                                                                                                        LE06_BIOGL
ID LE06_BIOGL
AC P80745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPAC_BACME
P56948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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NON_TER
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PPAC_BACME
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Gaps
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Biochemistry 15:1928-1933(1976).
FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING CHOLESTEROL FROM TISSUES AND BY ACTING AS A COFACTOR FOR THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
SUBCELLULAR LOCATION: EXTRACELLULAR.
TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mahley R.W., Weisgraber K.H., Innerarity T., Brewer H.B. Jr.; "Characterization of the plasma lipoproteins and apoproteins of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Erythrocebus patas (Red guenon) (Hussar).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Erythrocebus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE APOAl / APOA4 / APOE FAMILY.
PIR; A05313; A05313.
                                                                                                                                                                                          Score 21; DB 1; Length 16;
Pred. No. 1.4e+03;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
-!- COFACTOR: REQUIRES MANGANESE FOR ITS ACTIVITY.
-!- SUBECLLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE PPASE CLASS C FAMILY.
Hydrolase: Manganese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasma; Lipid transport; HDL; Cholesterol metabolism.
                                                                                                                        3C0E6735D98B38A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 AA; 2387 MW; 9C970997C7FC976A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20.5; DB 1;
Pred. No. 2.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 28, Created)
(Rel. 28, Last sequence update)
(Rel. 33, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APOLIPOPROTEIN A-I (APO-AI) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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MEDLINE=76184721; Pubmed=178359;
                                                                                                                                                                                             18.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.4%;
                                                                                                                   16 AA; 1828 MW;
                                                                                                                                                                                             Ouery Match 18.6
Best Local Similarity 44.4
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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Best Local Similarity
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Length 18;

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Query Match
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                                                                                                          Regul. Pept. 32:39-45(1991).
-!- FUNCTION: GASTRIN STIMULATES THE STOMACH MUCOSA TO PRODUCE AND SECRETE HYPROCHOLORIC ACID AND THE PANCREAS TO SECRETE ITS DIGESTITVE ENZYMES. IT ALSO STIMULATES SMOOTH MUSCLE CONTRACTION, INCREASE BLOOD CIRCULATION AND WATER SECRETION IN THE STOMACH AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS. MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
                                                                    Yu J., Xin Y., Eng J., Yalow R.S.;
"Rhesus monkey gastroenteropancreatic hormones: relationship to human
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Min Y., ping Z., Yaoshi 2., and "Purification and primary structures of duck fibrinopeptides A and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Anserlformes; Anatidae; Anas.
                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: SECRETED.
-!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
PIR; A60071, A60071.
InterPro; IPR001651; Gastrin.
PROSITE; PS00259; GASTRIN: 1.
Hormone; Amidation; Sulfation.
                                                                                                                                                                                                                                                                                                                                                          Score 20; DB 1; Length 17; Pred. No. 2.2e+03; 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                              PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BOF15E7768F8A1F9 CRC64;
                                                                                                                                                                                                                                                                                                                       6F6E92C73611D39A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; JP0102; JP0102.
InterPro; IPR002181; Pibrinogen_C.
SO051E; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
Blood coagulation; Plasma; Sulfation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIBB_ANAPL STANDARD; PRT; 18 AA. P12802; 01-0CT-1989 (Rel. 12, Created) 1-0CT-1989 (Rel. 12, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                           SULFATION. AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anas platyrhynchos (Domestic duck)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-85168193; PubMed-3983613;
                                                      MEDLINE-91164506; PubMed-2003150;
                                                                                                                                                                                                                                                                                                                                                               17.78;
40.08;
                                                                                                                                                                                                                                                                                                                       2076 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2028 MW;
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
Cercopithecinae; Macaca
                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 2; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 AA;
                                                                                                                                                                                                                                                                                                                     17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIBRINOPEPTIDE B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=8839;
                                                                                                                                                                                INTESTINE.
                                                                                                                                                                                                                                                                                                                                                                                                                     3 PWITD 7
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MOD_RES
MOD_RES
SEQUENCE
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NON_TER
SEQUENCE
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FIBB_ANAPL
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SUBUNT: MONOMER (BY SIMILARITY).
MISCELLANGOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA
BACKBONE BOND, IT SIMULTANBOUSLY FORMS A PROTEIN-DNA LINK, IN
WHICH A TYROSYL OXYGEN IN THE BNZYME IS JOINED TO A DNA PHOSPHORUS
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OSTCOWSKI J., Jagura-Burdzy G., Kredich N.M.;

"DNA sequences of the cysB regions of Salmonella typhimurium and

"Escherichia coli,";

J. Biol. Chem. 262:5999-6005(1987).

-!- FUNCTION: THE REACTION CATALIZED BY TOPOISOMERASES LEADS TO THE

CONVENSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.

-!- CONVENSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.

-!- CATALITIC ACTIVITY: ATP-INDEPENDENT BREAKAGE OF SINGLE-STRANDED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Last annotation update)
DNA TOPOISOMERASE I (EC 5.99.1.2) (OMEGA-PROTEIN) (RELAXING ENZYME)
(UNTWISTING ENZYME) (SMIVELASE) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95203287; PubMed-7895732;
Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
"The human myocardial two-dimensional gel protein database: update
1994.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Electrophoresis 15:1459-1465(1994).
-:- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 6.0, ITS MW IS: 55.3 KDA.
NON-TER 9 9 9
                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                          5;
                                                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF HEART (SPOT 5603) (FRAGMENT).
                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 AA; 1104 MW; 8874B1BB5B01B2CA CRC64;
Score 20; DB 1;
Pred. No. 2.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 19; DB 1;
Pred. No. 1e+05;
                                                                                                                                                                                                                            9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 AA.
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(Rel. 31, Last sequence update)
                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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17.78;
35.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.8%;
50.0%;
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                              STANDARD;
                                                                                8 STDRIFATRDQDTI 21
                                                                                                                        3 STD--YDDEDESTV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 3; Conserv
                     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 ITDSTD 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :1: |1
3 VTEYTD
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01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOP1_SALTY P40686;
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P40929;
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8 STDRI 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUSCLES
                                                                                         TISSUE-Gut;
                                                                                                                                                                                                                                                                                                                                                                                         TKNM_RANMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYNTHESIS.
                                                                                                                                                                                                                               SEQUENCE
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TKNM_RANMA
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
UNKNOWN PROTEIN FROM 2D-PAGE OF HEART TISSUE (SPOT 7520) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dunn M.J., Corbett J.M., Wheeler C.H.;
"HSC-2DPAGE and the two-dimensional gel electrophoresis database of
Ano heart profesins":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 6.9, ITS MW IS: 55.4 KDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
AT ONE END OF THE ENZYME-SEVERED DNA STRAND. SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                  Score 19; DB 1; Length 10;
Pred. No. 1.8e+03;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.8%; Score 19; DB 1; Length 13; 33.3%; Pred. No. 2.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                   2C25B67B02D37338 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9F5BD94B9306D76A CRC64;
                                                                                                                                                                    Interpro, IPR000380; Pro_topoisomrse.
PROSITE; PS00396; TOPOISOMERASE_I_PROK; PARTIAL.
Isomerase; Topoisomerase; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MX14_PHEVI STANDARD; PRT; 14 AA. P46980; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Electrophoresis 18:2795-2802(1997).
                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98163340; PubMed=9504812;
                                                                                                                                   EMBL; M15040; AAA27044.1; -.
                                                                                                                                                                                                                                                    16.8%;
40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 AA; 1457 MW;
                                                                                                                                                                                                                   10 AA; 1145 MW;
                                                                                                                                                                                                                                                   Query Match 16.8
Best Local Similarity 40.0
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                             topA.
                                                                                                                                                HSSP; P06612; 1YUA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dog heart proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                           StyGene; SG10515;
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FITDPVEXV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Heart;
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                                                                                                                                                                                                                                                                                                1 DSPWI
                                                                                                                                                                                                                                                                                                                     DGKWV
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P56535;
                      FAMILY
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SEQUENCE
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MY14_PHEVI
ID MY14_P
AC P46980
DT 01-NOV
DT 01-NOV
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MEDILINE=90026852; PubMed=2803524; Tang Y.Q., Tian S.H., Wu S.X., Hua J.C., Wu G.F., Zhao E.M., Lu Y.A., Zhu Y.Q., Zou G., Tsou K.; "Isolation and structure of ranamargarin, a new tachykinin from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ranamargarin.";
Sci. China, B, Chem, Life Sci. Earth Sci. 33:170-177(1990).
Sci. China, B, CHEM, EACHY SCI. EARTH SEPTIDES WHICH EXCITE NEURONS,
FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
01-NOV-1995 (Rel. 32, Last annotation update)
MYOACTIVE TETRADECAPRETIDE (PTP).
Pheretima vittata (Earthworm)
Elwaryota; Metazoa; Annolida; Clitellata; Oligochaeta; Haplotaxida;
Lumbricina; Megascolecidae; Pheretima.
                                                                                                                                                                                                                                                                                                                                          Ukena K., Oumi T., Matsushima O., Ikeda T., Fujita T., Minakata H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rana margaratae (Chinese frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=121156;
                                                                                                                                                                                                                                                                                                                                                                        "A novel gut tetradecapeptide isolated from the earthworm, Eisenia foetida.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -! - FUNCTION: HAS A STIMULATIVE EFFECT ON THE CONTRACTION OF GUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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"Synthesis and biological activity of a new frog skin peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     skin of Chinese frog Rana margaratae.";
Sci. China, B, Chem. Life Sci. Earth Sci. 32:570-579(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 19; DB 1; Length 14;
Pred. No. 2.6e+03;
0; Mismatches 1; Indels
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INTERPO, IPR002040; Tachykinin.
PROSITE; PS00267; TACHYKININ; 1.
Tachykinin; Neuropeptide; Amidation; Amphibian skin.
MOD_RES 14 AMIDATION.
AMIDATION.
AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMIDATION.
DA40BEE67CCD91AD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -! - SIMILARITY: TO INSECTS ALLATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                    MEDLINE=96087879; PubMed=8532604;
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptides 16:995-999(1995)
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neuropeptide; Amidation.
MOD RES 14 14
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                                                                                                                                                                                                                                       SEQUENCE, AND SYNTHESIS.
                                                                                                                                                               NCBI_TaxID=46674;
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Score 19; DB 1; Length 14;

16.8%;

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0; Gaps Best Local Similarity 60.0%; Pred. No. 2.6e+03; Matches 3; Conservative 2; Mismatches 0; Indels

0;

7 DSTDR 11 |::|| 2 DASDR 6 οy

Op

Search completed: February 21, 2002, 16:52:21 Job time: 520 sec

09vit3 bovine circ 056132 porcine cir 09qv03 rattus sp. 09ur28 filobasidie 09ur61 shimonella 09ur61 homo sapien

Q9YIT3 O56132 Q9QV03 Q9UR28

Q9RQ21 Q9UCF3 Q9F5X2 Q9TRH3 Q9PRN1

062645 saguinus oe 09yr03 porcine cir

Oguqwo homo sapien Ogucqg homo sapien Q63935 rattus norv Q9epx6 mus musculu Q79459 human immun

P82262 Q62546 Q9TR10 Q9UQW0 Q9UCW0 Q9UCQ9 Q63935 Q9EPX6 Q79459

11 11 12 4

Q62546 mus spretus

Ogtrh3 sus scrofa Ogprn1 petromyzon P82262 aspergillus

musculu

Q9tr10 bos taurus Q9jhb6 mus muscul

99uce7 homo sapien 09ep50 unidentifie

Q9UCE7 Q9EP50

092Y75 003977

Q9TWH2

cenocoelius escherichia oxytricha g

092y75 c 003977 e 09twh2 c

ALIGNMENTS

Q9um85 homo sapien Q9uce7 homo sapien

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26 05:52:58 2002
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Ogucgo homo sapien
Q62256 mus musculu
Q9qv38 mus sp. erp
Q9tqz8 sus scrofa
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Q31687 artemia par
Q9prn6 scyliorhinu
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                                                     February 21, 2002, 16:51:54; Search time 60.03 Seconds
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                        473505 segs, 146272329 residues
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                                    - protein search, using sw model
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090C99
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090V38
090GN8
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                                                                                                                                                                                                                                                                                                                                                                                          sp_unclassified:*
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sp_human:*
sp_invertebrate:*
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sp_phage:*
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                                                                                                                                                                                                                                                                                                                                                             sp_rodent:*
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Maximum DB s
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MINOR
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-!- FUNCTION: HEMOCYANIN ARE COPPER-CONTAINING OXYGEN CARRIERS
OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: COMPOSED OF 3 MAJOR SUBUNITS (IB, II AND III) AND 1 SUBUNIT (IA) WHICH FORM HOMOHEXAMERS AND HETEROHEXAMERS. MAX FORM LARGER STRUCTURES.
-!- SUBCELLULAR LOCATION: EXTRACELLULAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN SUBFAMILY.
                                                                                                                                                                                                                                                                                     Makino N., Kimura S.; "Subunits of Panulirus japonicus hemocyanin. 1. Isolation and
                                                                                                                    Panulirus japonicus (fanomicus).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Palinura;
Palinuroidea; Palinuridae; Panulirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 AA; 2154 MW; 313BE8E456DDDE09 CRC64;
                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Respiratory protein; Oxygen transport; Copper.
NON_TER 20 20
SEQUENCE 20 AA; 2154 MW; 313BEBE8456DDDE09
                                 AA.
                                 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000896; Hemocyanin.
InterPro; IPR00227; Tyrosinase.
PROSITE; PS00209; HEMOCYANIN_1: PARTIAL.
PROSITE; PS00210; HEMOCYANIN_2; PARTIAL.
PROSITE; PS00497; TYROSINASE_1; PARTIAL.
PROSITE; PS00498; TYROSINASE_2; PARTIAL.
                                 PRT;
                                                                                                               HEMOCYANIN IA SUBUNIT (FRAGMENT)
                               PRELIMINARY;
                                                                                                                                                                                                                                                                     PubMed=3360019;
                                                                                                                                                                                                                                                                                                                                                                                          ARTHROPODS.
                                                                                                                                                                                                                                                                                                                      properties.";
                                                                                                                                                                                                                                                     TISSUE=SERUM;
                                                                                                                                                                                                                                    SEQUENCE
                                               P82310;
                               P82310
RESULT
                 P82310
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Score 36; DB 5; Length 20;

31.9%;

Query Match

Q83489 turnip yell Q9rrd8 oryctolagus O91329 human immun Q9n188 equus cabal Q46747 escherichia Q9s8d5 cynara card P97135 mycobacteri

046747 0958D5 P97135

090594 gallus gall 09t2v5 crithidia f 09urc7 saccharomyc

Q9n1x1 equus cabal

19 AA.

Created)

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Mazzarella R.A., Marcus N., Haugejorden S.M., Balcarek J.M.,
Baldassare J.J., Roy B., Li L.J., Lee A.S., Green M.;
"Erp6l Is GRP58, a stress-inducible luminal endoplasmic reticulum
protein, but is devoid of phosphatidylinositide-specific phospholipase
C activity.";
                                                                             01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
ERP61, GRP58-STRESS-INDUCIBLE LUMINAL ENDOPLASMIC RETICULUM PROTEIN.
                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10095;
                                                                                                                                                                                                                                                                                 Arch. Biochem. Biophys. 308:454-460(1994).
SEQUENCE 19 AA; 2113 MW; 5A62F136268E3CF4 CRC64;
                                                                                                                                                                                                    MEDLINE=94153092; PubMed=8109975;
                                                                                                                                                                                                                                                                                                                                      25.7%;
                                                                     13,
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                                         PRELIMINARY;
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 4; Conserv
                                                                   01-MAY-2000
                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                        Q9QV38
Q9QV38;
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Q9TQZ8;
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               RESULT
                             09QV38
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EMBL: M55181; AAA40127.1.
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                Gaps
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MEDLINE-90287163; Pubmed-2355920;
Kilpatrick D.L., Zinn S.A., FitzGerald M., Higuchi H., Sabol S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                          Ø
                                                                                                                                                                                                                                                                                          MEDLINE-95028770; PubMed-7524281; Schroder J.M., Kameyoshi Y., Christophèrs E.; Schroder J.M., Kameyoshi Y., Christophèrs E.; Platelets secrete an eosinophil-chemotactic cytokine which is member of the C-c-chemokine family."; Adv. Exp. Med. Biol. 351:119-128(1993). SEQUENCE 16 AA; 1786 Mw; 8B041B46AEACC2Al CRC64;
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Pred. No. 3.3e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       27.4%; Score 31; DB 4; Length 16; 46.2%; Pred. No. 2e+02;
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             Indels
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Last sequence update)
Last annotation update)
                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2000 (TrEMBLrel. 13, Last annotation update) EOCP-1=EOSINOPHIL-CHEMOTACTIC CYTOKINE.
               4.
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                                                                                                                                   16 AA.
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Pred. No. 42;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
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                                                                                                                                                              Created)
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             3;
                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
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Q62256;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1999 (TrEMBLrel. 01,
01-NOV-1999 (TrEMBLrel. 12,
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58.3%;
46.28;
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             Conservative
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                                                      2 SPWITDSTDRIFA 14
                                                                                                                                                                                                                 Homo sapiens (Human)
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 7; Conserv
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SEQUENCE
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Score 29; DB 11; Length 19; Pred. No. 5.1e+02; 7; Indels

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01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
20 KDA PHOSPHORYLATION-DEPENDENT PROTEIN PHOSPHATASE-1 INHIBITORY
                                                                                                                                                                                 Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                Eto M., Ohmori T., Suzuki M., Turuya K., Morita F.;
"A novel protein phosphatase-linhibitory protein potentiated by protein kinase C. Isolation from porcine aorta media and characterization.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 17;
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                                                                                                                                                           Sus scrofa (Pig).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae;
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biochem. 118:1104-1107(1995).
SEQUENCE 17 AA; 2109 MW; 4728B9943FC5AB15 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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Pred. No. 9.2e+02;
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17
                                              Created)
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25.0%;
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001-NOV-1996 (TrEMBLrel. 01, 01-17AN-1999 (TrEMBLrel. 09;
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Best Local Similarity 46.7
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01-JUN-2001 (TrEMBLEEL.
GLOBIN (FRAGMENT).
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 UROTENSIN I HOMOLOG
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Best Local Similarity
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                                                                                        NCBI_TaxID=7830;
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7 PWVT 10
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SEQUENCE
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J. Mol. Evol. 38:156-168(1994).

EMBL, X67263; CAA47685.1;
                                                                                                                                                    Roberts D.L., Dalgleish R., Cohen G.M., MacFarlane M.; "The mammalian CED4 homologue, APAFI, exists as two distinct forms in human cells.";
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Artemia parthenogenetica.
Mitochondrion.
Bukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;
Artemidae; Artemia.
NCBI_TaxID=6663;
                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                       Score 27; DB 4; Length 18;
Pred. No. 9.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                         3; Indels
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                                                                                                                                                                                                Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AJ133645; CAB65087.1; -.
NON_TER 1
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                                                                                                                                                                                                                                                                                 2045 MW; 30D5FA30B885AEF5 CRC64;
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Last annotation update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
APAFI PROTEIN (FRAGMENT).
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=LA MATA;
MEDLINE=94223692; Pubmed=8169960;
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0
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                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Best Local Similarity
Matches 4; Conserv
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Matches 4; Conserv
                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 18 AA;
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2 WNTDSRSKV 10
                                                                                                   NCBI_TaxID=9606;
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01-MAY-2000 (
01-MAY-2000 (
01-MAY-2000 (
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PWIT 11
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SEQUENCE
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Q9PRN6
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                     Conion J.M.;
"A peptide from the caudal neurosecretory system of the dogfish Scyliorhinus canicula that is structurally related to urotensin I."; Gen. Comp. Endocrinol. 99:333-339(1995).
SEQUENCE 20 AA: 2305 MW: 77A92D52817E97B7 CRC64;
Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
Scyliorhinidae; Scyliorhinus.
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MEDLINE-20082971; bubmed=10613847;
Cactano A.R., Shiue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
Bowling A.T., Murray J.D.;
"A comparative gene map of the horse (Equus caballus).";
Genome Res. 9:1239-1249[1999].
EMBL; AF134056; AAF31299.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eŭkaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
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Waugh D., Anderson G., Armour K.J., Balment R.J., Hazon N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 27; DB 13; Length 20
Pred. No. 1.1e+03;
1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 10;
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Last annotation update)
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Last annotation update)
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Pred. No. 7.3e+02;
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Gaps

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Rommelaere H., Van Troys M., Gao Y., Melki R., Cowan N.J., Vandekerckhove J., Ampe C.; "Eukaryotic cytosolic chaperonin contains t-complex polypeptide 1 and seven related subunits."; Proc. Natl. Acad. Sci. U.S.A. 90:11975-11979(1993).
SEQUENCE 18 AA; 1884 MW; B608F6EBB5A8A2A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                         083489 PRELIMINARY; PRT; 21 AA. 083489; 087489; CTEMBLEG. 01, Created) 01-NOV-1996 (TEMBLEG. 01, Last sequence update) 01-NOY-1999 (TEMBLEG. 12, Last annotation update) 01-NOY-1999 (TEMBLEG. 12, Last annotation update) TYPE ISOLATE) COAT PROTEIN (FRAGMENT).

Turnip yellow mosaic virus. Virus. Viruses; ssrNA positive-strand viruses, no DNA stage; Tymovirus.
               Creutz C.E., Snyder S.L., Kambouris N.G.;
"Calcium-dependent secretory vesicle-binding and lipid-binding proteins of saccharomyces cerevisiae.";
Yeast 7:229-244(1991).
SEQUENCE 20 AA: 2388 MW; 594377CBC3E72B0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-88105991; PubMed-3426397;
Blok J., MacKenzie A., Guy P., Gibbs A.;
"Nucleotide sequence comparisons of turnip yellow mosaic virus isolates from Australia and Europe.";
Arch. Virol. 97:283-295(1987).
EMBL; M24802; AAA46597.1; -...
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pred. No. 1.7e+03;
2; Mismatches 1; Indels
                                                                                                                                                     Length 20;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2000 (TrEMBLrel. 14, Last annotation update)
CHAPERONIN (FRAGMENT).
                                                                                                                                                   Score 26; DB 3;
Pred. No. 1.6e+03;
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MEDLINE-91353077; PubMed=1882548;
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50.0%;
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62.5%;
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21 AA; 2177 MW;
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Best Local Similarity 62.5
Matches 5; Conservative
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13 SPLITDTS 20
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SEQUENCE 21
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                                                                         S., Salser W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Crithidia.
NCBI_TaxID=5656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Seccharomycetales; Saccharomycetaceae; Saccharomyces
NCbi_TaxID=4932;
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Speijer D., Muijsers A.O., Dekker H., de Haan A., Breek C.K.,
Albracht S.P., Benne R.;
                                                                                                                                                                                                                                                                                                                                          Score 26; DB 13; Length 15;
Pred. No. 1.2e+03;
0; Mismatches 2; Indels
                               SEQUENCE FROM N.A.

MEDLINE=81261952; PubMed=6266925;

Padayatty J., Cummings I., Manske C.L., Higuchi R., Woo S Padayatty J., Cummings I., Manske C.L., Higuchi R., Woo S "Cloning of chicken globin cDNA in bacterial plasmids.";
Gene 13:417-422(1981)
--- SIMILARITY: TO GLOBIN FAMILY.

EMBL; M10380; AAAA48803.1; --
HSSP; P02112; 1HBR.
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                                                                                                                                                                                                                                                                                   23E61DA734FA7962 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2000 (TrEMBLrel. 14, Last annotation update)
CYTOCHROME C OXIDASE SUBUNIT 5 (FRAGMENT).
Crithidia fasciculata.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
LIPID-BINDING PROTEIN.
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RESULT 11

Q9T2V5

Matches

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Matches

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Gaps

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        22.1%; Score 25; DB 6; Length 18;

        Best Local Similarity
        35.3%; Pred. No. 2e+03;

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        6; Conservative
        2; Mismatches
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22.1%; Score 25; DB 12; Length 19; 44.4%; Pred. No. 2.2e+03; ive 3; Mismatches 2; Indels

Ouery Match 22.1 Best Local Similarity 44.4 Matches 4; Conservative

1 DSPWITDST 9 :| | ::|| 11 NSTWYSNST 19

Qy Db Interleukin-5 bind Peptide #2092 enco Peptide #2196 enco Peptide #2077 enco Cry j I pollen all Cry j I Japanese C Anti Lill2 antibody Peptide useful in Mouse mammary tumo

Complementarity-de Peptide #562 enco Peptide #5912 enco Peptide containing Peptide binding in IL-IRtI binding pe

Interleukin-1 type IL-1 antagonist pe Human FSH antagoni

Autotaxin peptide Human Factor V pro Phobr pathway apta

Fragment of human

Human secreted pro Sequence of P85 po Immunopeptide #2 d

Immunogenic Hepati Synthetic HAV VP1 T cell epitope/MHC Human leucocyte an Proteasome digesti

Hepatitis C virus Hepatitis C virus Hepatitis C virus

Proteasome

us-08-753+851-7.rag

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

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Use of CD44 protein and new peptide derivs - for developing prods for inflammation, immune-mediated tissue damage and tumour cell
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                                                                                                                           AAY09987
AAB17767
AAR21764
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AAW64573
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AAY02864
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AAY10398
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AAR53478 standard; peptide;
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Homo sapiens
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AAR53478;
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RESULT
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HTLV-1 p27(rex) pr
LN clone E13 Vbeta
IL-5 receptor bind
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C3/C4/C5-derived c
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23.976 Million cell updates/sec
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                                                         February 21, 2002, 16:42:58; Search time 64.88 Seconds
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Copyright (c) 1993 - 2000 Compugen Ltd
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Listing first 45 summaries
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1 DSPWITDSTDRIFATRDQDTI 21
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                                                                                                                                                                                                                 Gaps
                          The peptide can be used for treating inflammation and immune-mediated tissue damage such as occurs in the course of autoimmune diseases, e.g. rheumatoid arthritis. It can also be used for determining metastatic potential or to treat or prevent tumor cell metastasis. This peptide corresponds to AA 200-219 of the CD44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptide(s) specific for human cytomegalovirus - useful to detect antibodies specific for the specified virus, and for
                                                                                                                                                                                 Score 60; DB 15; Length 21; Pred. No. 0.0062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CMV; detection; antibody specificity determination.
                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cytomegalovirus antibody specific peptide 3.2.
                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                 AAR33105 standard; peptide; 17 AA.
Claim 4; Page 14; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 24; 25pp; German.
                                                                                                                                                                                 53.1%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91DE-4128684.
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                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BEHW ) BEHRINGWERKE AG
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                                                                                                                                                                                                                                          1 DSPWITDSTDRI 12
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                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preparing vaccines
                                                                                                                                                                                                                                                           21 AA;
                                                                                                         protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                              29-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-AUG-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
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                                                                                                                                       Sequence
                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                AAR33105;
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Matches
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SXX CCCCCCXX SXX CCCCCCXXX
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and cells the genes are expressed in Examples of activities include: antiarthritis; immunosuppressive; antirhemmatic; antiproliferative; cytostatic; cardiant; vasotropic; creebroprotective; nootropic; cardiant; vasotropic; creebroprotective; nootropic; opposition in the polymetrial; virucide; fungicide; and ophthalmological. The polymedical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the present
                                                                                                                                                                                                                                                                                                                                                                                                       fungicide; ophthalmological; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arriest; cerebrovascular disorder; cerebrovascular disorder; anglogenesis; nervous system disorder; Alzheimer's disease; skin aging; ocular disorder; corneal infection; wound healing; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homologous to them, which are given in the exemplification of the preser
invention. Human secreted proteins have activities based on the tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e.g. cardiac arrest, cerebroascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fundi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase storage capabilities. AAR32690 to AAR32698 and AAB64421 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The polynucleotide sequences given in AAF32699 to AAF32747 encode the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human secreted proteins given in AAB64422 to AAB64470. AAB64471 to AAB64548 represent human secreted polypeptide sequences and proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                   Gene 25 human secreted protein homologous amino acid sequence #147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Komatsoulis GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 564; 593pp; English.
                                                                                                                                       AAB64509 standard; Protein; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2000; 2000WO-US14926.
                                                                                                                                                                                                                                    23-MAR-2001 (first entry)
|: | :: | | | | 4 daadevwalrdg 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200077255-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JUN-1999;
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                                                                                                                                                                                    AAB64509;
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Gaps

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Indels

3;

Score 36; DB Pred. No. 31; 3; Mismatches

31.9%; 50.0%;

Query Match Best Local Similarity

6; Conservative

Matches

DB 14; Length 17;

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WPI; 1992-080024/10.
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Best Local Similarity
Matches 6; Conserv
                                                        3 sdsxsrayxtrd
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                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                23-JUN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                        WO9202542-A.
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                                                                                                                                                                                                                                              Synthetic.
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                                                                                                                                           AAR21762;
Query Match
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                                                                                                                                                                                                                                                                    Key
Region
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                                                      Gaps
                                                                                                                                                                                                                                           Follicle stimulating hormone; FSH; thyroid stimulating hormone; TSH; contraceptive; in vitro fertilisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "amino acids 34-37 of beta-chain of hFSH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptide having glyco-protein hormone agonist or antagonist action - useful as vaccines for passive immunisation against glyco-protein hormone and to regulate fertility
                                                                                                                                                                                                                                                                                                                           from
                                                                                                                                                                                                                                                                                                                                                                                 Length 14;
                                                                                                                                                                                                                                                                                                                          /note= "amino acids 92, 88,89, 90 and 91
                                                     Indels
                                                     2;
                                                                                                                                                                                                                                                                                                                                      beta-chain of human FSH"
                               DB 22;
52;
                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "5-aminopentanoic acid"
                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Meloen RH;
                               Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                     AAR21758 standard; Protein; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Page 74; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER
                            30.1%;
60.0%;
                                                                                                                                                                                                                        Human FSH agonist peptide #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hage Van Noort M, Puijk WC,
                                                                                                                                                                                                                                                                                                                                                           /label= Acp
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                                                                                                                                                                                                  (first entry)
                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  /label=
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/note=
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                                          Best Local Similarity
                                                                          8 STDRIFATRD 17
                                                                                       || |:| |:|
3 stprvfttgd 12
14 AA;
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                                                                                                                                                                                                                                                                              Synthetic
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Sequence
                               Query Match
                                                                                                                                                                                                                                                                                                                Region
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                                                     Matches
                                                                                                                                RESULT
AAR21758
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Gaps
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Follicle stimulating hormone; FSH; thyroid stimulating hormone; TSH; contraceptive; in vitro fertilisation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "amino acids 34-37 of beta-chain of hFSH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptide having glyco-protein hormone agonist or antagonist action - useful as vaccines for passive immunisation against glyco-protein hormone and to regulate fertility
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 and 91 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "partial peptide from alpha-chain of glycopeptide hormones"
    Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 15;
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                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1..5
/note= "amino acids 92, 88,89, 90
beta-chain of human FSH"
  DB 13;
56;
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  Score 34; DB 1
Pred. No. 56;
2; Mismatches
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2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                  AAR21762 standard; Protein; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                               Human FSH antagonist peptide #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hage Van Noort M, Puijk WC,
30.1%;
50.0%;
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                             Best Local Similarity 50.0
Matches 6; Conservative
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(first entry)

us-08-753-851-7.rag

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AAW24962 standard; peptide; 14 AA.
                                                                       28-OCT-1997
                                                     AAW24962;
                          AAW24962
                                             Follicle stimulating hormone; FSH; thyroid stimulating hormone; TSH; contraceptive; in vitro fertilisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention also covers substitution, deletion and insertion variants having FSH antagonistic activity, as well as derivs. in which the free amino group of the N-terminal amino acid and/or the free carboxyl group of the C-terminal amino acid are blocked or otherwise modified. The antagonist can be used, e.g. as an alternative "steroid-free" pill to block ovulation or as an immunogen for active or passive immunisation against gonadotropins. See AAR21754-R21765 and AAR23788-9.
                                                                                                                                                                                                                                                                               12..15
/note= "amino acids 34-37 of beta-chain of hFSH"
                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptide having glyco-protein hormone agonist or antagonist action - useful as vaccines for passive immunisation against glyco-protein hormone and to regulate fertility
                                                                                                                                                                                              92, 88,89, 90 and 91 from of human FSH"
                                                                                                                                                                                                                                           "partial peptide from alpha-chain of glycopeptide hormones"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 13; Length 15; Pred. No. 56; 4; Indels.
                                                                                                                                                                                                                                                                                                                                                                                                 Meloen RH;
                                                                                                                                                                                              /note= "amino acids 92
beta-chain of
                                                                                                                                                                               Location/Qualifiers
                                                            AAR21763 standard; Protein; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Page 75; 82pp; English.
                                                                                                                 Human FSH antagonist peptide #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.1%;
50.0%;
                                                                                                                                                                                                                                                                       'label- bAla
                                                                                                                                                                                                                                                                                                                                                                                                 Puijk WC,
                                                                                                                                                                                                                           'label- Acp
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                                                                                                (first entry)
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3 sdsxsraygtrd 14
6 TDSTDRIFATRD 17
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                                                                                                                                                                                                                                                                                                                                                                                                 Hage Van Noort M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 AA;
                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                              Modified-site
                                                                                               23-JUN-1992
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                                                                                                                                                                                                                                                                                                                                                              27-JUL-1990;
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                                                                                                                                                             Synthetic
                                                                             AAR21763;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modulatory cpds. identified by screening peptide(s) derived from indels - esp. from regions involved in protein-protein interaction, useful as inhibitors or activators of the complement system
                                                              Indel; insertion; deletion; protein family; sequence alignment; interaction site; ligand; interface peptide; binding complex; modulation; complement; vaccine; antibody; tissue rejection; ischemia; aneurysm; chronic inflammation; autoimmune disease.
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C3/C4/C5-derived complement inhibitory peptide C4-B1.
                                                                                                                                                                                                                                                                                                                                                          /note= "acylated N-terminus"
                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 30; Page 23; 161pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.2%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-0000674.
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Best Local Similarity
Matches 5; Conser
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|spwlkds 14
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Modified-site
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                                                                                                                                                                                                                              Synthetic.
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Key

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Polymerase chain reaction; PCR; primer; amplify; human; T cell receptor; beta chain; TCR; myelin basic protein; BP; autoantigen; encephalitogen; experimental autoimmune encephalomyelitis; EAR; multiple sclerosis; MS; autoimmune disease; neurological disease; cerebrospinal fluid; therapy; central nervous system; complementarity determining region; CDR; T lymphocyte; optical nerve damage; anterior chamber inflammation.
                                                                                                                                                                                                                                             New HTLV-I antigenic peptide(s) - used for diagnosing HTLV-I infection(s), partic. HTLV-I associated myelopathy and adult T-cell
                                                                                                                                                                                                                                                                                                                                                 AAR74352-R74355 are claimed human T-cell lymphotropic virus type I (HTLV-1) p27(rex) protein antigenic peptides. They can be used to diagnose diseases caused by HITV-I, e.g. adult T-cell leukaemia, and HTLV-I associated myelopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methods for diagnosis and immune-related therapy of autoimmune diseases - partic. multiple sclerosis, by detecting marker T cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 30.5; DB 16;
Pred. No. 2.8e+02;
3; Mismatches 7;
                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                Claim 6; Columns 11-12; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vandenbark AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CONN-) CONNECTIVE THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR89243 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
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                                                                     93US-0103742
                                                                                                     93US-0103742.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LN clone E13 Vbeta8-CDR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; , Conservative
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Best Local Similarity
                                                                                                                                                                         Rudolph DL;
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                                                                                                                                                                                                         WPI; 1995-206307/27
                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                     06-AUG-1993;
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                                                                                                       06-AUG-1993;
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   US5420244-A.
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                                   30-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR89243;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                leukemia
                                                                                                                                                                         Lal RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            It has an amino acid sequence which corresp. to a naturally occurring amino acid sequence for an epitope of HIV, and which further has two Cys residues on each side of the epitope. It is stabilised by a sulphur bridge between the 2 Cys residues formed by a chemical oxidation step. Also claimed are peptides having a shorter sequence. It provides an assay for the detn. of antibodies induced by HIV for use in diagnostic immunoassay kits. It may also be used as an immunising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                   Artificial peptide containing a sequence which comprises an epitope
                                                                                                                                                     Artificial HIV peptide; HIV epitope; immunoassay kit; HIV vaccine;
artificial antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human T-cell lymphotropic virus type I; HTLV-I; p27(rex) protein; antigenic peptide; rex2; residues 16-35; adult T-cell leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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                                                                                                                                                                                                                                           /note="This sequence is specifically claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31; DB 10; Length 21; Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - having a sulphur bridge between 2 cysteine residues located on each side of a HIV epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTLV-1 p27(rex) protein antigenic peptide rex2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 21, lines 11-13; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       component in vaccine compsns. against HIV.
                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                  87SE-0004185.
AAP91156 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                  88WO-SE00570
                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Artificial HIV peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trojnar J, Wahren B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1989-150751/20.
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Matches 4; Conserv
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|16 pwvnds 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 PWITDS 8
                                                                                                                                                                                                                                                                                                                                                 27-OCT-1988;
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                                                                 26-APR-1990
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                                 AAP91156;
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AAR89215-R89251 represent clones of the Vbeta8 complementarity
determining region 3 (CDR3) of the T cell receptor beta (TCRbeta) chain.
These sequences were isolated from cerebrospinal fluid (CSF), spinal cord
(SC) and lymph nodes (LN) of clones of Lewis rats with experimental
autoimmune encephalomyelitis (BAB). By detecting the presence of a
marker TCR V gene bias in a body fluid which encapsulates all or part of
the target organ, an autoimmune disease (such as a neurological disease)
in a human can be identified. This method can also be carried out to
the vbeta gene bias, an immune-related disease that targets the central
correvous system can be diagnosed. Therapettic Vbeta peptide sequences can
the vbeta gene bias, an immune-related disease that targets the central
nervous system can be diagnosed. Therapeutic Vbeta peptide sequences can
the target tissue or organ of the disease, and selection
is carried out by identifying a vbeta gene bias in a body fluid that is
too the target tissue or organ of the disease, and selecting an
immunogenic peptide corresponding to the Vbeta gene bias. Multiple
sclerosis (MS) can be treated by identifying the CDR2 of a V gene peptide
con the surface of a Tymphocyte in the CSF of a patient and
also be used for the diagnosis and immune related therapy of optical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IL-5; interleukin-5 receptor; binding peptide; inflammatory disorder;
immunomediated inflammatory skin condition; respiratory tract; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide(s) that bind to interleukin-5- receptor - for treatment of asthma, inflammatory skin conditions, osteoarthritis etc.
receptor V gene bias and treating patients with selected V beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.5%; Score 30; DB 17; Length 8; 71.4%; Pred. No. 4.38+05; 1.4% 2; Mismatches 0; Indels
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                                                 Example 2; Fig 6c; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IL-5 receptor binding peptide #4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 71.4%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-0478312.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurological diseases.
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                                              AAW34409-W34412 represent the interleukin-5 (IL-5) receptor binding peptides of the invention. These sequences are based on the consensus sequences shown in AAW34403-W34408. The peptides can be used for the treatment of an inflammatory disorders of the respiratory tract, specifically asthma. They can also be used for the treatment of inmunomediated inflammatory skin conditions such as urticardi and angioedema, eczematous dermatitis, and hyperprolliferative skin disease such as psoriasis. Also for Theumatoid arthritis, inflammatory bowel disease spondylitis, osteoarthritis, gouty arthritis, inflammatory bowel disease chemical stability, enhanced pharmacological properties (e.g. half-life, absorption, potency and efficacy), altered specificity (e.g. a broad spectrum of biological activities) and reduced antigenicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interleukin-5; IL-5; binding peptide; core sequence; consensus sequence; lymphokine; T cell; mast cell; B cell; eosinophil; IL5 receptor; asthma; inflammatory disorder; rheumatoid arthritis; rheumatoid spondylitis; costeoarthritis; gouty arthritis; inflammatory bowel disease; angloedema; skin disease; urticaria; eczematous dermatitis; psoriasis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW30160-W30163 represent the interleukin-5 binding peptides used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  compound used in the method of the invention. The method is for the traatment of disorders mediated by interleukin-5 (IL-5), IL-5 is a lymphokine secreted by T cells and mast cells, and has biological activities on B cells and eosinophils. The method comprises administering a peptide or peptide analogue which has one of these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treatment of disorders mediated by interleukin-5, especially asthma - uses low molecular weight peptide(s) having affinity for
                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                         Score 30; DB 18; Length 18;
Pred. No. 2.9e+02;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sloan D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; Column 49-50; 43pp; English.
               Claim 9; Column 71; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW30163 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interleukin-5 binding peptide #4.
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                                                                                                                                                                                                                                                                                                                                                                           26.5%;
53.8%;
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Best Local Similarity 53.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 dgctrivatrswd 14
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                                                                                                                                                                                                                                                                                                                     18 AA;
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sequences a molecular weight below 5 kD, and an IC50 of 100 microM or less for binding to IL5 receptors. The peptide may have one or more peptide CONH linkages replaced, an altered N-terminal group, and a c-terminal group of formula COR2, where R2 = 0H, lower alkoxy or NR3R4, where R3 and R4 = H or lower alkyl, or the nitrogen atom of the -NR3R4 group can optionally be the amine group of the N-terminus of the peptide so as to form a cyclic peptide. The method may be used for treating an IL-5-mediated disorder that involves the accumulation of eosinophils. It is especially for treating an IL-5-mediated inflammarcry disorder of the respiratory tract, especially asthma, by administering an inhalant composition comprising a peptide or peptide analogue as above in an aerosolised carrier solution or dry powder. Other diseases that may be treated with the method include rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, inflammatory bowel disease, and various skin conditions (including urticaria, angloedema, eczematous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide #2092 encoded by probe for measuring cervical gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe; human; microarray; gene expression; cervical epithelial cell;
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                                                                                                                                                                                                                                                                                                                                                                       6; Indels
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Pred. No. 2.9e+02;
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53.8%;
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nes 7; Conserv
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26-MAY-2000;
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27-SEP-2000;
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Best Local S
Matches 7
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measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                          printed
                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                  Peptide #2196 encoded by probe for measuring placental gene expression.
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Pred. No. 2.9e+02;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                              Probe; microarray; human; placenta; antenatal diagnosis;
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Pred. No. 2.9e+02;
                                                                                   at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    analyzing gene expression in human placenta
                                                                                                                                                                                    Mismatches
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                                                                                                                                                       26.5%;
62.5%;
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Best Local Similarity 62.5
Matches 5; Conservative
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                                             cervical cancer
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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Search completed: February 21, 2002, 16:42:58 Job time: 232 sec

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The present invention relates to novel single exon nucleic acid probes see AAI00010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for preddicting, diagnosing, grading, staging, monitoring and prognosing adiseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. WIPO.Int/pub/published_pct_sequences.
                                                                                                                                                                                                                                        Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel single exon nucleic acid probe used to measuring gene expression
                                                                                                                                                                                                            Peptide #2077 encoded by probe for measuring breast gene expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rank DR;
                                                                                                            AAM03395 standard; Protein; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
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2000us-0207456.
2000us-0608408.
2000us-0632366.
2000us-0234687.
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                               10 spwcpnst 17
2 SPWITDST 9
                                                                                                                                                                                                                                                                                                                       WO200157270-A2
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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Gaps

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Score 30; DB 22; Length 18; Pred. No. 2.9e+02; 1; Mismatches 2; Indels

26.5%; 62.5%;

Query Match 26.59
Best Local Similarity 62.59
Matches 5; Conservative

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US-08-934-915-40 US-07-745-380-7 US-07-921-828-7 US-08-810-436-7 US-08-810-436-7 US-08-810-436-7 US-08-221-583-8 US-08-553-257A-49 PCT-US95-04018-8 US-08-451-947-32 US-08-451-947-32 US-08-451-947-32 US-08-951-29 US-08-951-29 US-08-951-29 US-08-951-29 US-08-851-843A-185 US-08-951-29 US-08-951-29

Sequence

Sequence Sequence Sequence Sequence

Sequence

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/143,311B
FILING DATE: 29-OCT 1993
CLASSIFICATION NUMBER: 07/973,339
FILING DATE: 30-OCT-1992
CLASSIFICATION NUMBER: 07/973,339
FILING DATE: 30-OCT-1992
CLASSIFICATION NUMBER: 07/69,730
FILING DATE: 15-MAR-1991
CLASSIFICATION NUMBER: 05-MAR-1091
CLASSIFICATION NUMBER: 05-MAR-1091
CLASSIFICATION NUMBER: 05-MAR-1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: AN ADHESION MOLECULE NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08143311B Patent No. 5863540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGIESTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HALE, LAURA P.
APPLICANT: PATTON, KAREN L.
APPLICANT: TELEN, MARILYN J.
APPLICANT: LIAO, HUA-XIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BARTON F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-143-311B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 703-c.c.
TELEPHONE: 703-816-4100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: HAYNES,
APPLICANT: HALE, LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: VIRGINIA COUNTRY: U.S.A. ZIP: 22201-4714
44EUUUUUUUUUUUUUUUUUUUUUUUUUUUUU
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US-08-143-311B-7
  (without alignments)
14.969 Million cell updates/sec
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Sequence 308, App
Patent No. 5217891
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Sequence 43,
                                                                                                                                                February 21, 2002, 16:43:36; Search time 31.57 Seconds
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-464-538B-251
US-08-463-076E-308
5217891-8
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US-08-460-874A-31
US-08-368-883B-31
US-08-221-583-31
PCT-USS-04018-32
PCT-USS-04018-32
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US-08-478-312-13
US-08-485-302-13
US-08-467-023-55
US-08-555-394-16
US-08-745-892-16
US-08-937-102-21
US-08-937-102-23
US-08-937-102-23
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US-08-977-221-43
                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                       212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                        protein search, using sw model
                                                                                                                                                                                                                                                                               1 DSPWITDSTDRIFATRDQDTI 21
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                    US-08-753-851-7
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 21
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                                                                                                                                                  Run on:
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Gaps
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                                                                       APPLICANT: Stuber, Werner
APPLICANT: Wieczorek, Leszek
APPLICANT: Ziegelmaier, Robert
TITLE OF INVENTION: HOMY-Specific Peptides, Agents Therefor
TITLE OF INVENTION: and the Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor TITLE OF INVENTION: and the Use Thereof NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Finnegan, Henderson, Farabow, Garrett & Dunner L.L.P.
                                                                                                                                                                                                                 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,874A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05552-1210-04000
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Mismatches
                                                                                                                                                                                                                                          STREET: 1300 I Street, N.W., Suite 700 CITY: Washington, STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/460,874A
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/936,219
FILING DATE: 27-Aug-1992
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 29-Aug-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36;
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              Sequence 31, Application US/08460874A Patent No. 5744298 GENERAL INFORMATION:
APPLICANT: Stuber, Werner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 31, Application US/0838883B
Patent No. 5859185
GENERAL INFORMATION:
APPLICANT: ST BER, Werner
APPLICANT: XIEGEOREK, Leszek
APPLICANT: ZIEGELMAIER, RObert
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 05.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Forman, David S. REGISTRATION NUMBER: 33,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.9%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                           NUMBER OF SEQUENCES: 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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20005-3315
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Best Local Similarity
Matches 6; Conserv
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ADDRESSEE:
US-08-460-874A-31
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                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                  Length 20;
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Pred. No. 0.0014;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.25
                                  ch 87.6%; Score 99; DB 2; I
1 Similarity 95.0%; Pred. No. 6.6e-10;
19; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: AN ADHESION MOLECULE NUMBER OF SEQUENCES: 28 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/143,311B
FILING DATE: 29-OCT-1993
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: NIXON & VANDERHYE P.C. 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
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APPLICATION NUMBER: 07/973,339
FILING DATE: 30-0CT-1992
CLASSIFICATION: 436
APPLICATION NUMBER: 07/669,730
FILING DATE: 15-MAR-1991
                                                                                                                                                                                                                                                Sequence 6, Application US/08143311B Patent No. 5863540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
EDDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REGISTRATION NUMBER: 15;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                         APPLICANT: HAYNES, BARTON F.
APPLICANT: HALE, LAURA P.
APPLICANT: PATTON, KAREN L.
APPLICANT: TELEN, MARILIYN J.
APPLICANT: LIAO, HUA-XIN
                                                                                                                1 DSPWITDSTDRIFATRDQDT 20
                                                                                                                                      1 DSPWITDSTDRIPATRDQDT 20
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91.7%;
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LENGTH: 21 amino acids
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Best Local Similarity 91.7
Matches 11; Conservative
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                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARLINGTON
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                                                                                                                                                                                                                                    US-08-143-311B-6
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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 17;
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TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36;
Pred. No. 7
                                                           APPLICATION NUMBER: US 08/388,883
FILING DATE: 13-FEB-1995
FILING DATE: 3-FEB-1995
APPLICATION DATA:
ATTORNEY SPECIFICATION NUMBER: DE P4128684.7
FILING DATE: 29-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAMME: FORMAT INFORMATION:
NAMME: FORMAT SPECIFICATION NUMBER: 33,694
      APPLICATION NUMBER: US/08/462,211A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: CCOR-0185 TELECOMMUNICATION INFORMATION:
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Patent No. 5486595
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 55
TELECOMMUNICATION INFORMATION
TELEPHONE: 202-408-4000
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50.0%;
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TELEFAX: (215) 568-3439
INFORMATION FOR SED ID NO: 31
SEQUENCE CHARACTERISTICS:
                           05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 50.0
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 17 amino acids
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                    202-408-4400
                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pennsylvania
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| DAADEVWALRDQ 15
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APPLICANT: Wiegzork, Leszek
APPLICANT: Ziegelmaier, Robert
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
TITLE OF INVENTION: and the Use Thereof
CORRESPONDENCE: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner L.L.P.
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington,
STATE: D.C.
                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.25
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7.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                   PAPLICATION NUMBER: US/08/388,883B
FILING DATE: 13-FEB-1995
CLASSIFICATION 13-FEB-1995
CLASSIFICATION 343:
APPLICATION NUMBER: US 08/300,305
FILING DATE: 23-FEB-1994
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/936,219
FILING DATE: 27-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4128684.7
FILING DATE: 29-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 31, Application US/08462211A Patent No. 6143493 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 55
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33,694
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50.0%;
                                                                                                                      Floppy disk
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Best Local Similarity 50.v.
کید 6; Conservative
                                        ZIP: 20005-3315
COMPUTER REDABLE FORM:
MEDIUM TYPE: Flore
COMPUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Forman, David S. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 17 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: peptide US-08-388-883B-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 DSTDRIFATRDQ 18
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4 DAADEVWALRDO 15
                       Washington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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Gaps

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APPLICANT: Heavner, George A.

APPLICANT: Heavner, George A.

Turne OF INVENTION: Tumor Necrosis Factor Inhibitors

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris

STREET: One Liberty Place 46th Floor

CITY: Philadelphia

STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
CORRESPONDENCE: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTOREY AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFRENCE/DOCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: One Liberty Place 46th Floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 32, Application PC/TUS9504018 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                            US-08-221583-32
Sequence 32, Application US/08221583
Patent No. 5486595
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.2%;
50.0%;
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Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: peptide US-08-221-583-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Pennsylvania
3 KVFATKTSDTV 13
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1 VFATKTSDTV 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                     0
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5; Length 15;
                                                                                                                         Length 15;
                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Meric, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Norris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.0%; Score 35; DB 945.5%; Pred. No. 9.9; tive 4; Mismatches
                                                                                                                         Score 35; DB
Pred. No. 9.9;
                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-ARR-1994
PRIOR APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-ARR-1994
FILING DATE: 01-ARR-1994
FILING DATE: 01-ARR-1994
FILING DATE: 01-ARR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
                                                                                                                                                                                                                                                                                                                RESULT 7
PCT-US95-04018-31
Sequence 31, Application PC/TUS9504018
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: DeLuca, Mark
REGISTRATION UNDBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR.
TELECOMMUNICATION INFORMATION:
TELEFAN: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 31:
                                                                                                                         31.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 45.5
Matghes... 5; Conservative
                                                                                                                                             Best_Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                    ; MOLECULE TYPE: peptide US-08-221-583-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pennsylvania
amino acid
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                                                                                                                                                                                                            11 RIFATRDQDTI 21
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3 KVFATKTSDTV 13
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                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US95-04018-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: I
                                                                                                                         Query Match
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Length 15; 2; Indels

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Gaps
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                                                                                                                                                                                                                                       ;;
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                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/478,312
FILING DATE: 07-JUN-1995
                                                                                                                                                                                             27.0%; Score 30.5; DB 1; 38.9%; Pred. No. 74;
                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Affymax Technologies, N.V 4001 Miranda Ave.
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application US/08478312
Patent No. 5654276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Barrett, Ronald W. APPLICANT: England, Bruce APPLICANT: Schatz, Peter APPLICANT: Sloan, Derek APPLICANT: Chen, Min-Jia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36,691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,
                                                                                                                                                                        Query Match
Best Local Similarity 38.9%,
-has 7; Conservative
                                                                                                                                                                                                                                                                           2 SPWIT-DSTDRIFATRDQ 18
                                                                                                                                                                                                                                                                                                 :|| | || || || || || || 3 TPWPTSQGLDRVFFSDTQ 20
                                        LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: . 415-424-0832
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                                                                                              TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-103-742-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 4001 Mirand
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 DSTDRIFATRDQD 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGCTRIVATRSWD 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-478-312-13
                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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APPLICANT: RUDOLPH, DONNA L.
APPLICANT: LAL, RENU B.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: DIAGNOSING HTLV-I ASSOCIATED MYELOPATHY AND ADULT T-CELL LEUKE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: Suite 1200, 127 Peachtree Street
CITY: ALLanta
STATE: Georgia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Pred. No. 21;
3; Mismatches 2; Indels
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                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-ARR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-ARR-1994
PRIOR APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-ARR-1994
ATTORNEY/AGENT INFORMATION:
NAME: DELUCA, MARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: DELUCA, MATK
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3409
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 32:
                                                          PCT/US95/04018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: SPRATT, GWENDOLYN D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 1414.080
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404/688-0770
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/103,742
FILING DATE: 06 AUG 1993
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application 08/103742 Patent No. 5420244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 15 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 29.2
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         404/688-9880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide PCT-US95-04018-32
                                    CURRENT APPLICATION DAT
                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : | | |: | |:
1 VFATKTSDTV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 IFATRDQDTI 21
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Sequence 16, Application US/0855394

Patent No. 5686247

GENERAL INFORMATION:
APPLICANT: HOLLAND, JAMES
APPLICANT: HOLLAND, JAMES
TITLE OF INVENTION: DETECTION OF MAMMARY TUMOR VIRUS ENV GENE;
TITLE OF INVENTION: LIKE SEQUENCES IN HUMAN BREAST CANCER
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 20;
               E: ImmuLogic Pharmaceutical Corporation, Inc. 610 Lincoln St
                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 08/350,225
FILING BAPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTONINY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3;
89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.5%; Score 30; 41.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,394
FILING DATE: 09-NOV-1995
CLASSIFICATION 435
PRICR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 55:
                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 26.5
Best Local Similarity 41.7
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: peptide
; FRACMENT TYPE: internal
US-08-467-023-55
                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 10112-0228
                       ADDAL.
STREET: blo
TTY: Waltham
                                                                                                         USA
                                                                                                       COUNTRY: US
ZIP: 02154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-08-555-394-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                 APPLICANT: Barrett, Ronald W.
APPLICANT: England, Bruce
APPLICANT: Schatz, Peter
APPLICANT: Schatz, Peter
APPLICANT: Chen, Min-Jia
TITLE OF INVENTION: Peeptides and Compounds That Bind to the IL-5
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: Affymax Technologies, N.V.
STREET: 4001 Miranda Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Allergenic Proteins And Peptides From Japanese Cedar Pollen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 30; DB 1; Length 18;
Pred. No. 79;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/485,302
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 55, Application US/08467023
Patent No. 6090386
GENERAL INFORMATION:
APPLICANT: Griffeth, Irwin J.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
                                                          Sequence 13, Application US/08485302
Patent No. 5668110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 1088
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 415-496-2300
TELEFAX: 415-496-230
                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yeung, Siu-mei H.;
Brauer, Andrew;
Exley, Mark A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Powers, Steven P.
TYTEE OF INVENTION: Allergeni
TITLE OF INVENTION: Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.5%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kuo, Mei-Chang;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 26.5
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 DSTDRIFATRDQD 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 DGCTRIVATRSWD 14
                                                                                                                                                                                                                                                                                                                                                        CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                  GENERAL INFORMATION:
APPLICANT: Barret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino av
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-467-023-55
                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
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Gaps

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Score 29, DB 3; Length 10, Pred. No. 56; 0; Mismatches 3; Indels

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Search completed: February 21, 2002, 16:43:37 Job time: 171 sec
                                                                                                                                                                         Query Match 25.7%;
Best Local Similarity 57.1%;
Matches 4; Conservative
                                  HYPOTHETICAL: NO
SANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
CRIGINAL SOURCE:
US-08-745-892-16
  .: peptide
NO
  TOPOLOGY: linear
                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                   4 DEPWFDD 10
                                                                                                                                                                                                                                                          1 DSPWITD 7
                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: HOLLAND, JAMES
APPLICANT: POGO, BEATRIZ
ATTLE OF INVENTION: DETECTION OF MAMMARY TUMOR VIRUS-LIKE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10112-0228
COMPUTER READBALE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/745,892
FILING DATE: 08-NOV-1996
CLASSITCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/555,394
FILING DATE: 09-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kole, Lisa B
REGISTRATION NUMBER: 35,225
REFRENCE/COCKET UNBER: 35,225
REFRENCE/COCKET UNBER: 35,225
REFRENCE/COCKET UNBER: A30363-A - 165/35211
TELEPHONE: 212-408-2628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
STREET: 30 Rockefeller Plaza
                                  NAME: KOLE, Lisa B
REGISTRATION NUMBER: 35,225
REFERENCE/DOCKET NUMBER: A30363 - 165/32494
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2628
TELEFAX: 212-765-2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 29; DB 1
Pred. No. 56;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16, Application US/08745892 Patent No. 6040146
                                                                                                                                                                             16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.78;
57.18;
FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                          N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 25.7
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 212-408-26;
TELEFAX: 212-765-2519
                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 30 ROCKE
CITY: New YORK
STATE: NY
                                                                                                                                                                                                                                                                                                                                      ; ANTI-SENSE: NO
; FRAGMENT TYPE: 1
; ORIGINAL SOURCE:
US-08-555-394-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 DEPWFDD 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DSPWITD 7
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                                                                                                                                                          TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

February 21, 2002, 16:50:51; Search time 13.27 Seconds Run on:

(without alignments)
200.913 Million cell updates/sec

US-08-753-851-8 Title:

Perfect score: Sequence:

1 CATRDQDTFHPSGGSHTTHESEDGHSHGSQEGGAN 35

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 219241 seqs, 76174552 residues Searched:

7547

seq length: 0 seq length: 35 Minimum DB Maximum DB

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

PIR\_68:\* Database :

pirl:\* pir2:\* pir3:\* pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Kex2/subtilisin-li histidine-rich pro hypothetical prote fibrinogen alpha c second envelope gl second envelope gl antigen, T-cell re lectin II, anti-H( chitinase (EC 3.2. hyaluronate recept hemopexin - chicke thaumatin-like pro fibrinopeptide A huma hypothetical prote hypothetical prote 34K ribonucleoprot hypothetical prote T cell receptor Vferredoxin al - Ja carbonic anhydrase second envelope gl second envelope gl capsid protein VP2 dnaK-type molecula Kex2/subtilisin-li
Kex2/subtilisin-li second envelope gl Kex2/subtilisin-li tau protein -Description SUMMARIES E45357 B45357 B32473 B82151 JP0101 C31514 PQ0548 PQ0263 B81078 B82138 S39455 PC2343 PC2344 159477 S13439 E44957 F45357 C45357 129501 DB % Query Match Length D  $\dot{\mathbf{w}} \mathbf{u} \dot{\mathbf{w}} \dot{\mathbf{w}} \dot{\mathbf{w}} \dot{\mathbf{w}} \dot{\mathbf{w}} \dot{\mathbf{w}} \dot{\mathbf{w}} \dot{\mathbf{u}} \dot{\mathbf{u}}$ Score Result . Ю

second envelope gl	PX3 protein - toma	pollen allergen DG	proline-rich prote	hypothetical prote	cytochrome c550 -	dehydrin 7.5K poly	hypothetical prote	alkaline serine pr	hypothetical profe	gag-junD mutant fu	erythrocyte membra	Ig H chain V-D-J r	hypothetical prote	redD protein - Str	histidine-rich pro
PC2334	S57798	A60359	A60692	G81891	S21191	PC4381	B30988	PQ0105	F70540	A49016	XCHUE	PH1582	T44539	S26243	A32473
7	~	7	7	7	7	7	ņ	7	7	4	7	7	7	7	7
27	27	78	28	33	35	21	23	26	27	32	10	15	23	23	23
14.5	14.5	14.5	14.5	14.5	14.5	14.2	14.2	14.2	14.2	14.2	14.0	14.0	14.0	14.0	14.0
29	29	29	29	29	29	28.5	28.5	28.5	28.5	28.5	28	28	28	28	28
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

```
C;Species: Homo sapiens (man)
C;Dactes 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 30-Sep-1993
C;Accession: A41683
R;Shtivelman, E.; Bishop, J.M.
Mol. Cell. Biol. 11, 5446-5453, 1991
A;Title: Expression of CD44 is repressed in neuroblastoma cells.
A;Reference number: A41683; MUID:92017823
                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; not compared with conceptual translation
                                     hyaluronate receptor CD44 (version 2) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-29 <SHT>
                                                                                                                                                                                                                                                                                                                                A; Accession: A41683
A41683
```

A;Cross-references: GB:M69215 C;Keywords: cell adhesion

Gaps ; DB 2; Length 29; 0; Query Match 31.5 Best Local Similarity 100. Matches 11; Conservative

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5 DQDTFHPSGGS 15 δ

19 DQDTFHPSGGS 29 qq

Demopexin - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 18-Jun-1993
C;Accession: C31514
R;Wellner, D.; Cheng, K.C.; Muller-Eberhard, U.
Biochem. Biophys. Res. Commun. 155, 622-625, 1988
A;Title: N-terminal amino acid sequences of the hemopexins from chicken, rat and rabb A;Reference number: A90148; MUID:88339942
A;Accession: C31514

A; Molecule type: protein A; Residues: 1-34 <WE3>

Gaps 0; 21.0%; Score 42; DB 2; Length 34; 35.0%; Pred. No. 52; 10; Indels ive 3; Mismatches 10; Indels 

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16 HTTHESEDGHSHGSQEGGAN 35 δ

9 Dp

RESULT

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5

Gaps

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R;Seidah, N.G.; Day, R.; Hamelin, J.; Gaspar, A.; Collard, M.W.; Chretien, M. Mol. Endocrinol. 6, 1559-1570, 1992
A;Title: Testicular expression of PC4 in the rat: molecular diversity of a novel germ A;Reference number: A45357; MUID:93078790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Macropus Sp. (Kangaroo)
C;Date: 21-Nov-1987 #sequence_revision 08-Jun-1990 #text_change 18-Aug-2000
C;Date: 21-Nov-1987 #sequence_revision 08-Jun-1990 #text_change 18-Aug-2000
C;Accession: 129501
Unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and A;Reference number: A29501
A;Reference number: A29501
A;Status: preliminary
                      A;Cross-references: EMBL;AF016328; NID:g2454603; PIDN:AAB71681.1; PID:g2454604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rex2/subtilisin-like proprotein convertase PC4-C - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C;Accession: F43357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kex2/subtilisin-like proprotein convertase PC4-C - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Jun.1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C;Accession: C43557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: profein
A;Residues: 1-15 <BLO>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology
                                                                                                                                                                        Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 24;
                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: nucleic acid
A; Residues: 1-24 <SEI>
A; Note: sequence extracted from NCBI backbone (NCBIP:118888)
                                                                                                                                                                      Score 34.5; DB 2;
Pred. No. 3.5e+02;
l; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 2; I
Pred. No. 3.1e+02;
2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33; DB 2
Pred. No. 5e+02
1; Mismatches
                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                         11 PSGGSHTTHESEDGHSHGSQEGG 33
                                                                                                                                                                                                                                                                                                     3 PGGG----HSSPPGHG-GRQDLG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
                                                                                                                                                                      17.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.5%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.5%;
60.0%;
                                           A) Experimental source: cv. Morex C)Genetics:
A)Gene: perm2
                                                                                                                                                                                               Best Local Similarity 43.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               fibrinopeptide A - kangaroo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TKDEGTFIAEGG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 TRDQDTFHPSGG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserv
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||| || || GGSTATHSSQ 24
A; Residues: 1-26 <SKA>
                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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C45357
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                                   C; Species: human herpesvirus 1
C; Date: 03-Teb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C; Accession: PQ0548
R; Davison, M.D; Rixon, F.J.; Davison, A.J.
J; Gen. Virol. 73, 2709-2713, 1992
A; Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of herpes A; Reference number: PQ0544; MUID: 93019027
A; Accession: PQ0548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-28 <DEN>
A; Note: translation of the nucleotide sequence is not complete
C; Comment: This protein plays a role both in protein import into the lumen of the endopl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Description: involved in protein folding and assembling/disassembling of protein compl
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R; Demecke, J.; Goldman, M.H.S.; Demolder, J.; Seurinck, J.; Botterman, J. Plant Cell 3, 1025-1035, 1991
A; Title: The tobacco luminal binding protein is encoded by a multigene family. A; Reference number: J01360; MUID: 92361242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: luminal binding protein BLP-3
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 30-Jun-1992 #sequence_revision 10-Mar-1994 #text_change 13-Mar-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thaumatin-like protein - barley (fragment)
C;Species: Hordeum vulgare (barley)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dnaK-type molecular chaperone BLP-3 - common tobacco (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone
F;25-28/Region: endoplasmic reticulum retention signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 2; Pred. No. 3.3e+02;
            protein VP26 - human herpesvirus 1 (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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R; Skadsen, R.W.; Herbst, J.M.
submitted to the EMBL Data Library, July 1997
A; Reference number: Z15316
A; Accession: T04371
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                             19.0%;
58.3%;
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Similarity 57.1%;
8; Conservative
                                                                                                                                                                                                                                     A Molecule type: protein
A; Residues: 1-19 < CDAV>
A; Residues: 1-19 < CDAV>
C; Genetics:
A; Gene: UL35
C; Keywords: capsid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 19.0
Best Local Similarity 58.3
Matches 7; Conservative
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Best Local Similarity
Matches 8; Conserv
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Gaps

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C; Species: Mus musculus (house mouse)
C; Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C; Accession: E45357
R; Seidah, N.G.; Day, R.; Hamelin, J.; Gaspar, A.; Collard, M.W.; Chretien, M. Mol. Endocrinol. 6, 1559-1570, 1992
Mol. Endocrinol. 6, 1559-1570, 1992
A; Title: TestLocular expression of PC4 in the rat: molecular diversity of a novel germ A; Reference number: A45357; MuID: 93078790
A; Reference number: A45357
A; Molecule type: nucleic acid
A; Molecule type: nucleic acid
A; Residues: 1-34 < SEL>
A; Note: sequence extracted from NCBI backbone (NCBIP:118887)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Species: Rattus norvegicus (Norway rat)
C.Species: Rattus norvegicus (Norway rat)
C.Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C.Accession: 845357
R.Seidah, N.G.; Day, R.; Hamelin, J.; Gaspar, A.; Collard, M.W.; Chretien, M. Mol. Endocrinol. 6, 1559-1570, 1992
Affithe: Testicular expression of PC4 in the rat: molecular diversity of a novel germ A.Reference number: A45357; MuID:93078790
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R;Walte, J.H.; Rice-Ficht, A.C.
Biochemistry 28, 6104-6110, 1989
A;Title: A histidine-rich protein from the vitellaria of the liver fluke Fasciola hep A;Reference number: A32473; MUID:89375343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 1-18 <WAI>
A;Note: 18-61y and 18-His were also found
C;Superfamily: period clock protein; EGF homology
C;Keywords: egg yolk
F;1,5/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B32473
histidine-rich protein C, peptide P-5 - liver fluke (fragment)
C;Species: Fasciola hepatica (liver fluke)
C;Species: 25-Sep-1989 #sequence_revision 03-May-1994 #text_change 26-May-2000
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                                                                                                        Kex2/subtilisin-like proprotein convertase PC4-B - mouse (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 2; Length 34; Pred. No. 7.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 2; Length 34;
Pred. No. 7.1e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 18;
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60.0%;
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60.0%;
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Best Local Similarity 60.00
6. Conservative
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Best Local Similarity
Matches 6; Conserv
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25 GGSTATHSSQ 34
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tau protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: 15223
R;Mori, H; Hamada, Y.; Kando, J.; Ihara, Y.
R;Mori, H; Hamada, Y.; Kandohi, M.; Honda, T.; Kondo, J.; Ihara, Y.
R;Morien: Biophys. Res. Commun. 159, 1221-1226, 1989
A;Title: A distinct form of tau is selectively incorporated into Alzheimer's paired heli
A;Reference number: 152232
A;Accession: 152232
A;Accession: 152232
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-31 cRES>
A;Cross-references: GB:M25298; NID:g602470; PIDN:AAA57264.1; PID:g602471
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Date: 21-Mar-1995 #sequence_revision 26-May-1995 #text_change 08-Oct-1999
C;Accession: PC2342
Biochem. Biophys. Res. Commun. 206, 863-869, 1995
A;Title: Susceptibility of human T-lymphotropic virus type I infected cell line MT-2 to
A;Reference number: PC2334; MUID:95134269
A;Accession: PC2342
A;Accession: PC2342
A;Accession: PC2342
A;Residues: 1-27 <KAT>
A;Residues: 1-27 <KAT>
A;Cross-references: DDBJ:D43654; NID:9882093; PIDN:BAA07769.1; PID:d1008354; PID:g882094
A;Experimental source: isolate D-1, inoculum
                                                                                 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
PC2342
second envelope glycoprotein, gp70, hypervariable region 1 - hepatitis C virus (isolate
R;Seidah, N.G.; Day, R.; Hamelin, J.; Gaspar, A.; Collard, M.W.; Chretien, M. Mol. Endocrinol. 6, 1559-1570, 1992
A;Title: Testicular expression of PC4 in the rat: molecular diversity of a novel germ A;Title: Testicular expression of PC4 in the rat: molecular diversity of a novel germ A;Accession: C45357
A;Accession: C45357
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-24 <SEI>A;Note: sequence extracted from NCBI backbone (NCBIP:118879)
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                                                                                                                                                                                                                                                                                                                                Length 24;
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Pred. No. 6.5e+02;
2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 2; Length 27;
Pred. No. 5.6e+02;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                             Score 33; DB 2;
Pred. No. 5e+02;
1; Mismatches
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40.0%;
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60.0%;
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Best Local Similarity 46.2%;
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserva
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Best Local Similarity
Matches 6; Conserv
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Gaps

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A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-teferences: GB: AE004259; GB: AE003852; NID: 99656353; PIDN: AAF94978.1; GSPDB: GNO01
A; Experimental source: serogroup 01; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                         hypothetical protein VC1830 [imported] - Vibrio cholerae (strain N16961 serogroup O1) (Species: Vibrio cholerae (Species: Na-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 (SAccession: B82151 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; R:Heidelberg, J.F.; Eisen, J.A.; Vanathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. Nature 406, 477-483, 2000 (Species of Doth chromosomes of the cholera pathogen Vibrio cholerae. A; Reference number: A82035; MUID:20406833
                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fibrinogen alpha chain - duck (fragment)

N;Contains: fibrinopeptide A

N;Contains: fibrinopeptide A

C;Species: Anas platyrhynchos (domestic duck)

C;Date: 30-Jun-1987 #sequence_revision 28-Dec-1987 #text_change 26-Jan-1996

C;Date: 30-Jun-1987 #sequence_revision 28-Dec-1987 #text_change 26-Jan-1996

C;Accession: JP0101

R;Min, Y:; Ping, Z:; Yaoshi, Z

Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. 28, 31-35, 1985

A;Title: Purification and primary structures of duck fibrinopeptides A and B.

A;Reference number: A94238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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A; Residues: 1.15 < MINN
C; Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology
C; Keywords: blood coagulation; plasma; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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Pred. No. 8.6e+02;
3; Mismatches 2; Indels
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                                 Indels
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                              0; Mismatches
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Matches 6; Conservative
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A;Gene: VC1830
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Search Completed: February 21, 2002, 16:53:30 Job time: 159 sec

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Anas platyrhynchos (Domestic duck).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
NCBI_TaxID=8839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIBA_ANAPL STANDARD; PRT; 15 AA. P12801; 01-0CT-1989 (Rel. 12, Created) 01-0CT-1989 (Rel. 12, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) FIBRINOPEPTIDE A.
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FIBA_ANAPL
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(without alignments)
125.934 Million cell updates/sec
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homo sapien
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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1 CATRDODTFHPSGGSHTTHESEDGHSHGSQEGGAN 35
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                                                                                                                                                                       100059 segs, 36664827 residues
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YL55_CAEEL
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C550_BACHA
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Listing first 45 summaries
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                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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Q09290 caenorhabdi	P82144 agkistrodon O83196 treponema p	P54440 bacillus su	P82537 spinacia ol	P11385 carausius m	P01370 tremella me	P21225 pisum sativ	P30800 octopus vul	P80554 narcissus p	Q38199 bacteriopha	P22296 lactobacill	
YOK8_CAEEL	PG25_AGKBL Y161_TREPA	YRKM_BACSU	TL1X_SPIOL	HTF2_CARMO	TA13_TREME	CHI1_PEA	A2M_OCTVU	BULB_NARPS	DNIV_BPD10	YHV4_LACHE	
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34	9 2	37	38	39	40	4.1	42	43	44	45	

## ALIGNMENTS

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Gaps

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Length 19;

Score 31; DB 1; Ler Pred. No. 3.3e+02;

15.5%; 62.5%;

Conservative

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19 HESEDGHS 26
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                                                                    Sci. Sin., B, Chem. Biol. Agric. Med. Earth Sci. 28:31-35(1985).
-1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phylogeny and classification of species.";
Ark. Kemi 25:411-428(1966).
-!- FUNCTION: FIBRINGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                    -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA, 6 GAWAA), LINKED TO EACH OFHER BY DISULFIDE BONDS.
-!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES PIR; JP0101; JP0101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
-1- MISCELLANEOUS: CONVERSION OF FIBRINGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR HE FORMATION OF THE SOFT CLOT.
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES-E.asinus;
Blomback B., Blomback M., Grondahl N.J., Holmberg E.;
"Structure of fibrinopeptides-its relation to enzyme specificity and
                                             "Purification and primary structures of duck fibrinopeptides A and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebráta; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                 Length 15;
                                                                                                                                                                                                                       PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                             D78A51FF88B40373 CRC64;
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Pred. No. 2.6e+02;
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PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
Blood coagulation; Plasma; Sulfation.
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-JAN-1990 (Rel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blomback B., Blomback M., Grondahl N.J.;
"Studies on fibrinopeptides from mammals.";
Acta Chem. Scand. 19:1789-1791(1965).
                                                                                                                                                                                                                                                                                                        2; Mismatches
                     MEDLINE=85168193; PubMed=3983613;
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50.0%;
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                                    Min Y., Ping Z., Yaoshi Z.;
                                                                                                                                                                                                         Blood coagulation; Plasma.
                                                                                                                                                                                                                                                                                                          Conservative
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Best Local Similarity
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                                                                                                          AGGREGATION.
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P14471;
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NON_TER
SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                   "A multicenter comparison of methods for typing strains of Pseudomonas aeruginosa predominantly from patients with cystic fibrosis. The International Pseudomonas aeruginosa Typing Study
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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FMK7_PSEAE STANDARD; PRT; 23 AA. 053391; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) FIMBRIAL PROTEIN (FILIN) (STRAIN KB7) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00114; pilin; 1. PROSITE; PS00409; PROKAR_NTER_METHYL; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 31;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR001120; Prok_N_methyltn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Infect. Dis. 169:134-142(1994).
                                                                                                                                                                                                                                                                                                                         MEDLINE=94103636; PubMed=7903973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96110702; PubMed=8845350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; S67809; CAB32861.1; -. PDB; 1kB7; 29-JAN-96. PDB; 1KB8; 29-JAN-96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001082; Pilin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUCTURE BY NMR OF 7-23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                   Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   NCBI_TaxID=287;
                                                                                                                                                                                                              Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9;
                                                                                                                                                                                                                                                                                                    STRAIN=KB7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=KB7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
DISULFID
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1 CATRDODTFHPSG 13

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TISSUE=Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HF40_MAIZE
ID HF40_MAIZE
AC P82865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C550_BACHA
P80091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_CONS
NON_TER
SEQUENCE
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C550_BACHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=BRISTOL N2;
MEDLINE-94150718; PubMed=7906398;
Milson R., Anderson K., Baynes C., Berks M.,
Milson R., Anderson K., Edynes C., Berks M.,
Denfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laister E., Jier M.,
Latreille P., Lighthing J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Wohldman P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               r.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               '2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CYTOCHROME C OXIDASE POLYPEPTIDE VA (EC 1.9.3.1) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 3.4 KDA PROTEIN F44E2.5 IN CHROMOSOME III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0744BB516215EC75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 30.5; DB 1;
Pred. No. 6.5e+02;
1; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 AA.
                                                                                                                                          32 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 GGSHTTHESEDGHSHGSQEGGAN 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 GGGGTAGEFE-----EEGAAN 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.2%;
39.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 32 AA; 3393 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L23646; AAK67233.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WormPep; F44E2.5; CE00183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 368:32-38(1994)
                 8 CATTVDAKFRPNG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COXA_CANFA P99501;
                                                                                                                                       YL55_CAEEL
P34435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        elegans
                                                                                                                                                                                                                                                                                      F44E2.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COXA_CANFA

ID COXA_CI

AC P99501

DT 15-JUL

DT 30-MAY

DE CYTOCH

GN CANFA

OC EUKATYI

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OC MARMATI
                                                                                                                 YL55_CAEEL
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                    Electrophoresis 18:2795-2802(1997).
-!- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
-!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      El-Shemy H.A.-A., Nishimura T., Saneoka H., Fujita K.; "Characterization and localization of a novel protein (HFN40) in some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
MEDLINE-98163340; PubMed-9504812;
Dunn M.J., Corbett J.M., Wheeler C.H.;
"HSC-2DPAGE and the two-dimensional gel electrophoresis database of
don heart proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
HSC-2DPAGE; P99501; DOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 29; DB 1; Length 11; Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 29; DB 1; Length 33;
Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              maize genotypes without husk leaf blades.";
Submitted (NOV-2000) to the SWISS-PROT data bank.
-!- FUNCTION: SUPPRESSES EXPANSION OF HUSK LEAF BLADES.
NON_CONS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A4C66AFEE0253A43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          11 AA; 1274 MW; 910B35C5B1AB11F5 CRC64;
                                                                                                                                                                                                                                                                                                                      Oxidoreductase; Heme; Mitochondrion; Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SUPPRESSOR PROTEIN HFN40 (FRAGMENTS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
Bacillus halodenitrificans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LINE F1; TISSUE=Seed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.5%;
31.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3492 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 GGPFSASAKYFGQAHGGXE 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 GGSHTTHESEDGHSHGSQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                              dog heart proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 SHTTHESED 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              || :||::
SHGSHETDE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zea mays (Maize)
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Thunnus obesus (Bigeye tuna).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
Scombridae; Thunnus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  žea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                               Eur. J. Biochem. 248:99-103(1997).

-i- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.

-i- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + 0(2) = 2 H(2)0 + 4 FERRICYTOCHROME C.
                                                                                                                                                                                                                                                                                                                                  "The subunit structure of cytochrome-c oxidase from tuna heart and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 206)
                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CYTOCHROME C OXIDASE POLYPEPTIDE VA-2 (EC 1.9.3.1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
Oxidoreductase; Heme; Mitochondrion; Inner membrane.
                                                                                                                                                                                                                                                                                                      Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 28; DB 1; Length 24;
Pred. No. 9.9e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 AA; 2903 MW; 20998FB91F22E43B CRC64;
                                     24 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                    TISSUE=Heart, and Liver;
MEDLINE=97454291; PubMed=9310366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Coleoptile;
                                                                                                                                                                                                                  NCBI_TaxID=8241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 SHGSQE 31
                                                                                                                                                                                                                                                                                                                       Kadenbach B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SHGKQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UC09_MAIZE
P80615;
                                     COXC_THUOB
P80973;
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NON_CONS
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                  COXC_THUOB
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                                                                                                                                                                                                                                                                                                                HEME (COVALENT) (BY SIMILARITY).
HEME (COVALENT) (BY SIMILARITY).
IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                              Bacillus halodentrificans.";

Eur. J. Blochem. 204:1131-1139(1992)

- FUNCTION: MONOHEME CYTOCHROME WHICH FUNCTIONS AS AN ELECTRON

- CARRIER IN THE REDUCTION OF MITRITE BY MEMBRANE VESICLES.

-1- PTM: BINDS ONE HEME GROUP PER MOLECULE.
                                                                                                                                       11.; and EPR studies on a monoheme cytochrome c550 isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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0
                                                                                                                   Saraiva L.M., Denariaz G., Liu M.-Y., Payne W.J., le Gall J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 29; DB 1; Length 35;
Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 28; DB 1; Length 10; Pred. No. 4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Indels
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239BFEEAA1F5B1E8 CRC64;
 Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
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1; Mismatches
Bacteria; Firmicutes; Bacillus/Clostrid:
Bacillus/Staphylococcus group; Bacillus
                                                                                                                                                                                                                                                                InterPro; IPR000345; CytC_heme_bind.
PROSITE; PS00190; CYTOCHROME_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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ERYTHROCYTE MEMBRANE GLYCOPEPTIDE.
                                                              SEQUENCE, AND STRUCTURE BY NMR. STRAIN-SP. NOV. / ATCC 49067; MEDLINE-92201200; Pubmed-1312933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 SGGSHTTHESEDGHSHGSQEGGA 34
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Best Local Similarity 30.4%;
Matches 7; Conservative
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Best Local Similarity
Matches 4; Conserv
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                                NCBI_TaxID=1482;
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SEQUENCE
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MEDLINE=84032400; PubMed=6630187;
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                                                                                                                                                                                                                                                                                                                                  Can. J. Biochem. Cell Biol. 62:426-433(1984).
-!- SIMILARITY: BELONGS TO THE L15P FAMILY OF RIBOSOMAL PROTEINS.
PIR; S08555; S08555.
                                                                                                                                                                                                                                                                                                                certain 50S ribosomal subunit proteins from the archaebacterium Halobacterium cutirubrum.";
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Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=6491;
                                                                                                                                                                                                                                      Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gray W.R., Luque A., Olivera B.M., Barrett J., Cruz L.J.;
"Peptide toxins from Conus geographus venom.";
J. Biol. Chem. 256:4734-4740(1981).
                                                 Score 28; DB 1; Length 32;
Pred. No. 1.3e+03;
1; Mismatches 8; Indels
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                      8841DBE253F211D6 CRC64;
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Pred. No. 1.4e+03;
2; Mismatches 7;
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4AY-2000 (Rel. 39, Last annotation update)
RIBOSOMAL PROTEIN L15P (HL16) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-NOV-1988 (Rel. 09, Last annotation update)
                                                                                                                                                          29 AA.
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PROSITE; PS00475; RIBOSOMAL_L15; PARTIAL.
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37.5%;
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32
3249 MW;
                                                  14.0%;
35.7%;
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                                                                     Conservative
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                                                                                                                                                          STANDARD;
                                                                                      14 GSHTTHESEDGHSH 27
                                                                                                         14 GGYVXXLGEAGHHH 27
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                                       Query Match
Best Local Similarity
'... 5; Conserve
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Best Local Similarity
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32
AA;
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                      32
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50S RIBOSOMA
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P01520;
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P05971;
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CXA2_CONGE
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RL15_HALCU
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-!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA, & GAMMA), LINKED TO EACH OFHER BY DISULFIDE BONDS.
-!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
                                                                                                                                                                                                                                                                                                                      Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Syncerus.
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                                                                                                             MEDLINE=89024586; PubMed=3052286; Gray W.R., Olivera B.M., Cruz L.J.; Peptide toxins from venomous Conus snails."; Annu. Rev. Biochem. 57:665-700(1988).
-!-FONGTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND INHIBIT THEM.
Gray W.R., Rivier J.E., Galyean R., Cruz L.J., Olivera B.M.;
"Conotoxin MI. Disulfide bonding and conformational states.";
J. Biol. Chem. 258:12247-12251(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                     DEEE831C39297EBD CRC64;
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Pred. No. 8.1e+02;
0; Mismatches 6;
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01-JAN-1990 (Rel. 13, Last sequence update)
01-JAN-1990 (Rel. 13, Last annotation update)
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50.0%;
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HSSP; P01519; 1NOT.
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Best Local Similarity
Matches 6; Conserv
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DP20_CAEBR
LD DP22_CAEBR
STANDARD; PRT; 22 AA.

TD DP22_CAEBR
STANDARD; PRT; 22 AA.

TD DP22_CAEBR
STANDARD; PRT; 22 AA.

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DR 01-OCT-1996 (Rel. 34, Last sequence update)

CR 01-OCT-1996 (Rel. 34, Last sequence update)

CR 02-CAEVALY (Relational Proportional Proportion
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Search completed: February 21, 2002, 16:56:16 Job time: 184 sec

23 DGHSHGS 29 ||||: | 2 DGHSNTS 8

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SEQUENCE FROM N.A.
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037250
RESULT
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01897 hepatitis g
056472 hepatitis c
099900 hepatitis c
09995 hepatitis c
07834 human immun
078378 human immun
099488 porcine cir
056126 porcine cir
056126 porcine cir
099755 hepatitis c
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056521 hepatitis c
Q9j5v4 hepatitis c
Q96240 arabidopsis
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233.875 Million cell updates/sec
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Q78345 human immun
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                                                                                                                                                                                February 21, 2002, 16:52:56; Search time 21.89 Seconds
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                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                         1 CATRDQDTFHPSGGSHTTHESEDGHSHGSQEGGAN
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## ALIGNMENTS

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37250, PRELIMINARY; PRT; 27 AA.

10 037250, PRELIMINARY; PRT; 27 AA.

37250, PRAMINITION OF TEMBLEEL 17, Last annotation update)

58 GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2/NS1 (GP68)]

59 Hepacitis C virus.

50 Hepacitis C virus.

51 Hepacitis C virus.

52 VITURESS; SSRNA positive-strand viruses, no DNA stage; Flaviviridae; DC viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae; DC viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae; DC viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae; DC viruses; SSRNA martin J., Quiroga J.A., Castillo I., Carreno V.; RX MAYS S., MARTIN J., Quiroga J.A., Castillo I., Carreno V.; RY VIRUS STAIN=15; PROME NA.

50 NEBLINE-98105815; Pubmed-9445070; PRT VIRUS SENVELOPE GLYCOPROTEIN E2/NSI IS CONTAINE IN THE REPORTEINS SENVELOPE GLYCOPROTEIN E2/NSI IS CONTAINED WITHIN THE BENNELOPE GLYCOPROTEIN E1 ENVELOPE CC CONTAINED WITHIN THE BENNELOPE GLYCOPROTEIN E1 ENVELOPE THAT CONTAINED WITHIN THE BENNELOPE GLYCOPROTEIN E (BY SIMILARITY): TO HEPATITIS C VIRUS IS COVERED BY A LIPOPROTEIN E(BY SIMILARITY): TO HEPATITIS C VIRUS NON-STRUCTURAL PROTEIN E2/NSI FAMILY.

50 EMBL. APDIASS 9. AARODISS46.1; PRAMILY.

51 SMILLARITY: TO HEPATITIS C VIRUS NON-STRUCTURAL PROTEIN E2/NSI FAMILY.

51 SMILLARITY: TO HEPATITIS C VIRUS NON-STRUCTURAL PROTEIN E2/NSI FAMILY.

52 FAMILY.

53 FAMILY.

54 PROTEIN: BRANCHOPE PROTEIN: GLYCOPROTEIN E2/NSI FAMILY.

55 FAMILY.

56 PROTEIN: MAN STRUCTURAL PROTEIN: MAN SHEN PROTEIN E2/NSI FAMILY.

56 FAMILY.

57 FAMILARITY: TO HEPATITIS C VIRUS NON-STRUCTURAL PROTEIN E2/NSI FAMILY.

58 FAMILY.

59 FAMILY.

50 FAMILY.

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51 FAMILARITY: TO HEPATITIS C VIRUS NON-STRUCTURAL PROTEIN E2/NSI FAMILY.

50 FAMILY.

51 FAMILARITY: TO HEPATITIS C VIRUS NON-STRUCTURAL PROTEIN E2/NSI FAMILY.

51 FAMILY.

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E2/NS1; NONSTRUCTUBAL PROTEINS NS2, NS3, NS4A, NS4B, NS5A AND NS5B. THE VIRION OF THE VIRUS IS COVERED BY A LIPOPROTEIN ENVELOPE THAT CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sandres K., Dubois M., Pasquier C., Payen J.L., Alric L., Duffaut M., Vinel J.P., Pascal J.P., Puel J., Izopet J.; "Genetic heterogeneity of hypervariable region 1 of the hepatitis C virus (HCV) genome and sensitivity of HCV to alpha interferon
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pfam, PF01560; HCV_NS1, 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy.";
J. virol. 74:661-668(2000).
-!- SUBUNIT: HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E2/NSF1 IS
CONTAINED WITHIN THE GENOME POLYPROTEIN THAT CONTAINS: CAPSID PROTEIN C; THE ENVELOPE GLYCOPROTEIN E1; ENVELOPE GLYCOPROTEIN MC3. NCAA NSAA AND
                                                                                                                                                                                                                                                                                                                                             Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2/NS1 (GP68)]
                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2/NS1 (GP68)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
-!- SIMILARITY: TO HEPATITIS C VIRUS NON-STRUCTURAL PROTEIN E2/NS1
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Pred. No. 1.5e+02;
1; Mismatches 8; Indels
                                                                       Length 27;
                                                                                                    Indels
                             2769BD33B878BCD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CB80D3F44ECBEAC4 CRC64
                                                                      DB 12;
1.5e+02;
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                                                                                                                                                                                                                                 27 AA.
                                                                                                  Mismatches
                                                                      Score 39;
Pred. No.
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MEDLINE-20091320; PubMed=10623727;
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50.0%;
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66.7%;
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                             2637 MW;
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NON_TER 27 27
SEQUENCE 27 AA; 2934 MW;
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27
27 AA;
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Best Local Similarity
Matches 11; Conserv
                                                                                      Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus
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01-MAY-2000
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Matches 8
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Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBMIT: HEPAITIS C VIRUS ENVELOPE GLYCOPROTEIN EZ/NSF1 IS
--- CONTAINED WITHIN THE GENOME POLYPROTEIN THAT CONTAINS: CAPSID PROTEIN C: THE ENVELOPE GLYCOPROTEIN E1: ENVELOPE GLYCOPROTEIN E2/NS1: NOSTRUCTURAL PROTEINS NS2, NS3, NS4A, NS4B, NS5A AND NS5B. THE VIRION OF THE VIRUS IS COVERED BY A LIPOPROTEIN ENVELOPE THAT CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E (BY
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF040799; AAB95524.1; -.
InterPro; IPR002531; HCV_NS1.
Pthm; PF01560; HCV_NS1; 1.
CCdt.protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                   Gonzalez-Perez M.A., Norder H., Bergstrom A., Lopez E., Visona K.A.,
                                                                                                                                                                                                                                      Hepatitis GB virus C. Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; GBV-C/HGV group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FRAGMENT).
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2/NS1 (GP68)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: TO HEPATITIS C VIRUS NON-STRUCTURAL PROTEIN E2/NS1
                             2;
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 DB 12; Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; DB 12; Length 20. Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                        EB10B7DCA5DBB5AB CRC64;
                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                            26 AA
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                             5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
Score 46; DB
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                         Created)
                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                          10 HPSGGS--HTTHESEDGHSHGSQE 31
                                                                          3 HTTGGSAVRTTHRLANLFSHGAKQ 26
23.0%;
41.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                      01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-AUG-1998 (TrEMBLrel. 07, POLYPROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                         26 26
26 AA; 2944 MW;
                                                                                                                                                                                                                                                                                                                                                                              J. Med. Virol. 0:0-0(0).
EMBL; U86121; AAB58565.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CATRDQDTFHPSGGSHT 17
                             Conservative
                                                                                                                                                                                                                                                                                                                                     STRAIN=353-96, NICARAGUA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Conservative
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                                                                                                                                                            PRELIMINARY;
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Best Local Similarity
              Similarity
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                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                   Magnius L.O.;
                                                                                                                                                                                                                                                                                                                                                                                                             Polyprotein.
NON_TER
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  Query Match
                Best Local
Matches 1
                                                                                                                                                                          011897;
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011897
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InterPro; IPR002531; HCV_NS1.
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NON_TER
SEQUENCE
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NON_TER
SEQUENCE
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-!- SUBUNIT: HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E2/NSF1 IS

-!- SUBUNIT: HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E2/NSF1 IS

CONTAINED WITHIN THE GENOME POLYPROTEIN E1; ENVELOPE GLYCOPROTEIN

PROTEIN C; THE ENVELOPE GLYCOPROTEIN E1; ENVELOPE GLYCOPROTEIN

E2/NS1; NONSTRUCTUREAL PROTEINS NS3, NS4A, NS4B, NS5A AND

NS5B. THE VIRION OF THE VIRUS IS COVERED BY A LIPOPROTEIN ENVELOPE

THAT CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E (BY
                                                                                                                                                                                                                          ENVELOPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                        Sandres K., Dubois M., Pasquier C., Payen J.L., Alric L., Duffaut M., Vinel J.P., Pascal J.P., Puel J., Isopet J., Genetic heterogeneity of hypervariable region 1 of the hepatitis C virus (HCV) genome and sensitivity of HCV to alpha interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sandres K., Dubbis M., Pasquier C., Payen J.L., Alric L., Duffaut M., Vinel J.P., Pascal J.P., Puel J., Izopet J., "Genetic heterogeneity of hypervariable region 1 of the hepatitis C virus (HCV) genome and sensitivity of HCV to alpha interferon
                                                                                                                                                                                                                                                                                                    Interpro; IPR002531; HCV_NS1.
Pfam; PF01560; HCV_NS1; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
                                                                                                                                                      J. Virol. 74:661-668(2000).

-1- SUBUNIT: HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E2/NSF1 IS
CONTAINED WITHIN THE GENOME POLYPROTEIN THAT CONTAINS: CAPSID
PROTEIN C; THE ENVELOPE GLYCOPROTEIN E1; ENVELOPE GLYCOPROTEIN
E2/NS1; NONSTRUCTURAL PROTEINS NS2, NS3, NS4A, NS4B, NS5A AND
NS5B. THE VIRION OF THE VIRUS IS COVERED BY A LIPOPROTEIN ENVELC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses: ssRNA positive strand viruses, no DNA stage: Flaviviridae;
Hepacivirus.
             Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                 SIMILARITY).
SIMILARITY: TO HEPATITIS C VIRUS NON-STRUCTURAL PROTEIN E2/NS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2/NS1 (GP68)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
SIMILARITY: TO HEPATITIS C VIRUS NON-STRUCTURAL PROTEIN E2/NS1
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                                                                                                                                                                                                                                                                                                                                                                                                                              Length 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                                                                     27 AA; 2934 MW; CB80D3F44ECBEAC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB 12;
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
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                                                                            MEDLINE=20091320; PubMed=10623727;
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MEDLINE=20091320; PubMed=10623727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 SGG--SHTTHESEDGHSHGSQE 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 SGGTASHTTRRLTSLFSFGSQQ 26
                                                                                                                                                                                                                                                                                                                                                                                                                            19.5%;
50.0%;
                                                                                                                                                                                                                                                                                         EMBL; AF166573; AAD52231.1;
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                                                                                                                                                                                                                                                                                                                                            Polyprotein; Transmembrane
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 50.07
Matches 11; Conservative
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                                                             SEQUENCE FROM N.A.
 Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus
                                      NCBI_TaxID-11103;
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SEQUENCE
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Gaps
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
VIRAL SAMPLE FLPAR5B (FLORIDA PATIENT A), PARTIAL ENV CDS, V5 REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
VIRAL SAMPLE FLPBR5A (FLORIDA PATIENT B), PARTIAL ENV CDS, V5 REGION
(FRAGMENT).
              Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92271245; PubMed=1589796;
Ou C.Y., Ciesielski C.A., Myers G., Bandea C.I., Luo C.C.,
Korber B.T.M., Mullins J.I., Schochetman G., Berkelman R.L.,
Economou A.N., Witte J.J., Furman L.J., Satten G.A., MacInnes K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Curran J.W., Jaffe H.W.;
"Molecular epidemiology of HIV transmission in a dental practice.";
Science 256:1165-1171(1992).
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                                                                                                                                                                                     Length 27;
                                                                                                                                                                                  Score 39; DB 12; Length 27
Pred. No. 1.5e+02;
1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Zhang L.Q., Leigh-Brown A.J.;
Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3473A0BB802CA370 CRC64;
                                                                                                               CB80C3F54ECBEAC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38; DB 12;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                   12 SGG--SHTTHESEDGHSHGSQE 31
                                                                                                                                                                                                                                                                                                              5 SGGTASHTTRRLASLESFGSQQ 26
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50.0%;
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50.0%;
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                                                                                                                  2904 MW;
Pfam; PF01560; HCV_NS1; 1.
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                                                                                                                                                                                                                                 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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5 TKGSETFRPGGG 16
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                                                                                      27
27 AA;
                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Nucleotide sequence of porcine circovirus associated with postweaning
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11 HPTAASHKSHQ 21
                                                                                                                                                                                                                                                                                              clinical syndromes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 AA;
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Matches 5; Conserv
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Q9QRT5
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                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Hamel A.L., Navar G.P.S.;
"Genetic characterization of four novel type-2 Porcine circoviruses.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF117753; AAD12312.1;
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                           MEDLINE-92271245; PubMed-1589796; Ou C.Y., Ciesielski C.A., Myers G., Bandea C.I., Luo C.C., Korber B.T.M., Mullins J.I., Schochetman G., Berkelman R.L., Economou A.N., Mitte J.J., Furman L.J., Satten G.A., MacInnes K.A., Curran J.W., Jaffe H.W.;
                                                                                "Molecular epidemiology of HIV transmission in a dental practice."; Science 256:1165-1171(1992).
EMBL; M92123; AAA44493.1; -.
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                                                                                                                                                                         Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38; DB 12; Length 21;
Pred. No. 1.6e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                              4; Indels
Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
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17 AA; 1723 MW; 34757935D12CA370 CRC64;
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BD26E338284C1013 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     056126 PRELIMINARY; PRT; 21 AA. 056126; O9YJ58; 01-JUN-1998 (TrEMBLrel. 06, Created) 01-JUN-2001 (TrEMBLrel. 06, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) STRAIN PAWS PCV, COMPLETE GENOME (ORF-8). POYING CIRCOVITUS,
                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                          porcine circovirus type 2-D.
Viruses; ssDNA viruses; Circoviridae; Circovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Circovirus.
                                                                                                                                                                      Score 38; DB 12;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SRECIES-porcine circovirus; STRAIN-PMWS PCV;
MEDLINE-98241772; PubMed-9573301;
Hamel A.L., Lin L.L., Nayar G.P.S.;
                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          porcine circovirus type 2-E, and porcine circovirus type 2-E. Viruses: SEDNA Viruses: Circoviridae; NCBI_TaxID-46221, 85542, 85544, 85709;
                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                      19.0%;
50.0%;
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                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                            | : :|| | ||
5 TNETETFRPGGG 16
                                                                                                                                                          Query Match
Best Local Similarity
6; Conserve
                                                                                                                                                                                                                 3 TRDQDTFHPSGG 14
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||1 HPTAASHKSHQ 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 5; Conserv
                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 AA;
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NON_TER
SEQUENCE
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Best Local S
Matches 5
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Q9YQS8;
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056126
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RY
RA
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Hamel A.L., Nayar G.P.S.; "Independent isolates of circovirus detected "Nucleotide sequence of four different isolates of circovirus detected in pigs with various clinical syndromes."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               circovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=bovine circovirus;
Hamel A.L., Nayar G.P.S.;
"Nucleotide sequence of a circovirus detected in cattle with various
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Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-98418498; Pubmed-9747726;
MEDLINE-98418498; Pubmed-9747726;
Mechan B.M., Mondeilly F.M., Todd D., Kennedy S., Jewhurst V.,
Ellis J.A., Hassard L.E., Clark E.G., Haines D.M., Allan G.M.;
Characterization of novel circovirus DNAs associated with wasting syndromes in pigs.";
J. Gen. Virol. 79:2171-2199(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2/NS1 (GP68)]
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"Nucleotide sequence of four different isolates of porcine detected in pigs with various clinical syndromes.";
Submitted (DEC-1988) to the EMBL/GenBank/DDBJ databases.
EMBL; AF027217, AAC59469.1;
EMBL; AF055392; AAC35314.1;
EMBL; AF109397; AAD11935.1;
EMBL; AF1093997; AAD11935.1;
EMBL; AF1093997; AAD03094.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES-porcine circovirus; STRAIN-PORCINE CIRCOVIRUS TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38; DB 12; Length 21;
Pred. No. 1.6e+02;
3; Mismatches 3; Indels
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                                                                                                    SEGUENCE FROM N.A. SPECIES—POTATION—PMMS PCV; SPECIES—portaine circovirus; STRAIN—PMMS PCV; Hamel A.L., Lin L.L., Nayar G.P.S.; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
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multisystemic wasting syndrome in pigs.";
J. Virol. 72:5262-5267(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES-porcine circovirus type 2-E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-porcine circovirus type 2-B;
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45.5%;
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DFED6FAE38A8BCD4 CRC64;

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2808 MW;
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Best Local Similarity
27 AA;
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Best Local S
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                                                                                               "Replication of hepatitis C virus in the ascitic mononuclear cells and development of distinct quasispecies in the ascitic fluid."; submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- SUBMINT: HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN EZ/ASF1 IS CONTAINED WITHIN THE GENOME POLYPROTEIN THAT CONTAINS: CAPSID PROTEIN C; THE ENVELOPE GLYCOPROTEIN HAT CONTAINS: CAPSID PROTEIN NOSTRUCTURAL PROTEINS NS2, NS3, NS4A, NS5A AND NS5B. THE VIRLON OF THE VIRUS IS COVERED BY A LIPOPROTEIN ENVELOPE THAT CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ross S., Viazov S., Roggendorf M.;

"An outbreak of Hepatitis C in a municipal hospital: A unique case of patient-to-provider-to-patient transmission."

"Loprovider-to-patient transmission."

Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

-!- SUBUNT: HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E2/NSF1 IS CONTAINED WITHIN THE GENOME POLYPROTEIN THAT CONTAINS: CAPSID PROTEIN C: THE ENVELOPE GLYCOPROTEIN ENVELOPE GLYCOPROPEIN E2/NS1; NONSTRUCTURAL PROTEINS NS2, NS3, NS4A, NS5A AND NS5B. THE VIRUS IS COVERED BY A LIPOPROTEIN ENVELOPE THAT CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E (BY
                                                                                                                                                                                                                                                                                                 LuterPro; IPR002585.1; -...Coat protein; IPR04251; 1...Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; NoN_TER 1 1 1 1 1 NON_TER 26 26 SEQUENCE 26 Ab.
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InterPro; IPR002531; HCV_NS1.
Pfam; PF01560; HCV_NS1; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
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Hepacivirus.
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SIMILARITY: TO HEPATITIS C VIRUS NON-STRUCTURAL PROTEIN E2/NS1
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2/NS1 (GP68)]
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SIMILARITY: TO HEPATITIŞ C VIRUS NON-STRUCTURAL PROTEIN E2/NS1
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Pred. No. 1.9e+02;
2; Mismatches 4;
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50.0%;
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NON_TER 1 1
NON_TER 27 27
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Best Local Similarity 50.0
احد 6; Conservative
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2 TYTTGGSAHTTH 13
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                                       SEQUENCE FROM N.A.
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NCBI_TaxID=11103;
                                                          STRAIN-G-SE;
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MEDLINE=97169154; PubMed=9016961;
Bruno R., Bradbury A.;
A natural langer glycine-rich region in IKe filamentous phage confers no selective advantage.";
Gene 184:121-123(1997).
                                                Gaps
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
VIRAL SAMPLE FLPBRSF (FLORIDA PATIENT B), PARTIAL ENV CDS, V5 REGION
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Korber B.T.M., Mullins J.I., Schochetman G., Berkelman R.L.,
Economou A.N., Witte J.J., Furman L.J., Satten G.A., MacInnes K.A.,
Curran J.W., Jaffe H.W.;
"Molecular epidemiology of HIV transmission in a dental practice.";
Science 256:1165-1171(1992).
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0
  Length 27;
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Pred. No. 2.1e+02;
0; Mismatches 16; Indels
                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. Zhang L.Q., Leigh-Brown A.J.; Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 AA; 2074 MW; AE01C5995681DE45 CRC64;
                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
  Score 38; DB 12;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                Bacteriophage IKe.
Viruses; ssDNA viruses; Inoviridae; Inovirus.
NCBI_TaxID=10867;
                                                                                                                                                                                                                                                              28 AA.
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                                              1; Mismatches
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-NOV-1998 (TrEMBLrel. 08, Last anno
                                                                                                                                                                                                                                                                                                            Created)
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19.0%;
66.7%;
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                     Similarity 66.7
8; Conservative
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
VIRAL SAMPLE FLPARSF (FLORIDA PATIENT A), PARTIAL ENV CDS, V5 REGION (FRAGMENT).
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                                          Score 37; DB 12; Length 17; Pred. No. 1.7e+02; Aismatches 4; Indels
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                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Zhang L.Q., Leigh-Brown A.J.;
Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
NON_TER 17 17 17 SEQUENCE 17 AA; 1708 MW; 347570D2D12CA370 CRC64;
                                                                                                                                                                                                                                         Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                 17 AA.
                                                                                                                                                                  PRT;
                                          Query Match 18.5%;
Best Local Similarity 50.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 18.0°
Best Local Similarity 50.0°
Matches 6; Conservative
                                                                                                                                                                 PRELIMINARY;
                                                                                                   | : :|| | ||
5 TNNTETFRPGGG 16
                                                                                      3 TRDODTFHPSGG 14
                                                                                                                                                                078345
                                                                                                                                            RESULT 15
                                                                                                                                                       078345
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Search completed: February 21, 2002, 16:55:59 Job time: 183 sec

| :|| | || 5 TNGSETFRPGGG 16

3 TRDQDTFHPSGG 14

g G Peptide #98 encode Peptide #100 encod Peptide #96 encode Cyclitol-ubiquinon Fusion protein com Conserved sequence

Cyclitol-ubiquinon Human colon cancer Human SAPL peptide

Phage-derived flex

myc oncogene prote

Human high polymer

deletio

c-myc encoded BSP-GST 5' del

Mutant TD regulato Threonine dehydrat Human high molecul Human pancreatic P

Human complementar

Human secondary si Peptide #3643 enco Peptide #3741 enco Peptide #3588 enco

Fragment of human

Human high molecul Hexahistidine-cont

Modified VP1 pepti

ragment of human

HIV peptide #34. CD44 peptide CD44-Human ovarian tumo Peptide #1816 enco Peptide #1904 enco

4

Title: Perfect score:

Sequence:

protein

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Run on:

Scoring table:

Searched:

Database

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Use of CD44 protein and new peptide derivs - for developing prods for inflammation, immune-mediated tissue damage and tumour cell
                                                                                                                                                                                                                                                                                                                                                                                                          Cell adhesion molecule; CD44; antiinflammatory; rheumatoid; arthritis; tumor cell metastasis; autoimmune disease; immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Telen MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patton KL,
                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                         AAY05710
AAY81997
                                                                                                                                                                         AAB98752
AAM17209
                                                                                                                                                                                                                                         AAW08049
AAR53479
                                                                       AAM13664
AAM26063
                                                                                                AAW36466
AAY44209
                                                                                                                                                         AAY25326
AAB12350
                                                                                                                                                                                         AAM29704
AAM04906
                                                                                                                                                                                                                                                        AAY76576
AAM15382
                                                                                                                                                                                                                         AAY51161
AAY76261
                                                        AAB62422
                                                                AAW17096
                                                                                        AAM01414
                                                                                                                AAB08789
                                                                                                                         AAG97418
                                                                                                                                AAY32946
                                                                                                                                                                                                         AAY81994
                                                                                                                                                                                                                  AAR60513
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                                                                                                                                                                                                                                                                                                                                          AAR53480 standard; peptide; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liao H,
 93WO-US10412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92US-0973339
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
 Hale LP, Haynes BF,
                                                                                                                                                                                                                                                                                                                                                                                           CD44 peptide CD44-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1994-167121/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYDU-) UNIV DUKE.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-0CT-1992;
                                                                                                                                                                                                                                                                                                                                                                           01-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9409811-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-MAY-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metastasis
                AAR53480;
                                                                                                                                                                                                                                                                                                                                    AAR53480
 RESULT
                                                                                                                                                                                                                                                                                                                                          Surrounding sequen
Peptide #1318 enco
Peptide #1310 enco
Peptide #1311 enco
Peptide #757 enco
Surrounding sequen
Myc.His tag. Synt
Ubiquitin peptide
Human ANC_2H01 pro
Human zinc finger
                                                              (without alignments)
108.612 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD44 peptide CD44-
                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                      February 21, 2002, 16:44:21; Search time 23.87 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                       /SIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT:
/SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:
/SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:
/SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT:
/SIDS8/gcgdata/geneseq/geneseqp/AA1993.DAT:
/SIDS8/gcgdata/geneseqp/geneseqp/AA1994.DAT:
/SIDS8/gcgdata/geneseqp/geneseqp/AA1995.DAT:
/SIDS8/gcgdata/geneseqp/geneseqp/AA1995.DAT:
/SIDS8/gcgdata/geneseqp/geneseqp/AA1997.DAT:
/SIDS8/gcgdata/geneseqp/geneseqp/AA1998.DAT:
/SIDS8/gcgdata/geneseqp/geneseqp/AA1999.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*
                                                                                                                                                                                                                                                       /SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1982.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1984.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*
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/SIDSB/gcgdata/geneseq/geneseqp/AA1987.DAT:*
                                                                                                                                                                253143
                                                                                                                                                                                                                                                 /SIDS8/gcgdata/geneseq/geneseqp/AA1980.
       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                      CATRDQDTFHPSGGSHTTHESEDGHSHGSQEGGAN 35
                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                               522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                       - protein search, using sw model
                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY15202
AAM14904
AAM27333
AAM02629
AAM33720
AAM33720
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AAR67264
AAE06626
AAB49884
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Gapop 10.0 , Gapext 0.5
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200
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23
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Maximum DB seq length: 35
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Match 1
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23.5
23.5
23.5
22.5
22.5
22.1
22.1
20.5
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111: 122: 133: 114: 115: 116: 119: 20:

Score

. 9 Result

96 447 447 441 441 441 441

4 5 7 7 10 11 11

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Gaps

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Indels

Length 20;

us-08-753;851-8.rag

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Peptide #1338 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                          human; microarray; gene expression; cervical epithelial cell;
           Score 96; DB 20; Lk
Pred. No. 5.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen W, Rank DR;
                                                                                                                                                           AAM14904 standard; Protein; 29 AA.
                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31
                                                                                                                                                                                                                                                                                                                                                                                            2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.5%; 42.9%;
                      48.0%;
                                   94.48;
                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US00670
                                                                        5 DQDTFHPSGGSHTTHESE 22
                                                                                      11 PSGGSHTTHESEDGHSHGSQE
                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 23.5
Best Local Similarity 42.9
Matches 9; Conservative
                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-488901/53
                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cervical cancer.
                                                                                                                                                                                                                                                                        cervical cancer
                                                                                                                                                                                                                                                                                                                      WO200157278-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                               03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
04-OCT-2000; 2
                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                          12-OCT-2001
                                                                                                                                                                                                                                                                                                                                              09-AUG-2001
                                                                                                                                                                                  AAM14904;
                         Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                              Matches
                                                                                                                                               AAM14904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The fusion protein may be used to target proteoglycans to a given site, which causes local accumulation of GAG-binding proteins. Therefore the protein may be used as adjuvants for vaccination and in the targeting of chemokines to non-immunogenic tumour cells to enhance cellular antitumour reconses. In addition, the fusion protein can also enhance the half-life of non-GAG binding growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The recombinant fusion protein may be administered to a patient to enhance the biological activity of a GAG-binding protein within the body. The protein also enhances wound healing and may be used to treat rheumatoid arthritis, asthma. Chronic obstructive pulmonary disorder, Lupus, inflammatory bowel disease, psoriasis, osteoarthritis or
                                                                                                                                                                        Gaps
                    The peptide can be used for treating inflammation and immune-mediated tissue damage such as occurs in the course of autoimmune diseases, e.g. rheumatoid arthritis. It can also be used for determining metastatic potential or to treat or prevent tumor cell metastasis. This peptide corresponds to AA 221-255 of the CD44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is part of the surrounding sequence of one of the potential assembly sites in a CD44 exon.
                                                                                                                                                                                                                                                                                                                                                          Surrounding sequence of potential assembly site E15-Rg, in CD44.
                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                               isoform; CD44; expression vector; exon; modification; proteoglycan; glycosaminoglycan binding protein; rheumatoid; arthritis; asthma; immunological disorder; assembly site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New artificial proteoglycans useful for treating rheumatoid
                                                                                                                                               Length 23;
                                                                                                                                                                       Indels
                                                                                                                                                        Pred. No. 4.3e-11;
Mismatches 0;
                                                                                                                                               Score 126; DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wolff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Greenfield WB,
                                                                                                                                                                                                                                                                                   AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 30; 63pp; English.
                                                                                                                                     63.0%; Scur
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BRIM ) BRISTOL-MYERS SQUIBB CO.
Claim 4; Page 14; 83pp; English
                                                                                                                                                                                                                                                                                 AAY15202 standard; Peptide; 20
                                                                                                                                                                                            1 CATRDQDTFHPSGGSHTTHESE 22
                                                                                                                                                                                                                    22
                                                                                                                                                                                                             1 catrdddtfhpsggshtthese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0072416
                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                       22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-478982/40
                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 AA;
                                                                                                          23 AA;
                                                                                    protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9937317-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JAN-1999;
                                                                                                                                                                                                                                                                                                                                 26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aruffo AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                             Query Match
Best Local Si
Matches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arthritis
                                                                                                                                                                                                                                                                                                        AAY15202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                           Sequence
                                                                                                                                                                                                                                                                   AAY15202
8XXCCCCCCXX8
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                                                                                                                                                                   The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPS are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
6
                                 analyzing gene expression in human cervical epithelial cells
Human genome-derived single exon nucleic acid probes useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22; Length 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                    Claim 27; SEQ ID No 19730; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                        Peptide #1370 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide #1311 encoded by probe for measuring breast gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                       genome-derived single exon nucleic acid probes useful for
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                                                                                                              Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 47; DB 22;
Pred. No. 7.3;
                                                                                                                                                                                                                                                                                                                                                                                                                     gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID No 27602; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                              Rank DR;
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                     AAM27333 standard; Protein; 29 AA.
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                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                             Chen W,
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                                                                                                                                                                                                                                          2000US-0180312.
2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.5%;
                                                                                                                                                                                                                     2001WO-US00663
                                                                                                                                                                                                                                                                             2000US-0632366
                                                                                                                                                                                                                                                                                         2000US-0234687
2000US-0236359
                                                                                                                                                                                                                                                                                                               2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM02629 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 pspqhhkslenqqphnhgsge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 PSGGSHTTHESEDGHSHGSQE
                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                          genetic disorder
                                                                                                                                                                       WO200157272-A2
                                                                                                                                                                                                                                                                          03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                    30-JAN-2001;
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26-MAY-2000;
                                                                  17-0CT-2001
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                                                                                                                                                                                              09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                     analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 27;
                                                                                                                                                                                                                                                                                                                                                             Penn SG,
                                            AAM27333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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         AAM27333
RESULT
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such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic acid cate of the human breast, particularly those diseases with polygenic acid of the human breast, particularly those diseases with polygenic acid of the human breast, fibrocystic changes, proliferative inflammatory diseases of the breast, fibrocystic changes, proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               breast disease and non-carcinoma tumours.
Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide #7757 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                           Novel single exon nucleic acid probe used to measuring gene expression in a human breast \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel single exon nucleic acid probes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 47; DB 22;
Pred. No. 7.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                       27; SEQ ID No 11369; 322pp; English.
                                                                                                                                                                                                                                                                       Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM33720 standard; Protein; 35
                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22
                                                                                                                                                                                                                                                                      Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.5%;
                                                                                                                                         2000US-0207456.
2000US-0608408.
                                                                                                                                                                      2000US-0632366
                                                                                                                                                                                                               2000GB-0024263
                                                                                              2001WO-US00661
                                                                                                                                                                                   2000US-0234687
                                                                                                                                                                                                 2000US-0236359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       || | : |:: |:||| | 2 pspqhhkslenqqphnhgsge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 PSGGSHTTHESEDGHSHGSQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                      Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                  WPI; 2001-476286/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genetic disorder
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                                       WO200157270-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29
                                                                                                                                                                   03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
             Homo sapiens
                                                                                              29-JAN-2001;
                                                                                                                                                                                                            04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                           04-FEB-2000;
                                                                                                                                                         30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-0CT-2001
                                                                                                                                         26-MAY-2000
                                                                   09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM33720;
                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM33720
δ
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assembly sites in a CD44 exon.

The recombinant fusion protein may be administered to a patient to enhance the biological activity of a GAG-binding protein within the body. The protein also enhances wound healing and may be used to treat rheumatoid arthritis, asthma, chronic obstructive pulmonary disorder, Lupus, inflammatory bowel disease, psoriasis, osteoarthritis or The fusion protein may be used to target proteoglycans to a given site, which causes local accumulation of GAG-binding proteins. Therefore the protein may be used as adjuvants for vaccination and in the targeting of chemokines to non-immunogenic tumour cells to enhance cellular antitumour responses. In addition, the fusion protein can also enhance the half-life
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This peptide comprises a myc-his tag composed of a c-myc oncoprotein epitope and a polyhistidine sequence. It is useful for the purification of an expressed fusion protein by using either anti-myc or anti-his affinity columns, or metalloprotein binding columns. New human breast-specific BS202 polypeptides (see AAW97643) have been expressed in mammalian cells as myc-his
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New breast specific gene, BS202 - used to develop products for detecting, diagnosing, staging, preventing or treating diseases or conditions of the breast such as breast cancer
                                              part of the surrounding sequence of one of the potential \ell sites in a CD44 exon.
                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kratochvil JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BS202 protein; breast cancer; tumour; metastasis; diagnosis; therapy; antigen; epitope; human; myc-his tag.
                                                                                                                                                                                                                                                                                                                                         21.5%; Score 43; DB 20; Length 15; 100.0%; Pred. No. 12; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M, Colpitts TL, Friedman PN;
Hodges SC, Klass MR, Kratoch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 11b; Page 72-73; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW97649 standard; Peptide; 34 AA.
                                                                                                                                                                                                                                                             non-GAG binding growth factors.
                  Example 1; Page 30; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US14046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0888894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                             Query Match 21.5
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cohen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Granados EN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-120783/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Billing-Medel PA,
                                                                                                                                                                                                                                                                                              15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                              5 DQDTFHP 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       409902559-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gordon J, G
Russell JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myc-His tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW97649;
                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                          6
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                                                                                                                                                                                                                                                                                                                                         The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Surrounding sequence of potential assembly site V10-Rg, in CD44.
                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isoform; CD44; expression vector; exon; modification; proteoglycan; glycosaminoglycan binding protein; rheumatoid; arthritis; asthma; immunological disorder; assembly site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New artificial proteoglycans useful for treating rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22; Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wolff EA;
                                                                                                                                                                                                                                                                             analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45; DB
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                             Claim 27; SEQ ID No 33989; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Greenfield WB,
                                                                                                                                                                                               DR;
                                                                                                                                                                                             Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 DTFHPSGGSHTTHESED--GHSHGSQE 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY15206 standard; Peptide; 15
                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                               Chen W,
                                              2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.5%;
40.7%;
2001WO-US00663
                                                                                                                              2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US01411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bennett KL,
                                                                                                                                                                                                                                                                                                                                                                                                                           human genetic disorders
                                                                                                                                                                                            Penn SG, Hanzel DK,
                                                                                                                                                                                                                             WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WP#; 1999-478982/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                            03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                             04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
30-JAN-2001;
                                                                                                                                04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9937317-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY15206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Human; ANC\_2H01 protein; catenin-binding protein; signal transduction; gene regulation; zinc finger protein; alphaN-catenin; drug screening; therapy; cancer; neurological disorder; cytostatic; neuroprotective.

Human ANC\_2H01 protein zinc finger motif 5.

(first entry)

25-SEP-2001

AAE06626;

AAE06626 standard; Protein; 24 AA.

AAE06626

2 ggmefmheseeeehss 18

(VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.

99EP-0204512

18-MAY-2000; 2000WO-EP04535

WO200147954-A2.

05-JUL-2001.

Homo sapiens

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Vanlandschoot A,

Van Roy F,

WPI; 2001-418220/44.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         extensions which are used in the method of the invention for assaying enzymes that modify peptide chains. These sequences represent extensions which are known to be modified in the presence of an enzyme being assayed for, and the reaction mixture formed is then analysed. This method may be used for assaying protein kinases or enzymes which modify the C-terminal end of Ha-RAS protein, such as farnesyl-protein transferase, or carboxy methyl transferase. These peptides are less expensive to synthesise than standard
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                         Ha-RAS protein; farnesyl-protein kinase; C-terminal; carboxy methyl transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assay for enzymes that modify peptide chains - using a substrate comprising a ubiquitin-peptide extension contg. a sequence modified by the enzyme
fusion proteins. BS202 cDNA clones and polypeptides are useful for developing products for detecting, diagnosing, staging, preventing or treating diseases or conditions of the breast,
                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequences given in AAR67262-70 represent ubiquitin-peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptides used in these methods and they may be purified from
                                                                                                                 Length 34;
                                                                                                                                              Indels
                                                                                                                                            ;
9
                                                                                                                 Score 43; DB 20;
Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bacterial extracts by simple acid extraction.
                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                          Ubiquitin peptide extension, PEST4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 23; Column 23; 14pp; English.
                                                                                                                                                                                                                                                                        AAR67264 standard; peptide; 18 AA.
                                                                                                                 21.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 910S-0791935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             910S-0791935
                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                  Query Match
Best Local Similarity 43.8.
Local 7; Conservative
                                                                                                                                                                                        : |: || : || 10 asasnmthsthrghsh 25
                                                                                                                                                                     12 SGGSHTTHESEDGHSH 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rechsteiner MC, Yoo YJ;
                                            including breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-005826/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UTAH ) UNIV UTAH.
                                                                       34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-NOV-1991;
                                                                                                                                                                                                                                                                                                                                27-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5366871-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                           AAR67264
                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                        οy
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                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human catenin-binding proteins and their corresponding cDNA molecules which functions in signal transduction and gene regulatory pathways. The invention also provides an isolated and/or recombinant nucleic acid or its functional fragment, homologue or derivative, corresponding to a alpha-catenin binding protein. The invention also relates to a novel human zinc finger protein binding with a member of the a-catulin/vinculin family, preferably with a human the field of drug discovery, diagnosis, prognosis and treatment of cancer and neurological discovery. The present sequence is human ANC_2HOI protein zinc finger motif.
                                                                                                                                                                                                                                                                                                                                    Novel recombinant nucleic acids useful for diagnosing, prognosing and/or treating cancer and neurological disorders, corresponds to a protein binding to alpha-catenin protein and with signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB 22; Length 24;
Pred. No. 40;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB49884 standard; Peptide; 24 AA.
                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Fig 3; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 58.5
Pest Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 HTTHESEDGHSH 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 hetndpedlhsh 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB4984;
                                                                                                                                                                                                                                                                                                                                                                             function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
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qq
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Gaps

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Indels

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Mismatches Score 42; Pred. No.

1;

8; Conservative

Best Local Similarity

Query Match Matches

Length 18;

DB 16;

21.0%;

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Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a fragment of the light chain of human high molecular weight kininogen. It is used to produce compounds of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endothelial cell proliferation, using compound
                                                                                                                                                                                                               The present peptide, and its claimed fragment, are derived from residues 402-498 of the human high polymer quininogen L-chain. They are useful in cell adhesion, cancer metastasis or platelet aggregation inhibitors, and in wound, inflammatory disease, arteriosclerosis or glomerular nephritis treating agents. The present peptide was synthesised using a solid phase method, and purified using a YMC-DOS-120A-S15/13 column.
                                                                                        inhibitor - comprises partial amino acid sequence of human high polymer quininogen L chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Light chain of human high molecular weight kininogen fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                               Score 40.5; Di
Pred. No. 38;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Method for inhibiting endothelial cell p
that inhibit endothelial cell migration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY93344 standard; peptide; 21 AA.
                                                                                                                                                                                Claim 3; Page 2; 14pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 35; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 20.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0107844.
   94JP-0259451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US26377.
                                    (SUMU ) SUMITOMO SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 HPSGGSHTTHESEDGHSH 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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(DUPO ) DUPONT PHARM CO.
(COLM/) COLMAN W R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mousa AS;
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Thes 8; Conserve
                                                                       WPI; 1996-421988/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-376306/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOUS/) MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                               20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200027415-A2.
 28-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY93344;
                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention is related to the coding sequence and protein fragments of a human catenin-binding zinc finger protein. The coding sequence was isolated from a human kidney cDNA library, but is expressed in most human tissue. The sequences provided by the invention can be used in the diagnosis and treatment of cancer and neurological disorders, and in drug screening to identify compounds capable of the same.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                cancer and neurological disorders, corresponds to a catenin-binding protein in signal transduction and gene regulatory pathways
                                    Catenin-binding zinc finger protein; cancer; neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid or its fragments, useful for diagnosing and treating
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cancer metastasis; platelet aggregation; inhibition; wound;
inflammatory disease; arteriosclerosis; glomerular nephritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.5%; Score 41; DB 22; Length 24; 58.3%; Pred. No. 40; 3; Indels iive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human high polymer quininogen L-chain derived peptide.
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/note= "claimed peptide (claim 1)"
                                                                                                                                                                                                                                                                       (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 52; 71pp; English.
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                                                                                                                                                                                                                                                                                                        Vanlandschoot A,
                                                                                                                                                                                                 99EP-0201543
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Human zinc finger motif
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|hetndpedlhsh 19
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Matches 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 AA;
                                                     drug screening
                                                                                                                         EP1054059-A1:
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                                                                                          Homo sapiens
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                                                                                                                                                            22-NOV-2000
                                                                                                                                                                                                                                                                                                          Van Roy F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treatment.
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Peptide

RESULT 12

AAW07626

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Gaps

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us-08-753-851-8.rag

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oncogenes which are bound by the monoclonal receptors of the invention. The monochoal receptor molecules are immunoglobulins which bind to both (a) a protein ligand and (b) a polypeptide having an amino acid residue sequence containing 7-40 amino acid residues corresponding to a sequence of a portion of the protein, the receptor molecule having been raised to an immunogen containing the polypeptide. High yields of monoclonal receptors can be obtained which bind to or immunoreact with
the invention. High molecular weight kininogen is a 120 kDa gycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monoclonal receptors to protein, esp. onco-protein ligands - prepd. using a polypeptide corresp. to a portion of the protein aminoacid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oncogene; monoclonal receptor; antibody; immunoglobulin; ligand; immunogen; epitope; oncoprotein; detection.
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                                                                                                                                                                                                                                                                       DB 21; Length 21;
                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                     Score 40.5; DB
Pred. No. 40;
1; Mismatches
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84US-0001304.
85US-0701954.
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Best Local Similarity 44.4.
Best Local Similarity 44.4.
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                                                                                                                                                                                                                    21 AA;
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Sequences AAY52601-Y52675 represent oncoprotein epitopes used to raise monoclonal antibodies which bind to both the epitopes and the proteins that comprise them. Certain retroviruses are able to cause the formation of solid tumours within a short period of time after infection of the host. Oncogenes, and the oncoproteins they encode, are responsible for the tumorigenic potential of these retroviruses. Retroviral oncogenes are closely related to and are derived from cellular oncogenes, which cencode proteins with mitogenic activity such as growth factors. The invention relates to monoclonal anti-oncoprotein antibodies, and the method used to purify them. The method of the invention may be used for obtaining purified oncoprotein ligands from aqueous solutions. It may be used in this way to detect proteins produced in tumour cells to diagnose cancers caused by retroviruses. It may also be used for the prognostication of foetal development (and other growth states including
                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oncoprotein; epitope; oncogene; retroviral; infection; cellular; amonoclonal; antibody; Mab; purification; cancer; tumour; growth factor; mitogenic; expression; detection; diagnosis; prognosis; immunoassay; growth; development; neoplasia; foetus; non-invasive.
known predetermined epitopes of protein molecules such as oncoproteins. The receptors can be used for e.g. detection of oncoprotein ligands or in affinity sorbants for binding and purifying oncoprotein ligands. This sequence is specifically derived from normal human cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Purifying oncoprotein ligands using monoclonal antibodies, useful for diagnosing cancers caused by retroviruses
                                                                                                                                                                         Gaps
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                                                                                                                                     Score 40; DB 12; Length 24; Pred. No. 56;
                                                                                                                                                                       Indels
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                                                                                                                                                                       2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                     c-myc encoded oncoprotein epitope #24
                                                                                                                                                                                                                                                                                                                             AAY52624 standard; peptide; 24 AA.
                                                                                                                                     20.08;
46.78;
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91US-0772702.
84WO-US01304.
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                                                                                                                                                      Local Similarity 46.7 ses 7; Conservative
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                                                                                                                                                                                                                           Lerner RA, Niman HL;
                                                                                   24 AA
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07-OCT-1991;
17-AUG-1984;
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Best Local S
Matches 7,
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                                                                                     Sequence
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neoplasia) using either urine or other body fluid obtained by non invasive methods, the antibodies being used to assay for oncoprotein. As the antibodies bind to epitopes of known amino acid sequence, the type of oncoprotein being expressed in the patient may be determined. 888888

24 AA; Sequence

0; Gaps Query Match
20.0%; Score 40; DB 21; Length 24;
Best Local Similarity 46.7%; Pred. No. 56;
Matches 7; Conservative 2; Mismatches 6; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: RECHESTBINER, MARTIN C.
APPLICANT: XOO, YUNG JOON
TITLE OF INVENTION: UBIQUITIN-PEPTIDE EXTENSIONS PATITLE OF INVENTION: BNZYME SUBSTRATES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thorpe, No. 5366871th & Western
STREET: 9035 South 700 East, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      storage
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US-08-464-134-89

US-08-461-361-85

US-08-461-361-89

US-08-485-910-89

PCT-US95-06266-69

PCT-US95-06266-73

US-08-444-733-97

US-08-461-34-97

US-08-461-361-97

US-08-331-362-10
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Pred. No. 9.9;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720
COMPUTER: compaq LTE/286
OPERATING SYSTEM: DOS 4.01
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,935B
FILING DATE: 19911113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/07791935B Patent No. 5366871 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 amino acid residues
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TELECOMMUNICATION INFORMATION:
TELEFAN: (801) 566-6633
TELEFAX: (801) 566-0750
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22,788
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: na ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Western, M. Wayne REGISTRATION NUMBER: 22,
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        Query Match
Best Local Similarity
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     ADDALL
STREET: YULL
TV: Sandy
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COUNTRY: USA
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US-07-791-935B-3
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        RESULT
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                                                                                                                                                                                                             (without alignments) 62.609 Million cell updates/sec
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Sequence 3, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, 2 Sequence 11, 2 Sequence 85, 2
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Sequence 20,
                                                                                                                                                                                February 21, 2002, 16:50:06; Search time 12.58 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTuS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTuS_COMB.pep:*
                             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                     CATRDQDTFHPSGGSHTTHESEDGHSHGSQEGGAN 35
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US-08-444-733-89
US-08-464-134-85
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                  protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                  US-08-753-851-8
200
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Match Length
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Maximum DB seq length: 35
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Gaps

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Score 42

No. Result

2 GGMEFMHESEEEEHSS 18

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APPLICANT: Hutchens, T. William
Yip, Tai-Tung
TITLE OF INVENTION: Surface-Enhanced Neat Desorption for the
Detection of Analytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,407
FILING DATE: 10-Jun-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5639-PCT-US-D1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                          ADDRESSEE: Fulbright & Jaworski L.L.P. STREET: 1301 McKinney, Suite 5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jiang, Shibo
APPLICANT: Lin, Kang
APPLICANT: Lin, Kang
APPLICANT: Neurath, A. Robert
TITLE OF INVENTION: SYNTHETIC POLYPEPTIDES AS
TITLE OF INVENTION: INHIBITORS OF HIV-1
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/068,896
FILING DATE: 28-MAY-1993
APPLICATION NUMBER: WO PCT/US94/06064
FILING DATE: 27-MAY-1994
FILING DATE: 27-MAY-1994
FILING DATE: 27-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-095-407-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (713) 651-5325
TELEFAX: (713) 651-5246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/07859923A Patent No. 5444044 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 НРИСИНРИСИИРИСИИРИС 26
                    Sequence 2, Application US/09095407 Patent No. 6124137 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 26 amino acids
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33.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                      CITY: Houston
                                                                                                                                                                                                                                                                                                STATE: Texas
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Best Local Similarity
Matches 8; Conserva
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US-07-859-923A-20
US-09-095-407-2
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                                                                                                                            APPLICANT: TEMPLE UNIVERSITY - OF THE COMMONWEALTH SYSTEM OF TITLE OF INVENTION: INHIBITION OF ANGIGGENESIS BY PEPTIDE ANALOGS OF HIGH TITLE OF INVENTION: MOLECULAR WEIGHT KININOGEN DOMAN 5 FILE REFERENCE: 6056-258 CT1 CURRENT APPLICATION NUMBER: US/09/612,126 CURRENT FILING DATE: 2000-07-07 PRIOR PLICATION NUMBER: 60/107,844 PRIOR PLILNG DATE: 1999-11-10 PRIOR PLILNG DATE: 1999-11-10 PRIOR FILING DATE: 1999-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Yip, Tai-Tung
APPLICANT: Yip, Tai-Tung
APPLICANT: Yip, Tai-Tung
APPLICANT: Hutchens, T. William
TITLE OF INVENTION: Method and Apparatus for Desorption and Ionization of
TITLE OF INVENTION: Analytes
FILE REFERENCE: Hutchens
CURRENT APPLICATION NUMBER: US/08/785,636
EURRENT FILING DATE: 1997-01-17
EARLIER APPLICATION NUMBER: 08/068,896
EARLIER FILING DATE: 1993-05-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTHER INFORMATION: Description of Artificial Sequence: Human high OTHER INFORMATION: molecular weight kininogen light chain amino acids; OTHER INFORMATION: Lys(420) through Gly(440)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Unknown Organism: US-08-785-636-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.0%; Scor.
33.3%; Pred. No. 55,
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Pred. No. 19;
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Patent No. 6027942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 HPHGHHPHGHHPHGHHPHG 26
                                                              Sequence 3, Application US/09612126
Patent No. 6284726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.28;
                                                                                                                                                                                                                                                                                                                                                                                PatentIn Ver. 2.1
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SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 33.3
Matches 8; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Ve
                                                                                                          GENERAL INFORMATION:
APPLICANT: TEMPLE (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Unknown
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LENGTH: 26
TYPE: PRT
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LENGTH: 21
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                                                                                                                                                                                                                                                                                                                    APPLICANT: Thoegersen, Hans Christian
APPLICANT: Thoegersen, Thor Las
APPLICANT: Holtet, Thor Las
APPLICANT: Etzerodt, Michael
TITLE OF INVENTION: Improved method for the refolding of
TITLE OF INVENTION: proteins
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 1; Length 15;
Pred. No. 52;
0; Mismatches 3; Indels
                                                                       Score 38; DB 2; Length 33;
Pred. No. 70;
                                                                                                            8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version SOFTWARE: #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/469,486
                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 06363/002001
TELECOMMUNICATION:
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                  Sequence 48, Application US/08469486 Patent No. 5739281
                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Fish & Richardson 225 Franklin Street
                                                                       19.0%;
38.9%;
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52.6%;
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                                                                                                                                              16 HTTHESEDGHSHGSQEGG 33
                                                                                                                                                                               15 HLIEESQNQQTKNEQEGG 32
                                                                                        Best Local Similarity 38.99
Matches 7; Conservative
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LENGTH: 15 amino acids
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Best Local Similarity 52.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
   ; TOPOLOGY:
US-08-484-107-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                     US-08-469-486-48
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                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Indels
                                                                                                                                                       MEDIUM TYPE: Diskette - 5.25 inch, 360 kb
COMPUTER: IBM XT compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/859,923A
FILING DATE: 19920326
FLING DATE: 19920326
FLING DATE: No. 5444044e
FILING DATE: No. 5444044e
INFORMATION FOR SEQ ID NO. 20:
SEQUENCE CHARACTERESTICS:
LENGTH: 33 Annio Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jiang, Shibo
APPLICANT: Jiang, Rang
APPLICANT: Lin, Kang
APPLICANT: Neurath, A. Robert
TITLE OF INVENTION: SYNTHETIC POLYPEPTIDES AS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER EXADABLE FORM:
MEDIUM TYPE: Diskette - 5.25 inch, 360 kb
COMPUTER: IBM XT compatible
OPERATING SYSTEM: MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
ADDRESSEE: The Lindsley F. Kimball ADDRESSEE: Research Institute of the ADDRESSEE: New York Blood Center STREET: 310 E. 67th Street
                                                                                      New York
: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             us/07/859,923
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APPLICATION NUMBER: US/08/484,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20, Application US/08484107 Patent No. 5840843 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/85
FILING DATE: March 26, 1992
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 Amino Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.0%;
38.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 HLIEESQNQQTKNEQEGG 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 HTTHESEDGHSHGSQEGG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                    Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                      New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                         10021
                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY:
US-07-859-923A-20
                                                                    CITY: Nev
STATE: Ne
COUNTRY:
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qq

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18.0%; Score 36; DB 1; Length 20; 50.0%; Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: ARIINGTON STATE COUNTRY: U.S.A. ZOUNTRY: PADDIUM TYPE: F. FLOPPy disk COMPUTER: IBM PC COMPATIble OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/143,311B
                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/218,025A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: HAYNES, BARTON F.
APPLICANT: HALE, LAURA P.
APPLICANT: PATTON, KAREN L.
APPLICANT: TELEN, MARILYN J.
APPLICANT: LIRO, HUA-XIN
TITLE OF INVENTION: AN ADHESION MOLECULE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                        CLASSILICATION: 4.24

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/891,451
FILING DATE: 29-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST33A
TELECHONE: (215) 540-9206
TELEPHONE: (215) 540-9206
TELEPAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/973,339
FILING DATE: 30-0CT-1992
CLASSIFICATION: 436
APPLICATION NUMBER: 07/669,730
FILING DATE: 15-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08143311B Patent No. 5863540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 TNDTEIFRPGGG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-218-025A-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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US-08-143-311B-7
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Patent No. 5556744
GENERAL INFORMATION:
APPLICANT: Weiner, David B.
APPLICANT: Weiner, David B.
APPLICANT: Williams, William V.
TITLE OF INVENTION: Methods and Compositions for Diagnosing
TITLE OF INVENTION: and Treating Certain HIV Infected Patients
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson
(GTREET: P.O. Box 457, 321 No. 5556744ristown Road
                Patent No. 5917018
GENERAL INFORMATION:
APPLICANT: Th egersen, Hans Christian
APPLICANT: The carsen, Hans Christian
APPLICANT: Etzerodt, Michael
TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOLDING OF
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 15;
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                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION UNBER: US/08/469,658
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30.162
REFERENCE/DOCKET NUMBER: 06363/00202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 52;
                                                                                                                                                                                                                              ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
Sequence 48, Application US/08469658
Patent No. 5917018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEX: 200154
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 aming acids
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52.6%;
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Best Local Similarity 52.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                              CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-08-469-658-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                            APPLICANT: Uithoven, Keith TTLE OF INVENTION: Improved Antibodies to P. falciparum NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Becton, Dickinson and Company
One Becton Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 88;
2; Mismatches
                                                                                                                                                                                                                                                                                         E: Becton Dickinson and Company
One Becton Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.5%; Score 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/945,287
                                                                                              ; Sequence 1, Application US/08250309
; Patent No. 5478741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08343305
Patent No. 5580735
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32,135
                                                                                                                                                     APPLICANT: Feindt, Hans H.
APPLICANT: Hahn, Gerald D.
APPLICANT: Maret, Melissa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Malick, Adrien
APPLICANT: Feindt, Hans H.
APPLICANT: Hahn, Gerald D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Fugit, Donna R. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 07417
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: peptide US-08-250-309-1
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CITY: Franklin Lakes
STATE: NJ
                                                                                                                                                                                                                                                                                                                          CITY: Franklin Lakes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
   2 САННАННААДАН 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 5; Conserva
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                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                         RESULT 12
US-08-250-309-1
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                                                                                                                                                                                                                                                                                                                                              STATE:
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0
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                                                                                                                                                                                                                                                                                                                                              DB 2; Length 20; 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.5%; Score 35; DB 1; Length 18; 41.7%; Pred. No. 88; 5; Indels Live 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                   0;
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CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/001,907
FILING DATE: 19930104
                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                              18.0%; Score 36; 100.0%; Pred. No.
                                                                          1579-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
           ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/CDCKET NUMBER: 1579-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08001907
Patent No. 5393527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,1
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: MALICK, Adrien
APPLICANT: Feindt, Hans H.
APPLICANT: Hahn, Gerald D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-08-001-907-1
                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 436
                                                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 5; Conserva
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CLASSIFICATION:
                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              ||||||||
|14 ATRDQDT 20
                                                                                                                                                                                                                                                                                                                                                                                                                     2 ATRDQDT 8
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                                                                                                                                                                                                                                                                                     US-08-143-311B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-08-001-907-1
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STATE:
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Gaps

ZIP: 07417

COUNTRY:

14 GSHTTHESEDGH 25

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Gaps
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                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Feindt, Hans H.
APPLICANT: Hahn, Gerald D.
APPLICANT: Marct, Melissa
APPLICANT: Uithoven, Keith
TITLE OF INVENTION: Improved Antibodies to P. falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 18;
                                                                             DB 1; Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB 1;
Pred. No. 88;
2; Mismatches
                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Becton Dickinson and Company
STREET: One Becton Drive
CITY: Franklin Lakes
                                                                               Score 35; DB
Pred. No. 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: February 21, 2002, 16:53:10 Job time: 184 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT ARPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,092
FILING DATE: 21-MAR-1995
CLASSIFICATION A15
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/945,287
FILING DATE: 11-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: FUGIL, DONNA R.
REGISTRATION NUMBER: 32,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08408092 Patent No. 5604117
                                                                               17.5%;
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INFORMATION FOR SEQ ID NO: 1:
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Best Local Similarity 41...
Si Conservative
                                                                           Query Match 17.5 Best Local Similarity 41.7 Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 18 amino acids
; MOLECULE TYPE: peptide US-08-343-795-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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US-08-408-092-1
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Patent No. 5593843
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Malick, Adrien
APPLICANT: Hahn, Gerald D.
TITLE OF INVENTION: Stabilized Microspheres and Methods of
TITLE OF INVENTION: Preparation
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Becton, Dickinson and Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 18; 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,305
FILING DATE: 22-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/343,795
FILING DATE: 22-NOV-1994
CLASSIFICATION: 435
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APPLICATION NUMBER: US 08/001,907
FILING DATE: 04 -JAN-1993
ATTORNEY/AGENT INFORMATION:

NAME: FUGIT, Donna R.

REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: 9-2209/P-2539
INFORMATION FOR SEQ ID NO: 1:
SAGUINCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Becton, Dickinson and Company
STREET: One Becton Drive
CITY: Franklin Lakes
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                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/001,907
APPLICATION NUMBER: US 08/001,907
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: FUGIt, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-2209/P-2539
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 17.5
Best Local Similarity 41.7
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: peptide US-08-343-305-1
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

February 21, 2002, 16:56:02; Search time 12.77 Seconds (without alignments) 77.547 Million cell updates/sec Run on:

US-08-753-851-9 74 Title: Perfect score:

1 CRDGIRYVQKGEY 13 Sednence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 segs, 76174552 residues Searched:

1822 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 13

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

Database :

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	glycine cleavage s	6-phosphofructo-2-	protein QA300025 -	T-cell receptor be	dextransucrase (EC	matK protein - bee	proteinase E - bla	T-cell receptor be	T-cell receptor al	Ig heavy chain CRD	conotoxin au5a - c	conotoxin au5b - c	proteasome chain 1	Z protein - guinea	T-cell antigen rec	RNA-directed DNA p	calliFMRFamide 10	alpha-adaptin - bo	nitrogenase (EC 1.	precorrin methyltr	T-cell receptor be	T-cell receptor be	Ig heavy chain CDR	≥ .	T-cell antigen rec	_	٦	-	T-cell antigen rec
SUMMARIES	ID	PS0253	A43405	PA0030	PH0746	B39841	S18722	A34858	PH0771	PH0803	PT0245	A59146	B59146	S09082	S23168	S47373	A35890	A44787	B46250	S70251	S21127	PH0929	PH0914	PT0228	PT0331	S47365	S47371	S47372	S47380	847390
	DB	7	~	~	7	7	~	~	7	7	7	7	7	7	7	7	7	7	~1	7	~	7	~	7	~	7	7	7	7	7
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ж (	Query Match	31	31	38	28	27	27	25	25	24	24	24	24	24	24	2	53	23.	23	23	23	23	23	2	23	23	23	23	23	23
	Score	23	23	21	21	20	20	19	19	18	18	18	18	18	18	17.5	17	17	17	17	17	17	17	17	17	17	17	17	17	17
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T-cell antigen rec	glyceraldehyde-3-p	whey glycoprotein	rpsA protein - Erw	T-cell receptor be	conopressin G - co	lysine-conopressin	T-cell receptor al	alcohol dehydrogen	endo-1,4-beta-xyla	T-cell-specific tr	urease (EC 3.5.1.5	glucan endo-1,3-be	Ig heavy chain V r	R-phycoerythrin ga	photosystem I 9K c
47392	344	392	141	T0653	128495	040	РН0807	196	301	797	215	215	525039	565	14316
S47	S5434	PC439	S3714	PTO	A28	S3904(	PH0	866196	S1930	S61797	C49215	S2821E	S25	G2256	S14
7	7	7	7	7	7	7	7	7	7	a	7	a	7	7	7
13	13	9	∞	∞	5	σ	10	11	11	11	12	12	12	13	13
3.0	3.0	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	21.6	1.6	1.6	1.6	1.6
7	7	7	7	7	7	7	7	7	7	7	7	7	7	~	7
17	17	16	16	16	16	16	16	16	16	16	16	16	16	16	16
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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glycine cleavage system protein H - rice (strain Nihonbare) (fragment) N;Alternate names: glycine decarboxylase complex H protein C;Species: Oryza sativa (rice) C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 03-Feb-1994
                                                                                                                                                                        C'Accession: PS0253
R'Tsugitat, A.
Submitted to JIPID, April 1993
A'Reference number: PS0206
A'Accession: PS0253
A'Molecule type: protein
A'Residues: 1-9 < TSUS)
RESULT
PS0253
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Gaps ö 0; Indels Length 9; Score 23; DB 2; 1 Pred. No. 2.2e+05; 2; Mismatches 0; Query Match 31.1%; Best Local Similarity 60.0%; Matches 3; Conservative

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3 DGIRY 7 ||::| | DGLKY Op δ

A43405

A43405

A43405

A53405

A53406

A; Notestand Manager (1970), No. 1970 (1

Query Match 31.1%; Score 23; DB 2; Length 10; Best Local Similarity 100.0%; Pred. No. 5.9e+02; Matches 4; Conservative 0; Mismatches 0; Indels 10 KGEY 13

.; 0

Gaps

6

||||| 7 KGEY 10

δλ Db RESULT PA0030

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R;Morden, C.W.; Wolfe, K.H.; dePamphilis, C.W.; Palmer, J.D.
EMBO J. 10, 3281-3288, 1991
A;Title: Plastid translation and transcription genes in a non-photosynthetic plant: i
A;Reference number: S17794; MUID:92007779
A;Accession: S18722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.Accession: PH0771

R.Acasonova, J.L., Romerov, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991

A;Title: T cell receptor genes in a series of class I major histocompatibility comple allelic exclusion and antigen specific repertoire.

A;Reference number: PH0746; MUID:92078846

A;Accession: PH0771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Characterization of the venom from Crotalus molossus nigrescens Gloyd (black A;Reference number: A34858; MUID:90260877 A;Accession: A34858
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                                                                                                                                                                            matk protein - beechdrops plastid (fragment)
C;Species: plastid ppifagus virginiana (beechdrops)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Feb-1995
C;Accession: S18722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteinase E - blacktail rattlesnake (fragment)
C;Species: Crotalus molossus nigrescens (blacktail rattlesnake)
C;bate: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 18-Jun-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T-cell receptor beta chain (PES.1.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 2.4e+03;
2; Mismatches 0;
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Pred. No. 3.6e+03;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Accession: A34658
R;Ramirez, G.A.; Fletcher Jr., P.L.; Possani, L.D.
Toxicon 28, 285-297, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.7%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.0%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-12 <MOR>
A;Cross-references: BMBL:X61798
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0v
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A;Molecule type: protein
A;Residues: 1-12 <RAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Genome: plastid
C; Keywords: plastid
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8 LRYLQ 12
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| DGVR 4
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4 RYVZ 7
              3 DGIR 6
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                                                                       C; Accession: PA0030
R; Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A; Description: Separation and characterization of Arabidopsis proteins by two-dimensiona
A; Reference number: PA0001
A; Accession: PA0030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dextransucrase (EC 2.4.1.5) - Streptococcus sobrinus (fragment)
C.Species: Streptococcus sobrinus
C.Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 23-Jun-1993
C.Accession: B39841
R.Mooser, G.; Hefta, S.A.; Paxton, R.J.; Shively, J.E.; Lee, T.D.
J. Biol. Chem. 266, 8916-8922, 1991
A.Mitile: Isolation and sequence of an active-site peptide containing a catalytic asparting A.Mocession: B39841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: T cell receptor genes in a series of class I major histocompatibility complex-salelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846
A;Accession: PH0746
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protein QA300025 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T-cell receptor beta chain (B28) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C;Accession: PH0746
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J. Exp. Med. 174, 1371-1383, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X60837; NID:g50098; PIDN:CAA43230.1; PID:g50099 A;Experimental source: T lymphocyte C;Keywords: T-cell receptor
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                                                                                                                                                                                                                                                                                                                                                                      Length 12;
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Pred. No. 1.6e+03;
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A;Molecule type: protein
A;Residues: 1-9 <MOD>
C;Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  2;
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50.0%;
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Best Local Similarity 50.0
Matches 4; Conservative
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A,Residues: 1-12 <KAM>
A,Experimental source: seed
C,Keywords: seed
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Matches 4; Conserv
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1 CASSSRYEQ 9
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2 IEPIQEGE 9
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Rywalker, C.S.; Steel, D.; Jacobsen, R.B.; Lirazan, M.B.; Cruz, L.J.; Hooper, D.; She J. Biol. Chem. 274, 30664-30671, 1999
A,Title: The T-superfamily of conotoxins.
A; Reference number. A59147; MUID:99452958
A; Accession: A59146
A; Molecule type: protein
A; Residues: 1-11 < VAML>
C; Keywords: amidated carboxyl end; toxin; venom F; 2-9, 3-10/Disulfide bonds: #status experimental
F; 11/Modified site: amidated carboxyl end (Trp) #status experimental
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C;Accession: B59146
R;Walker, C.S.; Steel, D.; Jacobsen, R.B.; Lirazan, M.B.; Cruz, L.J.; Hooper, D.; She
J; Blol. Chem. 274, 30664-30671, 199
A;Title: The T:Superfamily of conctoxins.
A;Reference number: A59147; MUID:99452958
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N;Alternate names: multicatalytic proteinase chain 1
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Aug-1998
C;Accession: S09082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Conus aulicus (court cone)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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C;Reywords: amidated carboxyl end; toxin; venom
F;2-9,3-10/Disulfide bonds: #status experimental
F;11/Modified site: amidated carboxyl end (Trp) #status experimental
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A;Residues: 1-12 <LIL>
C;Superfamily: multicatalytic endopeptidase complex chain C9
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75.0%; Pred. No. 5.5e+03;
iive 1; Mismatches 0;
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Pred. No. 5e+03;
0; Mismatches
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Pred. No. 5e+03;
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FEBS Lett. 262, 327-329, 1990
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57.1%;
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57.1%;
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Best Local Similarity 57.1
Local 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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    C; Accession: A59146
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9 KDGI 12
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A.Reference number: PH0746; MUID:92078846
A.Accession: PH0803
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PT0245

PT0245

Igh heavy chain CRD3 region (clone 2-103C) - human (fragment)

C; Species: Homo sapiens (man)

C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C; Accession: PT0245

R; Yamda, M.: Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A; Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A; Reference number: PT0222; MUID:91108337

A; Accession: PT0245

A; Molecule type: DNA

A; Residues: 110 cYAM>
A; Experimental source: B lymphocyte
C; Keywords: heterotetramer; immunoglobulin
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PH0803
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J. Exp. Med. 174, 1371-1383, 1991
A;Cross-references: EWBL:X60865; NID:953624; PIDN:CAA43255.1; PID:953625 A;Experimental source: T lymphocyte C;Keywords: T-cell receptor
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Pred. No. 3.6e+03;
1; Mismatches 5; Indels
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2.2e+05;
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Pred. No.
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A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor
                                                                                                                           25.7%;
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42.9%;
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Best Local Similarity 42.5.
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Matches 3; Conserv
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Matches 3; Conserv
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A; Residues: 1-8 <CAS>
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A; Description: binds dehydroepiandrosterone sulfate, estrone sulfate, oleic acid, choles C; Keywords: liver; steroid binding
Z protein - guinea pig (fragment)
C; Species: Cavia porcellus (guinea pig)
C; Species: Cavia porcellus (guinea pig)
C; Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C; Accession: S23168
B; Nicollier, M.; Roblin, S.; Cypriani, B.; Remy-Martin, J.P.; Adessi, G.L.
Eur. J. Biochem. 205, 1137-1144, 1992
A; Title: Purification and characterization of a binding protein related to the Z class of A; Accession: S23168; MUID:92249319
A; Reference number: S23168
A; Molecule type: protein
A; Residues: 1-12 < NIC>
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R;Lehner, P.J.
R;Leference number: 847355
A;Accession: 847373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Status: preliminary
A:Status: preliminary
A:Status: 1-13 ALEH>
A:Residues: 1-13 ALEH>
A:Cross-references: EMBL:Z35672; NID:g527489; PIDN:CAA84741.1; PID:g527490
C:Keywords: T-cell receptor
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24.3%; Score 18; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: liver C; Function:
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5 GEY 7
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S47373
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Search completed: February 21, 2002, 16:59:02 Job time: 180 sec

ij,

Gaps

23.6%; Score 17.5; DB 2; Length 13; 38.5%; Pred. No. 7.2e+03; Live 1; Mismatches 6; Indels

Query Match 23.6 Best Local Similarity 38.5 Matches 5; Conservative

1 CRDGIRYVQKGEY 13 | | | : || 1 CASSIRSADE-EY 12

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 21, 2002, 16:57:07 ; Search time 10.22 Seconds
(without alignments)
46.638 Million cell updates/sec Run on:

US-08-753-851-9 74

1 CRDGIRYVQKGEY 13 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

530 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 13

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	P81755 conna texti	7 chlamv	_		P41853 artioposthi		P05486 conus geogr	ascari	-									P80863 bacillus su				_			P81731 helicoverpa	P81545 dictyosteli		locusta	locusta	locusta	81737	0860	P82684 carausius m
SUMMAKIES	ID	CXET CONTE	UXA6_CHLTR	FARA_CALVO	RLA2_MOUSE	FARP_ARTTR	RS1_ERWCH	CONO_CONGE	FAR2_ASCSU	AL17_CARMA	FAR7_ASCSU	AL11_CARMA	OXYT_BUFRE	OXYT_CYPCA	OXYT_RABIT	OXYV_SQUAC	SAP_STOVA	PSBF_CAPAN	SOI5_BACSU	LIGB_TRAVE	FAR5_HIRME	RS11_SALTY	TKC1_CALVO	TKL1_LOCMI	ULAD_HUMAN	AMPN_HELAM	SP34_DICMU	SPI_HALRO		TKL3_LOCMI	TKL4_LOCMI	TRP5_LEUMA	UHA3_HUMAN	PKC1_CARMO
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	Result No.		7	е	4	2	9	7	œ	σ,	10	11	12	13	14	15	16	17	18	19.	20	21	22	23	24	25	56	27	28	29	30	31	32	2,5

UXAG\_CHLTR STANDARD; PRT; 10 AA.
D38007;
D1-OCT-1994 (Rel. 30, Created)
D1-OCT-1994 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE FROM ELEMENTARY BODY (FRAGMENT).

RESULT 2 UXA6\_CHLTR ID UXA6\_CI AC P38007; DT 01-OCT-DT 30-MAY. DE UNKNOWI

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P41518 calliphora P56245 litoria xan P56246 litoria xan P50983 conus imper P17776 escherichia P1445 cavia porce P1667 pinus pinas P01373 periplaneta P01373 periplaneta P1889 ascaris suu P38499 procambarus P38498 procambarus	GESTROCTURE BY NWR.  STRUCTURE BY NWR.  Tiec E., Hambe B.,  Baleja J.D.,  ttranslational  C MEMBRANES, BLOCKING  AL-GALNAC.  Tr. Venom; Vitamin K;  ylation; Bromination;  IIC ACID.  IIC ACID.  IIC ACID.  IIC ACID.	gth 13; Indels 0; Gaps
TKC2_CALVO CD11_LITXA CD14_LITXA CXA1_CONIM Y2PY_ECOLI FIBA_CAVPO NUO2_PINPS FRR1_PERAM FAR1_ASCSU FAR1_PROCL FAR2_PROCL	update) on update) on update) on update) opoda; Caenogas onus. THR-10, AND ST Roepstorff P., h unusual postt Roepstorff P., h unusual postt Roepstorff P., AT PRESYNAPTIC ISACCHARIDE GAL OTEN INHIBITOR; OTEN HYDON: VLATION. YLATION. ED GALWAC. IED GALWAC. IED GALWAC.	core 21; DB 1; Len red. No. 9.4e+02; Mismatches 1;
T CCC	Created) Last seq Last ann f-gold c llusca: a; Conid a; Conid ler E., p., Bertil ler E., s textil LS. Calciu LS. Calciu acid; Gl B B B B B B B B C Calciu acid; Gl B B B B B	0
1111111 11111111 111111111111111111111	ALIG  CONTE  CXET_CCONTE  STANDARD; PRT; P81755; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence 20-AGG-2001 (Rel. 40, Last annotati EDSILON-CONOTOXIN TXIX. CONUS textile (Cloth-of-gold cone). EURAIYOta; Metazoa; Mollusca; Gastr Neogastropoda; Conoidea; Conidae; C (1) SEQUENCE, CARBOHYDRATE-LINKAGE SITE TISSUE-Venom; MEDLINE=99254114; Pubmed=10318957; Rigby A.C., Lucas Meunier E., Kalum Dahlqvist I., Fossier P., Baux G., Furie B.C., Furie B., Stenflo J.P.; A conotoxin from Conus textile with modifications reduces presynaptic Proc. Natl. Acad. Sci. U.S.A. 96:57 -: FUNCTION: CONOTOXIN WHICH ACTS -: FUNCTION: CONOTOXIN WHICH ACTS -: FUNCTION: CONOTOXIN WHICH ACTS -: THE CALCIUM CHANNELS: PTM: O-GLYCAN CONSISTS OF THE D PUBS: 1MCT; 08-JUN-99. DISGUELD 3 MOD_RES 4 4 GAMMA- MOD_RES 7 7 BROWIN MOD_RES 13 13 13 REQUENCE CARBOHYD 10 0-LINK SEQUENCE 13 AA; 1388 MW; 386C9B	28.4%; larity 75.0%; Conservative
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18 118 118 118 117 117	13 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	mila Co 4
14 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	CONTE CXET_CONTE CXET_CONTE STANDARD P81752 30-MAY-2000 (Rel. 39, L 30-MAY-2000 (Rel. 39, L 20-MG-2001 (Rel. 40, L EPSILON-CONOTOXIN TXIX CONUS textile (Cloth-of EUKATYOLE) Metazoa; Mol Neogastropoda; Conoidea NEOGASTROPOGA; CONOSTROPOGA; CONOSTROPOGA; CONOSTROPOGA; CONOSTROPOGA; CONOCANO; CONOCANOCANO; CONOCANOCANO; CONOCANOCANO; CONOCANOCANO; CONOCANOCANO; CONOCANO,	tch al Sir 3; CRDG 4 
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Platyhelminthes, Turbellarian Platyhelminths, Rhabditophora, Seriata, Tricladida, Terricola, Geoplanidae,
                                                                                                                                                                                                                                                                          SUBUNIT.
-:- PTM: PHOSPHORYLATED (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.
SWISS-2DPAGE; P99027; MOUSE.
Ribosomal protein; Phosphorylation.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94211927; PubMed-7909164;
Maule A.G., Shaw C., Halton D.W., Curry W.J., Thim L.;
"RYIRFamide: a turbellarian FMRFamide-related peptide (FaRP).";
Regul. Pept. 50:37-43(1994).
-:- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
                                                                                                                                                                                                       Submitted (AUG-1998) to the SWISS-PROT data bank.
                                                                                                                                                                                                                                       PROTEIN SYNTHESIS.
                                                                                                                                    TISSUE-Liver;
Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X.,
Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.6%; Score 16; DB 1; Length 5; llarity 50.0%; Pred. No. 1e+05; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 10 AA; 1186 MW; 07121E3B45BDC2DB CRC64;
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69D4004B44600000 CRC64;
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1; Mismatches 0;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
FMRFAAIDE-LIKE NENROPEPTIDE RYIRF-AMIDE.
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 ACIDIC RIBOSOMAL PROTEIN P2 (FRAGMENT).
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5.AA; 754 MW;
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Best Local Similarity
Thes 3; Conserve
                                 Mus musculus (Mouse)
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Best Local Similarity
Matches 2; Conserv
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P41853;
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1 MRYV
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| RYIR
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ID RS1_ER
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Oestroidea; Calliphoridae; Calliphora.
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                  Pallini V.;
Submitted (SEP-1994) to the SWISS-PROT data bank.
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 6.44, ITS MW IS: 38.6 KDA.
                                                                                                    Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
Comanducci M., Christianen G., Birkelund S., Vtretou E., Ratti G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I., Rehfeld J.F., Thorpe A.; "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2 neuropeptides (designated calliFMRFamides) from the blowfly Calliphora vomitoria,", Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
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Pred. No. 2.3e+03;
3; Mismatches 0; Indels
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Pred. No. 1e+05;
2; Mismatches 1; Indels
                                                                                                                                                                                                                        SEQUENCE 10 AA; 1243 MW; DAD39A33304B5339 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OR S OR A.
29D00699CAB40457 CRC64;
Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
CALLIFMRFAMIDE 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLA2_MOUSE STANDARD; PRT; 10 AA. 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 AA.
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MEDLINE-92196111; PubMed-1549595;
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40.0%;
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Best Local Similarity 50.0%;
Matches 3; Conservative
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Best Local Similarity 40.0%
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                                                                                  STRAIN-L2/434/BU;
                                   NCBI_TaxID=813;
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4 RDFMRF 9
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4 KYIKK 8
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P41865;
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RLA2_MOUSE
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P31890;
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P81820;
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       PROSITE;
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                              Hormone;
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Gray W.R., Olivera B.M.;
                                                                                                                                                                                                                                                                                               Submitted (AUG-1993) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: BINDS MRNA: THUS FACILITATING RECOGNITION OF THE INITIATION POINT. IT IS NEEDED TO TRANSLATE MRNA WITH A SHORT SHINE-DALGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE SIP FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Invertebrate vasopressin/oxytocin homologs. Characterization of peptides from Conus geographus and Conus straitus venoms."; J. Biol. Chem. 262:15821-15824(1987).
                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Pectobacterium.
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Gray W.R., Olivera B.M., Cruz L.J.;
Peptide toxins from venomous Conus snails.";
Annu. Rev. Biochem. 57:665-700(1988).
-!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
PIR; A28495; A28495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYS-CONOPRESIN G.
Conus geographus (Geography cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidea; Conius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.6%; Score 16; DB 1; Length 8; 100.0%; Pred. No. 1e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 AA; 837 MW; 9E18733DC5B339CD CRC64;
  OCT-1994 (Rel. 30, Created)
(Rel. 30, Last sequence update)
(OV-1995 (Rel. 32, Last annotation update)
RIBOSOMAL PROTEIN SI (FRAGMENT).
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01-NOV-1988 (Rel. 09, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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PIR; S37141; S37141.
Ribosomal protein; Repeat; RNA-binding.
                                                                                                                                                                                                                                                                              Toussaint A., Faelen M.;
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Best Local Similarity
                                                                                                                    Erwinia chrysanthemi
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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01-OCT-1994 (
01-OCT-1994 (
01-NOV-1995 (
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COWden C., Stretton A.O.W.;
"AF2, an Ascaris neuropeptide: isolation, sequence, and bioactivity.";
Peptides 14:423-430(1993).
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                           AMIDATION.
D4FC276EB4540059 CRC64;
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69D4073B5B11E350 CRC64;
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Pred. No. 1e+05;
0; Mismatches
                                                                                  Score 16; DB 1;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CARCINUSTATIN 17.
                                                                                                Pred. No. 1e+05;
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Last annotation update)
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01-JUL-1993 (Rel. 26, Last seq
01-FEB-1996 (Rel. 33, Last ann
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57.1%;
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9 AA; 1037 MW;
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Best Local Similarity 75...
                                                                                                               4; Conservative
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Amidation.
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Best Local Similarity
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-!- FUNCTION: DEVOID OF OXYTOCIC ACTIVITY.
-!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bufo regularis (African toad).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Bufonoidea, Bufonidae,
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                                                                                                                                                               Isolation and identification of multiple neuropeptides of the
                                                                                                                                                                             allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Biochem. 250:727-734(1997).
-!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide; Amidation; Multigene family.
MOD_RES.
9 AMIDATION.
                                                                                     TISSUE=Cerebral ganglion, and Thoracic ganglion,
MEDIINE=98121193; PubMed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpe A.;
       Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
NCBI_TaxID=6759;
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17FF476EA5A6D04B CRC64;
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                                                                                                                                                                                                                                                                                                                                       20.3%; Score 15; DB 1; 66.7%; Pred. No. 1e+05;
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Pred. No. 1e+05;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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66.7%;
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Best Local Similarity 66.7
Matches 2; Conservative
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Best Local Similarity
Matches 2; Conserv
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ID OXYT_CYPCA
AC P23879;
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SEQUENCE
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"Eight novel FMRFamide-like neuropeptides isolated from the nematode Ascaris suum.";
Peptides 16:491-500(1995).
-: SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascariddidea; Ascaridoidea;
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                                                                                     TISSUE-Cerebral ganglion, and Thoracic ganglion;
MEDLINE-98121193; PubMed-9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
NCBL_TaxID=6759;
                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
                                                                                                                                                                                                                                             Neuropeptide; Amidation; Multigene family.
MOD_RES 8 8 AMIDATION (POTENTIAL).
SEQUENCE 8 AA; 858 MW; C82879D5AB46D865 CRC64;
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9CD40059D417687D CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-EBB-1996 (Rel. 33, Last annotation update)
FMRFAMIDE-LIKE NEUROPEPTIDE AF7.
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66.7%;
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Best Local Similarity 66.7
Matches 2; Conservative
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NCBI_TaxID=6253;
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Best Local Similarity
Matches 2; Conserv
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2 GQY 4
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MEDLINE=71232719; PubMed=5406007;
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2 YIQ 4
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P43000;
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OXYV_SQUAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OXYTOCIN (OCTTOCIN).

OYYTOCIN (OCTTOCIN).

OYYCCIA (Sabit), Hippopotamus amphibius (Hippopotamus),

Balaenoptera physalus (Finback whale) (Common rorqual),

Tachyglossus aculeatus aculeatus (Australian echidna), and

Hydrolagus colliei (Spotted raffish) (Pacific raffish).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                       Cyprinus carpio (Common carp), and Petromyzon marinus (Sea lamprey). Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cypriniae; Cyprinidae; Cypriniae; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES—P. marinus; TISSUE—Pituitary;

K MEDLINE=88225976; PubMed=3371648;

Lane T.F., Sower S.A., Kawauchi H.;

T "Arginine vasotocin from the pituitary gland of the lamprey (Gen. Comp. Endocrinol. 70:152-157(1988).

C -!- FUNCTION: ANTIDIURETIC HORMONE.
-!- FUNCTION: ANTIDIURETIC HORMONE.
-!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

R PIR; 861364; B61364.

R PIR; S06375; S06375.
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MEDLINE=72215060; PubMed=5150741;
Chauvet J., Chauvet M.-T., Acher R.;
"Evolution of neurohypophyseal hormones: isolation of active
Principles from rabbits and rats.";
Biochimie 53:1099-1104(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 15; DB 1; Length 9;
Pred. No. 1e+05;
1; Mismatches 0; Indels
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01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Comp. Biochem. Physiol. 14:245-254(1965).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00220; hormone4; 1.
PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
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66.7%;
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Best Local Similarity
'hes 2; Conservē
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SPECIES=H.amphibius;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amidation.
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2 YIQ 4
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                                                                                                                          VASOTOCIN.
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OXYT_RABIT
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elasmobranch fish, Hydrolagus collei.";
J. Endocrinol. 45:597-606(1969).
-!- FUNCTION: OXYTOCIN CAUSES CONTRACTION OF THE SMOOTH MUSCLE OF THE
UTERUS AND OF THE MAMMARY GLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE.
MEDLINE=73031727; PubMed=5083097;
Acher R., Chauvet J., Chauvet M.-T.;
"Phylogeny of the neurohypophysial hormones. Two new active peptides isolated from a cartilaginous fish, Squalus acanthias.";
Eur. J. Blochem. 29:12-19(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Squalus acanthias (Spiny dogfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Squaloidei; Squalidae; Squalus.
NCBI_TaxID=7797;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Oxytocin as a neurophyophysial hormone in the holocephalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
PIR, A91466; A91466.
PIR, A92174, A921774.
PIR, A93147, A93147.
PIR, B9667; B9067.
PIR, B9667; B9067.
PDB; IXY1; 15-0CT-90.
                                                                                                                                                                                                                                                                                      MEDLINE-73223515; PubMed-4515919;
Acher R., Chauvet J., Chauvet M.-T.;
"Neurohypophysial hormones and evolution of tetrapods.";
Nature New Biol. 244:124-126(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                      Acher R., Chauvet J., Chauvet M.-T.;
"Isolation of finback whale oxytocin and vasopressin.";
Nature 201:191-192(1964).
Ferguson D.R., Pickering B.T.; "Arginine and lysine vasopressins in the hippopotamus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 9 AMIDATION.
9 AA; 1010 MW; 17F8376EB456D04B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 15; DB 1;
Pred. No. 1e+05;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS00264; NEUROHYPOPHYS_HORM; 1
                                                                Comp. Endocrinol. 13:425-429(1969)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR000981; Neurhypophys_horm.
                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=H.colliei;
MEDLINE=70088110; PubMed=5366118;
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66.7%;
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                                                                                                                                                                                                                                                                   SPECIES=A.aculeatus;
                                                                                                                                 SPECIES=B.physalus;
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Best Local Similarity
                                         neurohypophysis
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                                   MEDILINE=72128038; PubMed=4622083; Acher R., Chauvet J., Chauvet M.-T., Fontaine M.; Acher R., Chauvet J., Chauvet M.-T., Fontaine M.; Acher R., Chauvet J., Chauvet M.-T., Fontaine M.; Acher B., Chauvet J., Chauvet M.-T., Fontaine M.; Acher Spino of 2 new neurohypophyseal hormones, valitocin (val8-oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the spiny dog-fish (Squalus acanthias)...; C. R. Acad. Sci., D., Sci., Nat. 274:313-316(1972).

-I- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY. InterPro: IPR000981: Neurhypophys_horm.

PROSITE: PS00220; hormone4; 1.

PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.

BISULFID 1.
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20.3%; Score 15; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels

        MOD_RES
        9
        AMIDATION.

        SEQUENCE
        9 AA;
        996 MW;
        17EDD76EB456D04B CRC64;

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2 YIQ 4
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Search completed: February 21, 2002, 17:00:08 Job time: 181 sec

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GenCore version 4.5

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OM protein - protein search, using sw model

Run on: February 21, 2002, 16:56:52; Search time 22.09 Seconds

(without alignments)

86.081 Million cell updates/sec
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(without alignments)

Title:
Perfect score: 74
Sequence: 1 CRDGIRVVQKGEY 13
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 1983

Minimum DB seq length: 0 Maximum DB seq length: 13 Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database: SPTREMBL\_17:\*

1: Sp\_archea:\*
2: sp\_barchia:\*
3: Sp\_fungi:\*
4: Sp\_human:\*
5: Sp\_inwerterate:\*
6: Sp\_nammal:\*
7: Sp\_nnc:\*
8: Sp\_organelle:\*
9: Sp\_nhc:\*
10: Sp\_phage:\*
10: Sp\_phage:\*
11: Sp\_ordanelle:\*
12: Sp\_virus:\*
13: Sp\_virus:\*
14: Sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ			COLUMNICO	•
Result		Query				
NO.	Score	Match	Match Length DB	- BB	ID	Description
1	21	28.4	6	7	Q9R7H9	Q9r7h9 haemophilus
7	21	28.4	12	7	Q50959	Q50959 neisseria q
٣	19	25.7	13	4	016141	Q16141 homo sapien
4	18	24.3	10	9	Q9TR48	09tr48 bos taurus
2	18	24.3	12	æ	Q9T2U3	Q9t2u3 bos taurus
9	18	24.3	13	7	Q9RF24	Q9rfz4 mycoplasma
7	17	23.0	8	9	Q9BF92	
80	17	23.0	6	9	Q9XT05	
6	17	23.0	12	4	Q9UMR0	Q9umr0 homo sapien
10	17	23.0	12	12	Q9IF00	Q9if00 human adeno
11	17	23.0	12	12	Q91EZ9	Q9iez9 human adeno
12	17	23.0	13	9	Q9TU76	Q9tu76 ovis aries
13	17	23.0	13	œ	Q9MQK6	O9mqk6 rupicapra r
14	17	23.0	13	11	Ø9C006	Ogcu06 mus musculu
15	16	21.6	80	9	Q9BFC3	Q9bfc3 didelphis m
. 16	16	21.6	æ	9	Q9BFC2	Q9bfc2 macropus eu
17	16	21.6	80	9	Q9BFC1	Q9bfc1 choloepus h
18	16	21.6	80	9	Q9BFC0	Q9bfc0 choloepus d
19	16	21.6	80	9	Q9BFB9 .	Q9bfb9 euphractus

09bfb8 chaetophrac 09bfb7 tamandua te 09bfb6 myrmecophag 09bfb6 myrmecophag 09bfb4 talpa altal 09bfb3 condylura c 09bfb1 condylura c 09bfb1 echinops te 09bfb1 cchinops te 09bfb0 trichechus 09bfa9 procavia ca	, , , , , , , , , , , , , , , , , , , ,
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## ALIGNMENTS

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	late) ipdate)	subdivision; Pasteurellaceae;	MEDLINE-98083063; PubMed-9422600; MEDLINE-98083063; PubMed-9422600; Martin K., Morlin G., Smith A., Nordyke A., Eisenstark A., "The tryptophanase gene cluster of Haemophilus influenzae evidence for horizontal gene transfer."; J. Bacteriol. 180:107-118(1998). J. Bacteriol. 322; AAB96582.1;	CRC64; Length 9;	2; Indels	nate) podate)
9 AA.	ed) sequence update) annotation update)	vision;	A., phil	B4412D7 CR ; DB 2; 4 70+05:	O	; 12 AA. ed) sequence update) annotation update)
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RESULT 1 Q9R7H9 ID Q9R7H9	01-M 01-M	NLPD. Haemc Bacte Haemc NCBI	SEQU MEDL Mart "The evid J. BE EMBL	SEQUENCE SEQUENCE Query Match	Matches 3	30L)
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MEDLINE=96029671; PubMed=7592757;
Hori O., Brett J., Slattery T., Cao R., Zhang J., Chen J.X.,
Hori O., Brett J., Slattery T., Cao R., Zhang J., Chen J.X.,
Hori O., Brett J., Slattery T., Cao R., Zhang J., Chen J.X.,
Magashima M., Luddh E.R., Vijay S., Nitecki D.;
The receptor for advanced glycation end products (RAGE) is a cellular
binding site for amphoterin. Mediation of neurite outgrowth and co-
expression of rage and amphoterin in the developing nervous system.";
J. Biol. Chem. 270:25752-25761(1995).
HSSP, PO7155; 1HME.
SEQUENCE 10 AA; 1050 MW; 23BB9A286761EB18 CRC64;
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"The amino acid sequence of the 9 kDa polypeptide and partial amino acid sequence of the 20 kDa polypeptide of mitochondrial NADH-ubiquinone oxidoreductase.";
J. Blochem. 110:575-582(1991).
SEQUENCE 12 AA; 1335 MW; CC9702EC3C233DC2 CRC64;
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
NADH:UBIQUINONE OXIDOREDUCTASE (COMPLEX I) IRON-SULFUR PROTEIN
FRACTION 20 KDA POLYPEPTIDE PEPTIDE T-8.
Bos taurus (Bovine).
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Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 1.5 KDA PROTEIN (FRAGMENT).
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7.4e+03;
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Pred. No.-9.1e+03;
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75.0%;
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Best Local Similarity 75.0
Matches 3; Conservative
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Best Local Similarity
Local 3; Conserve
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NCBI_TaxID=40477;
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EMBU, X13965; CAB37342.1; -.
                Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseria.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
AMPHOTERIN (FRAGMENT).
Bos taurus (Bovine).
Bos taurus (Bovine).
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=94220089; PubMed=7545922;
Sadakane Y., Maeda K., Kuroda Y., Hori K.;
"Identification of mutations in DNA polymerase beta mRNAs from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Pred. No. 6.7e+03;
1; Mismatches 6; Indels
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EMBL: S69873; AAD14051.1; -.
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Pred. No. 2.8e+03;
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MEDLINE-89210824; Pubmed=2854063;
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75.0%;
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Best Local Similarity 36.4
Matches 4; Conservative
OPAEl PROTEIN (FRAGMENT).
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01-NOV-1996 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
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Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
NCBI_TaxID=9320;
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EMBL; AY011670; AAG47581.1; -.
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MEDLINES-99282512; PubMed-10353914;
MEDLINES-99282512; PubMed-10353914;
Shintani S., O'Huigin C., Toyosawa S., Michalova V., Klein J.;
"Origin of gene overlap: the case of TCP1 and ACAT2.";
Genetics 152:743-754 (1999).
EMBL: AF143499; AAD34976.1; -.
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MEDLINES-21082082; PubMed=11214319;
Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
O'Brien S.J.;
                                                                                                                                                                                                      Length 13
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                               of a putative membrane protein gene.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF162998; AAF15253.1; -.
Hyporteical protein.
NON_TER 1 1 1
SEQUENCE 13 AA; 1505 MW; 0B79431F5635573B CRC64;
                                                                                                                                                                                                                                            2; Indels
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CAMP RESPONSIVE ELEMENT MODERATOR (FRAGMENT).
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
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Pred. No. 1e+04;
1; Mismatches
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Hayashi S., Gillam I.C., McDonald T., Way D., Harris T.,
Sedgwick E.G.;
"ElA DNA of group C adenovirus integrates into human chromosomes.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF288220; AAF91488.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human adenovirus type 5.
Viruses; dSDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=28285;
                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Pred. No. 1.3e+04;
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Pred. No. 1.3e+04;
3; Mismatches 0; Indels
                                      Indels
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Tillmann H., Eschrich K.;
"Structure of human FBP2 gene.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ238483; CAB53359.1; -.
HSSP; P00636; IFRP.
 Length 9;
                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
(EC 3.1.3.11) (FRAGMENT)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
EIA NUCLEOPROTEIN (FRAGMENT).
Score 17; DB 6; L6
Pred. No. 4.7e+05;
1; Mismatches 0;
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12 AA; 1337 MW;
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                                        Conservative
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MEDLINE=99397042; PubMed=10467711;
Maddox J.F., Hawken R.J., Matthew P., Davies K.P.;
"Single strand conformational polymorphisms (SSCPs) in the ovine ILIA and ILG genes.";
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                                                                                                                                                                                    SEQUENCE FROM N.A.
Hayashi S., Gillam I.C., McDonald T., Way D., Harris T.,
Sedgwick E.G.;
Sudwirk B.G.;
Submitted (Jul. 2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF288641; AAF91494.1;
                                                                                                                                               Human adenovirus type 5.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
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Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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Last annotation update)
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1; Mismatches
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01-0CT-2000 (TrEMBLrel. 15, Last ann
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EMBL; AF117652; AAD25050.1; -.
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12 AA; 1337 MW;
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Matches 2; Conserv
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Matches 3; Conserv
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Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Yamanaka I., A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Relischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Nasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-PERIPPERAL BLOOD;
MEDLINE-20104876; PubMed=10641890;
Saulle E., Di Pasquale S., Tartaglia M.;
Saulle E., Di Pasquale S., Tartaglia M.;
Rapid communication nucleotide sequence of chamois, alpine ibex, and red deer tRNA(Lys) and ATPase8 mitochondrial genes.";
J. Anim. Sci. 77:3398-3399(1999).
Mitochondrion.
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                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Rupicapra.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
200A PELLOCIDA BINDING PROTEIN (FRAGMRT).
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Pred. No. 1.5e+04;
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MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                        Rupicapra rupicapra (Chamois).
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Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AK018876; BAB31470.1; -
MCD; MCI:1855701; Zpb.
SEQUENCE 13 AA; 1404 MW; D6A422099576B42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                              09BEC3;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CAMP RESPONSIVE ELEMENT MODERATOR (FRACMENT).
Didelphis marsupialis virginiana (North American opossum).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
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MEDLINE=21082082; PubMed=11214319;
Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
O'Brien S.J.;
"Molecular phylogenetics and the origins of placental mammals.";
Nature 409:614-618(2001).
Nature 409:614-618(2001).
NATURE 1.
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23.0%; Score 17; DB 11; Length 13;
Best Local Similarity 30.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 2; Mismatches 5; Indels
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Best Local Similarity 50.0
Matches 3; Conservative
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Immunogen; HLA; human leukocyte antigen; binding motif; antiviral; MHC; major histocompatability complex; viral infection; anticancer, prostate cancer; lymphoma; hepatitis; AIDS; diagnostic; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide which specifically binds selected MHC allele - used to induce an immune response for treatment or prevention of viral infection or cancer, or for diagnosis
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                                                                                                                                                                                                                 AAW97448
AAY38357
            AAW13796
AAP70356
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AAR66971
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AAY93853
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  WPI; 1994-065403/08.
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Homo sapiens
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07-AUG-1992;
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 AAY38367;
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 RESULT
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Immunogenic peptid
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Vpr/Vpx motif-deri
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Alpha5/beta1 integ
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Membrane dipeptida
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Aspergillus tubige
Human complementar
                                                                                                (without alignments)
40.665 Million cell updates/sec
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                                                                                     February 21, 2002, 16:53:32; search time 23.68 Seconds
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Copyright (c) 1993 - 2000 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
                                                              protein search, using sw model
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AAY48805
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score greater than or equal to
and is derived by analysis of
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Anti-2-phenylozazo Peptide that is us PAP-derived HLA-bi Histogranin deriva Immunogenic peptid HLA Al binding TAD Mutant leukocyte i Immunomodulatory p PAP-derived HLA-bi

Saccharomyces cere Saccharomyces cere

Histogranin deriva

anticancer;

Score

Result Ş. 11098765432

Polyclonal anti-HB Immunogenic peptid Immunogenic peptid Human ADAMTS-1 pep Arabidopsis thalia

Histogranin deriva

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commaily induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intext foreign antigen itself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful the rapeutically and for immunisation as above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes peptides that selectively home to a tissue or organ. The peptides can be used for identifying an organ or tissue, for identifying a target molecule expressed by an organ or tissue or for treating an organ or tissue pathology, where the organ or tissue is selected from prostate, lung, skin, retina, pancreas, gut, ovary, adrenal gland, liver, and lymph node. The peptide bind to the membrane dipeptidase (MDP). AAY48618 to AAX49066 represent sequences
Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptides which selectively home to organs or tissues, used for, e.g. identifying target ligands and for therapy of pathological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP; prostate; ovary; lymph node; adrenal gland; liver; gut; tumour; membrane dipeptidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 31; DB 20; Length 9;
Pred. No. 4.3e+05;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Membrane dipeptidase-binding skin homing peptide #21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.98;
71.48;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma; vaccine; immunisation.
                                                            The sequence is a specific example of a group of new immunogenic peptides having an HLA-A3.2 HLA-A1, HLA-A11 or HLA-A24.1 binding motif. For example, the peptides having an HLA-A3.2 binding motif each have 9-10 residues and contain, from the N-terminus to the C-terminus, (a) a first conserved residue selected from L, M, I, V, S, A, T, F, C, G, D and E and (b) a second conserved residue of K, R, Y, H or F, where the first and second conserved residues are separated by 6-7 residues. The peptides are capable of binding selected MHC molecules and inducing an immune response. They can be used to treat and/or prevent viral infection and cancer, e.g. prostate cancer, lymphoma, hepatitis or AIDS. They can also be used to produce antibodies for use as diagnostic or therapeutic agents. The peptides can also be used as diagnostic spents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 31; DB 15; Length 9;
Pred. No. 4.3e+05;
1; Mismatches 1; Indels
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                      Disclosure; Page 114; 150pp; English.
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71.48;
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Best Local Similarity 71.4°,
'-hos 5; Conservative
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AAB11009 standard; peptide; 13
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                                                          08-FEB-2001
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                                                                                                           TNF-alpha;
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                                       AAB11009;
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                                                                                                                                                                                                                                  Motif; Vpr; Vpx; human immunodeficiency virus; HIV; virion-associated; infection; penetration; uncoating; conserved; primate; lentivirus; antagonist; anti-proliferative; eukaryotic cell; cancer; leukaemia;
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                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vpr and Vpx proteins of HIV, and derived peptide(s) - useful as antagonists for the treatment of HIV, cell proliferative diseases and diseases caused by pathogens
which are used in the exemplification of the present invention.
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                                                                     Indels
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                                                Score 30;
Pred. No. 4
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50.0%;
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nes 5; Conservative
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Best Local Similarity
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ragtryfrrg 12
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                                                                                                                                                                                                                                                                                                                                                                 03-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                           25-MAR-1994;
                                                                                                                                                                                              10-MAY-1996
                                                                                                                                                                                                                                                                                                                           05-0CT-1995
                                                                                                                                                                                                                                                                 psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eukaemia
                                                                                                                                                                                                                                                                                     Synthetic.
                    Sequence
                                                                                                                                                                           AAR81762;
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Matches
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This invention describes a novel immunoadsorber (A) for treating sepsis which comprises a carrier of organic or synthetic polymer having bound to it poly- or monoclonal antibodies (Abl) against the complement factors (3a and/or C5a and against lippolysaccharide (LPS). Optionally other antibodies (Ab2) directed against other mediators of sepsis are also attached to the carrier. The products of the invention have anti-inflammatory and antisepsis activity. (A) are used for treatment, particularly by plasmapheresis, of sepsis and septic shock. The combination of antibodies used can be tailored to the requirements of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                 ; antigen; C3a; C5a; IL10; IL1-alpha; IL1-beta; IL6; immunoadsorber; treatment; sepsis; complement factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       support
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                         anti-inflammatory; antisepsis; plasmapheresis; septic shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 27; DB 21; Length 13
Pred. No. 1.7e+02;
!; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoadsorber for treating sepsis, comprises polymeric carrying antibodies specific for complement factors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Η;
Immunogenic peptide #1 for raising human C3a antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wagner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Meyer U, Kruschke P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           integrin binding peptide #13.
                                                                                                                                                                                                                                                                                                                                                                                                                                   (PRIV-) PRIVATES INST BIOSERV GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR79083 standard; peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Page 4; 8pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.5%;
66.7%;
                                                                                                                                                                                                                                                                                                                            99DE-1013707.
                                                                                                                                                                                                                                                                                                                                                                              99DE-1013707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heinrich H, Hahn H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-648176/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         individual patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lipopolysaccharide
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Best Local Similarity
Matches 4; Conserv
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98US-0094291.
98US-0103514.
                      99WO-US16596
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 AA;
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2 irvlqkgk 9
                      22-JUL-1999;
                                                                                                       10-MAY-1999;
19-MAY-1999;
                                                             27-JUL-1998
                                                                                     08-OCT-1998
                                                                                                                                                                                                                 Sidhu SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY48795;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      integrin binding peptides which bind to various integrins. Peptides which bind to various integrins. Peptides which bind to alphay/betas and alphay betas hard bind to alphay/betas and alphay betas integrins contain the motif given in AAR76187. Alphay/betas integrins are also bound by RGD containing peptides. These peptides assume a conformationally stabilised configuration which is due to the formation of a disulphide bond, a peptide bond or a lactam bond. These peptides may be used for isolating the complementary integrin from a sample mixture by contacting them under ionic conditions to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phage display; bacteriophage M13; fusion protein; major coat protein; protein VIII; phagemid vector; electroporation; combinatorial library; protein III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequences given in AAR76185-200 and AAR79073-94 are high affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 allow binding of the integrin to the peptide and then separating the integrin from the peptide. They can be used for attaching cells to a substrate, by binding them to the substrate with the cell. The peptides promote wound healing when applied locally and inhibit the metachment of osteoclasts to bone. They inhibit angiogenesis, metastasis of tumours and migration of smooth muscle cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                   High affinity integrin binding peptides - can be used to attach cells to a substrate, inhibit the attachment of osteoclasts to bone, promote wound healing, inhibit angiogenesis, metastasis of tumours and migration of smooth muscle cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.1%; Score 26; DB 16; L. 100.0%; Pred. No. 4.3e+05; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Linker g3-2 peptide, SEQ ID NO:136.
                                                                                                                                                                                                                                                        (LJOL-) LA JOLLA CANCER RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 9; Page 34; 86pp; English.
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                                                                                                                                                                                           94US-0286861.
93US-0158001.
                                                                                                                                                 94WO-US13542
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                                                                                                                                                                                                                                                                                                  Koivunen E, Ruoslahti E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                            WPI; 1995-206899/27.
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 AA;
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                                                             W09514714-A1.
                                                                                                                                                 22-NOV-1994;
                                                                                                                                                                                           04-AUG-1994;
                                                                                                                                                                                                              24-NOV-1993;
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| crdg 4
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                                                                                                       01-JUN-1995
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                      Synthetic.
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AAY81289
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0 X X O X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D 
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The invention relates to novel fusion proteins comprising a heterologous polypeptide fused to a variant (non-wild type) bacteriophage

CC major coat protein (protein VIII). The invention also relates to replicable expression vectors which contain a gene encoding the fusion protein; host cells containing the expression vectors; phages which contains the fusion protein on their surface; phage libraries displaying a plurality of different fusion proteins on viral surfaces; and methods of using these compositions. The fusion proteins for the major coat proteins can be used to alter the number of fusion proteins the invention are well to tolerated in phage display systems. Variants of the major coat proteins can be used to alter the number of fusion proteins incorporated into a virus particle. Hyper-functional variants can be used to increase the number of fusion proteins incorporated into a virus particle. Onversely, hypo-functional variants can be used to decrease the number of fusion proteins into virus particles to achieve a desired level of fusion proteins into virus particles to achieve a desired level of the transformation of cells by highly purifying DNA. The present concentration of cells by highly purifying DNA. The present invention uses affinity DNA purification to reduce ionic impurities and thus radvantageous in electroporation methods for increasing the concentration of DNA present. The increase in DNA entering the prior concentration of small library size using recombinant DNA. Sequences at throblem of small library size using recombinant DNA prior or at problem of small library size using recombinant DNA. The present or at problem of small library size using recombinant DNA prior or at problem of small library size using recombinant DNA present.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusion proteins comprising a heterologous protein and a viral variant major coat protein useful in phage display systems for improving transformation efficiency .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                display of a peptide fused to the C-terminal end of protein VIII (AAY81279-Y81283) or protein III (AAY81288-Y81290).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Membrane dipeptidase-binding skin homing peptide #11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 26; Page 85; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY48795 standard; Peptide; 13 AA.
99US-0133296
99US-0134870
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                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                          Weiss GA,
                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-183122/16.
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Huang KS;

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extracellular supernatant of rat peritoneal exudate cells. For tryptic fragment T17 (a) see AAR07929. The protein was isolated and sequenced to produce oligonucleotide probes in order to identify human lipocortin and N-lipocortin. See also AAQ05805-25, AAQ06581, AAR07926-37 and AAR07956-66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the culture filtrate of Aspergillus tuning. Probes (see AAX00982-87) based on residues 4-10 of the peptide were used to screen a DNA library prepared from Aspergillus higer DS16813 (now renamed Aspergillus tubigensis CBS 331-90) to isolate a xlnA gene (see AAX00973) encoding a new endoxylanase A (see AAW95553). The endoxylanase shows optimum activity at pH 3.5-5.5, making it useful for industrial processes requiring lower pH, such as lagering of beer, and can also be used in baking, preparation of animal feedstuff, lignin removal from Kraft mill pulp, and in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is an N-terminal peptide of a 25 kDa xylanase isolated from

    useful in the preparation of bread,

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Endoxylanase A; XlnA; xylanase; brewing; baking; pulp; paper; lignin removal; delignification.
                                                                                                                                                                                                                   Rat phospholipase A2 inhibitor protein was isolated from the
                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                          - useful for reducing
                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                       Schindler DG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aspergillus tubigensis xylanase N-terminal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                 Score 25; DB 11;
Pred. No. 4.3e+05;
2; Mismatches 0;
                                                                                                                                            inflammation or for treating arthritis, etc.
                                                       Garwin JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              animal foods, and in paper products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1.2; Fig 3; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW95554 standard; Peptide; 10 AA.
                                                                                                                          Pure fragment of human lipocortin
                                                                                                                                                                                Disclosure; Fig 2; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     5:
                                                                                                                                                                                                                                                                                                                                                                                                   33.8%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                     Wallner BP, Pepinsky RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KONN ) GIST-BROCADES NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New fungal xylanase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aspergillus tubigensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-083582/08.
                                                                                         WPI; 1990-274549/36
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
                    (BIOJ ) BIOGEN NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 YVQKGE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 fvqkgq 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JUL-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW95554;
                                                                                                                                                                                                                                                                                                                                               Sequence
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   P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes peptides that selectively home to a tissue or organ. The peptides can be used for identifying an organ or tissue, for identifying a target molecule expressed by an organ or tissue or for treating an organ or tissue pathology, where the organ or tissue is selected from prostate, lung, skin, retina, pancreas, gut, ovary, adrenal gland, liver, and lymph node. The peptide bind to the membrane dipeptidase (MDP). AAY48618 to AAY49066 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                              to organs or tissues, used for, for therapy of pathological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human N-lipocortin; placenta; inflammation reduction; arthritis; rat phospholipase A2 inhibitor; tryptic fragment T17 (b).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tryptic fragment T17 (b) of rat phospholipase A2 inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 26; DB 20;
Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                        Ruoslahti EI;
                                                                                                                                                                                                                                                                                                                                                          New peptides which selectively home e.g. identifying target ligands and
                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 6; Page 148; 193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR07967 standard; protein; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.1%;
50.0%;
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85US-0772892.
85US-0765877.
85US-0712376.
85US-0690146.
                                                                                                                                                           99WO-US05284
                                                                                                                                                                                             98US-0042107
99US-0042107
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                                                                                                                                                                                                                                                                                      Rajotte D, Pasqualini R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                   (BURN-) BURNHAM INST.
membrane dipeptidase.
                                                                                                                                                                                                                                                                                                                       WPI; 1999-571717/48
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Best Local Similarity
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                               Synthetic.
Homo sapiens.
                                                                                       WO9946284-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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15-MAR-1985;
10-JAN-1985;
                                                                                                                                                         10-MAR-1999;
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                                                                                                                                                                                               13-MAR-1998;
                                                                                                                        16-SEP-1999.
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Matches

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AAR07967

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13-DEC-2000; 2000WO-GB04776
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                                                                                                                                        99GB-0029464
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Best Local Similarity 80.0
امر 4; Conservative
                                                                                                                                                                            Roberts GW, Heal JR;
                                                                                                                                                          (PROT-) PROTEOM LTD.
                                                                                                                                                                                             WPI; 2001-408419/43.
                                                                                                                                                                                                                                                                                                                                             10 AA;
                                                                                  WO200142277-A2.
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Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                            9 QKGEY 13
                                                                                                                                        13-DEC-1999;
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                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9708304-A2
         18-SEP-2001
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                                                                                                    14-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                        A set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of the human genome, useful in an assay for screening and identifying of one or more novel peptides which are drug candidates or pro-drugs -
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a set of complementary peptide ligands generated from the human genome. The complementary peptides interact with their relevant target proteins encoded in the human genome. They can be used as reagents in drug discovery and as lead ligands to facilitate drug design and development. The present sequence is a complementary peptide provided in the specification.
                                                                                                                                                                                                                        Human; complementary peptide; ligand; drug discovery; drug design.
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                                             Length 10;
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                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 25; DB 22; L
Pred. No. 2.9e+02;
1; Mismatches 5;
                                           Score 25; DB 20;
Pred. No. 2.9e+02;
0; Mismatches 1
preparation of paper products (all claimed).
                                                                                                                                                                                                      SEQ ID NO: 617.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Page 128; 646pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG96391 standard; Peptide; 10 AA.
                                                                                                                                                AAG94423 standard; Peptide; 10 AA.
                                                                                                                                                                                                      Human complementary peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.8%;
                                            33.8%;
83.3%;
                                                                                                                                                                                                                                                                                               13-DEC-2000; 2000WO-GB04776
                                                                                                                                                                                                                                                                                                                  99GB-0029464
                                                                                                                                                                                    (first entry)
                                                               5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
                                                                                                                                                                                                                                                                                                                                                       Heal JR;
                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-408419/43.
                                                                                                                                                                                                                                                                                                                                     (PROT-) PROTEOM LTD
                                            Query Match
Best Local Similarity
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Matches 4; Conserv
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| glnyctsgay 10
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                   AA;
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                                                                                                                                                                                                                                                            WO200142277-A2
                  10
                                                                                  4 GIRYVQ 9
                                                                                           11 |||
2 gimyvg 7
                                                                                                                                                                                   18-SEP-2001
                                                                                                                                                                                                                                                                                                                                                      Roberts GW,
                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                  13-DEC-1999;
                                                                                                                                                                  AAG94423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG96391;
                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
AAG96391\
                                                                                                                              RESULT 11
                                                               Matches
                                                                                                                                        AAG94423
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A set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of the human genome, useful in an assay for screening and identifying of one or more novel peptides which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a set of complementary peptide ligands generated from the human genome. The complementary peptides interact with their relevant target proteins encoded in the human genome. They can be used as reagents in drug discovery and as lead ligands to facilitate drug design and development. The present sequence is a complementary peptide provided in the specification.
                                                                       Human; complementary peptide; ligand; drug discovery; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 25; DB 22; Length 10;
Pred. No. 2.9e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NS3; protease; HCV; inhibitor; antiviral; virucide
SEQ ID NO: 2585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= OTHER
/note= "OTHER = Ac-Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Page 412; 646pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                drug candidates or pro-drugs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.8%;
80.0%;
Human complementary peptide,
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natural, synthetic or recombinant DNA sources. The new agent causes bone tissues and cartilage to form and/or grow in humans and animals.
                                                                                                                                                                                                                     (first entry)
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                Barker S, Vinson GP;
                                                   Query Match
Best Local Similarity
'-has 4; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-147395/19.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 AA;
                                9 AA;
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dgikriq 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contraception.
                                                                                                     1 CRDGIR 6
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                                                                                                                                                                                                                                                                                                                                                                   27-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                               06-APR-1995
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                                Sequence
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                                                                                                                                                         RESULT 15
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  SSXS
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                                                                                                                                                              A synthetic peptide (AAW13795) corresponds to an N-terminally deleted version of the hepatitis C virus (HCV) polyprotein NS4A,4B junction (see also AAW13771). Unlike other related peptides (AAW13771-86) and depsipeptides (AAW13787-91), this peptide is not suitable as a substrate for assays of HCV NS3 protease activity.
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                   New isolated hepatitis C virus NS3 polypeptide(s) - useful in high-throughput assays for detecting inhibitors which can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A bone morphogenetic agent comprising a peptide displaying osteoinductive activity similar to bone morphogenetic protein (BMP) is new. The peptide may be obtained from any source, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New bone morphogenetic agent comprising osteo-inductive peptide is obtd. by recombinant DNA procedures etc. giving larger amts. for use in humans and animals
                                                    Steinkuehler C;
                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                            Length 12,
                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bone morphogenetic protein; osteoinduction; bone growth;
                                                    Pessi A,
                                                                                                                                                                                                                                                            Score 25; DB 18;
Pred. No. 3.6e+02;
                              (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.
                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         new bone morphogenetic agent.
                                                  De Francesco R, Narjes F,
Tomei L, Urbani A;
                                                                                                                                             Example 3; Page 18; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                           AAP70356 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                            33.8%;
27.3%;
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80US-0174906.
81US-0260726.
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          95IT-RM00573
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                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                         inhibit virus replication
                                                                                                                                                                                                                                                                                 3; Conservative
                                                                                WPI; 1997-179261/16.
                                                                                                                                                                                                                                                                                                     1 CRDGIRYVQKG 11
                                                                                                                                                                                                                                                                                                                   2 cashlpyiegg 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1987-058071/09
                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                             12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cartilage growth.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (REGC ) UNIV
         22-AUG-1995;
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                                                                                                                                                                                                                              Sequence
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                                                  Bianchi |
Taliani |
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AAP70356
ID AAP7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monoclonal antibody; AT1 receptor; subtype; Angiotenisin II receptor; rat vascular smooth muscle; conserved; mammalian AT1 receptor; detection; cancer diagnosis; sperm motility; contraception.
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monoclonal antibodies (MAbs) that bind to the ATI receptor (a subtype of Angiotenisin II receptor) are claimed. The Abs specifically bind to amino acid residues 8 to 17 of the rat vascular smooth muscle ATI receptor. This sequence is conserved in all memmellan ATI receptors so far cloned. The Mabs can be used for detection of ATI receptors, e.g. in cancer diagnosis. They can also be used to study and measure sperm motility and can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Epitope of rat vascular smooth muscle AT1 receptor (residues 8-17).
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Pred. No. 4.4e+02;
2; Mismatches 1; Indels
Score 24; DB 8; Length 9;
Pred. No. 4.3e+05;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibody to AT1 angiotensin receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detection and control of uterine contractions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vasoconstriction e.g. for treating hypertension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (QUEE-) QUEEN MARY & WESTFIELD COLLEGE.
                                                                                                                                                                                                                                                                                                                                               AAR72230 standard; Peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 13; 24pp; English.
                                                             ..
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57.1%;
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Search completed: February 21, 2002, 16:56:47 Job time: 195 sec

Sequence Seq

Sequence Sequence Sequence Sequence

Sequence

Sequence

Sequence Sequence

Sequence

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APPLICANT: Kubo, Ralph T.
APPLICANT: Kubo, Howard M.
APPLICANT: Grey, Howard M.
APPLICANT: Grey, Howard M.
APPLICANT: Greis, Hossandro
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSEE: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
San Francisco
                        US-08-250-789A-27
US-08-372-197-1
US-08-946-225-13
US-08-615-181-69
US-08-160-604-49
US-08-160-604-50
US-08-160-604-51
US-08-160-604-51
US-08-160-604-51
US-08-181-56
US-08-159-339A-944
US-08-159-339A-944
US-08-676-818-16
US-08-96-744-3
US-08-159-339A-944
US-08-159-339A-944
US-08-159-339A-944
US-08-16-801-818-16
US-08-16-801-818-16
US-08-16-801-818-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION 1424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: OF MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                           Sequence 628, Application US/08159339A
Patent No. 6037135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 9411-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             US-08-159-339A-628
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RESULT
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Sequence 186, App
Sequence 186, App
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23.479 Million cell updates/sec
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Sequence 195, App
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 195, A Sequence 28, A Sequence 7, Ap Sequence 8, Ap Sequence 8, Ap Sequence 17, A Sequence 1, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 444,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17,
                                                                                                 February 21, 2002, 16:55:12; Search time 12.46 Seconds
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Sequence 1
Sequence 3
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/FB_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5-09-258-754-186
5-09-042-107-186
5-08-159-339A-928
5-08-867-941-67
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US-08-867-941-67
US-07-768-286B-17
US-07-842-349-3
US-09-258-754-195
US-09-042-107-195
US-09-042-107-195
US-09-041-28
US-09-041-28
US-09-00536-8
US-09-100-536-8
US-09-100-536-8
US-09-101-961-17
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                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .08-836-561-42
.08-883-070-5
                                                                                                                                                                                                                                                                    212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                       Listing first 45 summaries
                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                        Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                         CRDGIRYVQKGEY 13
                                                                                                                                                       US-08-753-851-9
74
1 CRDGIRYVOKGEV 1
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Match
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Maximum DB
                                                                                                                                                                                            Sequence:
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                                                                                                 Run on:
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Result . ⊵ 1 CRDGIRYV

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US-08-159-339A-628

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APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Cells, Esteban
TITLE OF INVENTION: HIA Binding peptides and Their
TITLE OF INVENTION: Uses
                                                                                                                                                                                                                                                                                                                       Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                       STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                Sequence 928, Application US/08159339A Patent No. 6037135 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.2%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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Best Local Similarity
Matches 4; Conser
      5 CADGCRFI 12
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4 CRDTLKY 10
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US-08-159-339A-928
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                                                                                US-08-159-339A-928
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US-08-867-941-67
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                                                                                                                                                                                                                                                                                           APPLICANT: Pasquallin, Renata
APPLICANT: Basquallin, Renata
APPLICANT: Rajotte, Daniel
TITLE OF INVENTION: Membrads of Identifying Lung Homing Molecules Using
TITLE OF INVENTION: Membrane Dipeptidase
FILE REFERENCE: P-LJ 3443
CURRENT APPLICATION NUMBER: US/09/258,754
CURRENT FILING DATE: 1999-02-26
EARLIER APPLICATION NUMBER: 09/042,107
BARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 452
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 186
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rucsiahti, Erkki
APPLICANT: Rucsiahti, Erkki
APPLICANT: Rucsiahti, Renata
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
TITLE OF INVENTION: Tissues
FILE REFERENCE: P-L 2892
CURRENT APPLICATION NUMBER: US/09/042,107
CURRENT FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 436
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 186
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-042-107-186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-258-754-186
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Pred. No. 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
Score 31; DB 3; Length 9; Pred. No. 1.6e+05; 1; Mismatches 1; Indels
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                                                                                                                                                                                                                  Sequence 186, Application US/09258754
Patent No. 6174687
PERERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 186, Application US/09042107 Patent No. 6232287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.5%;
    41.98;
71.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.5%;
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Best Local Similarity 50.0°
  Query Match
Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity 50.0

Matches , 4: Conservative
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5 CADGCRFI 12
                                                                              7 YVQKGEY 13
                                                                                                        2 YFEKGEY 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 29; DB 3;
Pred. No. 20;
MEDICALION ALLE.

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 018623-005030US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                               PRIOR APPLICATION 17.3

PRIOR APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-A02-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 27; DB 1; Length 10;
Pred. No. 47;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAN DEN BROECK, HENRIETTE C.
                                      PCT/AU90/00603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DE GRAAFF, LEENDERT H.
HILLE R., JAN D.
VAN OOYEN J., ALBERT J.
VISSER, JACOB
HARDER, ABRAHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: WORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
                                               FILING DATE: 20-DEC-1990
ATTORNEY/ACENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)885-9300
TELEX: 899149
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/07842349 Patent No. 5358864
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NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (415) 813-5600
(415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 10 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 36.5
Best Local Similarity 44.4
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 494-07
TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 19920427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 IRYVQKGEY 13
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2 MQQIQKGSY 10
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APPLICANT: 1
APPLICANT: APPLICA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-07-768-286B-17
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                                                                                                                        ALTILE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA NUMBER OF SEQUENCES: 67 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,941
FILING DATE: US-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.25
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Pred. No. 42;
3; Mismatches
                                                                                                                                                                                                                                           ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1038-681 MIS: jb
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APPLICANT: RICHARDSON, Michael A.
TITLE OF INVENTION: VARIANTS OF PAI-2
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLBY & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/768,286B
FILING DATE: 19911011
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5444153
Loosmore, Sheena M
Du, Run-Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 103
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 67:
                                                         APPLICANT: Wang, Quijun
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
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Best Local Similarity 50.0
Matches 4; Conservative
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                TRY: Canada
M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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US-08-867-941-67
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STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                    CITY: Toronto
STATE: Ontario
COUNTRY: Canada
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 IRYVQKGE 12
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2 VQYTRKGE 9
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Gaps

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Length 13;

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APPLICANT: Du, Run-Pan
APPLICANT: Wang, Quijun
APPLICANT: Wang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LACTOFERRIN RECEPTOR GENES OF MORAXELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:

ZIP: M5G 1R7

COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,941
FILING DATE: 03-JUN-1997
FILING TATE: 03-JUN-1997
FILING TATE: OF TAT
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   Score 26; DB 4;
Pred. No. 97;
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Pred. No. 1.1e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
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US-09-074-658-28
Sequence 28, Application US/09074658
Patent No. 6184371
GENERAL INFORMATION:
APPLICANT: Run-Pan Du
                                                                                                                                                                                                                                                                                              US-08-867-941-28
; Sequence 28, Application US/08867941
; Patent No. 5977337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael 1
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1036
TELECOMMUNICATION INFORMATION:
35.1%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LOOSMORE, Sheena
APPLICANT: Du, Run-Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.8%;
57.1%;
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APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel I
TITLE OF INVENTION: LACTOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 10 amino acids
                                                             4; Conservative
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Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Ontario COUNTRY: Canada
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Matches 4; Conserv
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                                                                                                                                                                   5 CADGCRLI 12
                                                                                                                       1 CRDGIRYV 8
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1 QYTRKGE 7
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US-08-867-941-28
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                                                                                                                       δλ
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APPLICANT: Ruoslahti, Erkki
APPLICANT: Rajotte, Daniel
TILE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
TITLE OF INVENTION: Methods of IDeptidase
TITLE OF INVENTION: Membrane Dipeptidase
FILE REFERENCE: P-LJ 3443
CURRENT FILING DATE: 1999-02-26
EARLIER APPLICATION NUMBER: 09/042,107
NUMBER OF SEQ ID NOS: 452
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Patent No. 6232287
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
TITLE OF INVENTION: Tissues
FILE REFERENCE: P-LJ 2892
CURRENT FILITION DIMBER: US/09/042,107
CURRENT FILITION DAS: 436
NUMBER OF SEO ID NOS: 436
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-258-754-195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTMER INFORMATION: Description of Artificial Sequence: Synthetic US-09-042-107-195
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0
                                                                                                                                                                               Length 10;
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                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                               Score 26; DB Pred. No. 72; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 195, Application US/09258754
Patent No. 6174687
GENERAL INFORMATION:
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50.0%;
                                                                                                                                                                               35.1%;
83.3%;
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                                                                                                                                                                         Query Match 35.1
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 50.0
Matches 4; Conservative
                              single
   AMINO ACID
                                                       ; TOPOLOGY: linear
US-07-842-349-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 CADGCRLI 12
                              STRANDEDNESS:
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Length 10;

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Each Cys residue is protected at the S by an acetamidomethyl group. The C-terminus is an amide (i.e., than a carboxyl (i.e., -CO-OH).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Dean, Richard T.
APPLICANT: Dean, Richard T.
APPLICANT: Dean, Richard T.
TILE OF INVENTION: Radiolabeled Compounds for Thrombus Imaging;
FILE REFERENCE: 104D2
CURRENT APPLICATION NUMBER: US/09/100,536A
CURRENT FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 08/253,317
EARLIER APPLICATION NUMBER: 08/253,317
EARLIER FILING DATE: 1994-06-03
EARLIER FILING DATE: 1993-04-08
NUMBER OF SEQ ID NOS: 8
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VEr. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 25; DB 1; Length 12;
Pred. No. 1.4e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 25; DB 3; Length 12;
Pred. No. 1.4e+02;
                                                                NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07234/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
      US 07/653,012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-100-536-8; Sequence 8, Application US/09100536A; Patent No. 6022520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (12)
OTHER INFORMATION: acetamidomethyl
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OTHER INFORMATION: acetamidomethy
                                                                                                                                                                                                                                                                                              not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.8%;
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TYPE: PRT
ORGANISM: Artificial Sequence
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80.0%;
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OTHER INFORMATION: AMIDATION
                         FILING DATE: 08-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                        12 amino acids
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Best Local Similarity 80.0
Matches 4; Conservative
        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-08-439-905-7
                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dean, Richard T.
APPLICANT: Lister-James, John
APPLICANT: Civitello, Edgar
APPLICANT: Civitello, Edgar
TITLE OF INVENTION: RADIOLABLED COMPOUNDS FOR THROMBUS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,905
FILING DATE: 12-MAY-1995
                                        ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street CITY: Boston STATE: MA COUNTRY: USA ZIP: 0210-2804 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                    STATE: Ontario
COUNTRY: Canada
ZIP: MAG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/044,825
FILING DATE: 08-APR-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/074,658
FILING DATE: 08-MAY-1998
                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFRAX: (416) 595-1155
TELEFRAX: (416) 595-1155
TELEFRAX: (416) 595-1155
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08439905
Patent No. 5645815
GENERAL INFORMATION:
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57.1%;
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Best Local Similarity 57.10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 10 amino acids
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
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1 QYTRKGE 7
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US-09-074-658-28
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US-08-439-905-7
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C. STREET: 419 Seventh Street, N.W., Suite 300 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Xaa is Ac-Glu"
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                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/IT96/00163
FILING DATE: 20-AuG-1996
PRIOR APPLICATION NUMBER: IT RM95A000573
APPLICATION NUMBER: IT RM95A000573
APPLICATION NUMBER: IT RM95A000573
ATTONNEY/AGENT INFORMATION:
NAME: VUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: STEINKUHLER-TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPHONE: 202-628-5197
TELEPHONE: 202-628-5197
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                         омыек: US/09/011,961
23-FEB-1998
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Best Local Similarity 27.3
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                     APPLICATION NUMBER:
FILING DATE: 23-FEB
CLASSIFICATION: 435
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CTHER INFORMATION:
US-09-011-961-17
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                                                                               COUNTRY:
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APPLICANT: STEINGUELLER, Christian
APPLICANT: BIANCHI, Elisabetta
APPLICANT: BIANCHI, Elisabetta
APPLICANT: TALIANI, Marina
APPLICANT: TOMEI, Licia
APPLICANT: TOMEI, Licia
APPLICANT: TRESANCESCO, Raffaele
APPLICANT: NARJES, Frank
TITLE OF INVENTION: METHODOLOGY TO PRODUCE, AND PUBLFY AND
TITLE OF INVENTION: ASSAY POLYPERIDES WITH THE PROTEOLYTIC ACTIVITY OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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  Gaps
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APPLICANT: Dean, Richard T.
APPLICANT: Dean, Richard T.
TILE OF INVENTION: Radiolabeled Compounds for Thrombus Imaging;
FILE REFERENCE: 104D1
CURRENT APPLICATION NUMBER: US/09/100,537A
CURRENT FILING DATE: 1998-06-19
EARLIER FILING DATE: 1994-06-03
EARLIER FILING DATE: 1994-06-03
EARLIER FILING DATE: 1993-04-08
NUMBER OF SEQ ID NOS: 8
SOFTHARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 12
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    Indels
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0
  Mismatches
                                                                                                                                                                          Sequence 8, Application US/09100537A Patent No. 6022857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MOD_RES
LOCATION: (10)
OTHER INFORMATION: acetamidomethyl
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Patent No. 6197536
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MOD_RES
LOCATION: (12)
OTHER INFORMATION: acetamidomethyl
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 80.0°
Conservative
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CORRESPONDENCE ADDRESS:
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                                    2 RDGIR 6
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2 RDGVR 6
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2 RDGVR 6
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                                                                                                                                     RESULT 14
US-09-100-537-8
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Matches
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Length 12; 4; Indels

Score 25; DB 4; Pred. No. 1.4e+02;

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RESULT
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T-cell receptor be
T-cell receptor be
hucolin, 75K chain
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proctolin - Americ
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proctolin - Atlant
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ribulose-bisphosph
large granule L3 c
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alpha-amylase - ri
T-cell receptor be
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T-cell receptor be
T-cell receptor be
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dermorphin - Rohde
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41.920 Million cell updates/sec
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                                                                                    ; Search time 12.72 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
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                         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                 219241 seqs, 76174552 residues
                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                   February 21, 2002, 16:59:27
                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                OM protein - protein search, using sw model
                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
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B44787
PT06528
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S5324
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1: pir1:*
2: pir2:*
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7 - 7 - 7 - 7 - 7 - 7 - 7 - 7 - 7 - 7 -	Jenrs  Aug-1996 #text_cha ene arrangement of /EMBL/DDBJ	ore 17; DB 2; Length 4; ed. No. 2.2e+05; Mismatches 0; Indels	RESULT 2 S1077 alpha-amylase - rice alpha-amylase - rice c; Species: Oryza sativa (rice) C; Species: Oryza sativa C; Secession: S51077 C; Accession: S51077 Eur. J. Blochem. 226, 249-254, 1994 A; Riferance number: S51077; MUID:95045597 A; Reference number: S51077; MUID:95045597 A; Retarus: preclaimiary A; Rolecule type: protein A; Residues: 1-5 <ter></ter>	re 13; DB 2; Length 5; d. No. 2.2e+05; Mismatches 1; Indels
PT0515 A39690 A39690 A37114 PT0695 A126 A13406 PT0656 PT0656 PT06515 PT06516 PT06517 PT06110 PT06110 PT06110 PT06110 PT06110	(f ivi is is is	Scc Pr 0;	evision 0 wa, M.; I 1994 ked carbo D:9504559	Sco Pre 0;
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20222222222222222222222222222222222222	Citrobacter Citrobacter Aug-1996 #ss. 140697 .; Campbell 3n-211, 1988 anscription number: 14, 140697 reliminary; type: DNA 1-4 <res> erences: GB</res>	Similarity 3; Conser 7	rice za sativ -1995 #\$ 51077 m. 226, oles of mber: 55 51077 iminary e: prote	imi , 5
111111111111111111111111111111111111111	RESULT 1 140697 biotin A - Citrobacter C; Species: Citrobacter C; Date: 12-Aug-1996 #s/C; Accession: 140697 R; Shiuan, D.; Campbell Gene 67, 203-211, 1988 A; Title: Transcription A; Reference number: 14, A; Accession: 140697 A; Recents: preliminary; A; Molecule type: DNA A; Residues: 1-4 < RES> A; Cross-references: GB	rtch TDC TDC	mylase es: Ory; 01-Aug 101-Aug 1sion: Si shima, M Blocher 1: The ro ence nur 1sion: Si 1s: prel	sal sal SNF
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Length 6;

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Infect. Immun. 55, 2026-2031, 1987
A;Title: Antigenic and structural differences among six proteins II expressed by a si
A;Reference number: S16360; MUID:87306843
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A, Experimental source: strain FA1090
A; Note: expression of opacity proteins is regulated by the number of translated repea of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Ohta-Fukuyama, M.; Miyake, Y.; Emi, S.; Yamano, T.
J. Blochem. 88, 197-203, 1980
A;Title: Identification and properties of the prosthetic group of choline oxidase fro
A;Reference number: A15398; MUID:81006769
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C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000
C;Accession: A15398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 19-Mar-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997 C;Accession: S16365 R;Barritt, D.S.; Schwalbe, R.S.; Klapper, D.G.; Cannon, J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
F;l-7/Product: opacity protein P.IIf (fragment) #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                            opacity protein P.IIf - Neisseria gonorrhoeae (strain FA1090) (fragment) N.Alternate names: outer membrane protein P.IIf C.Species: Neisseria gonorrhoeae A.Variety: strain FA1090
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Pred. No. 2.2e+05;
1; Mismatches 0.
                   A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <FEE>
A;Experimental source: adult thymus, strain BALB/c
C;Keywords: T-cell receptor
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66.7%;
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66.7%;
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A; Residues: 1-7 <OHT>
C; Keywords: oxidoreductase
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A; Accession: PT0533
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                                  C; Species: Mus musculus (house mouse)
C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C; Accession: PT0601; PT0617; PT0694
R; Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A; Reference number: PT0509; MUID:91277601
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J. Exp. Med. 174, 115-124, 1991
A;Title, Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601
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C; Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Dec-1995
C; Accession: PQ0008
R; Maruyama, S: Miyoshi, S.; Tanaka, H.
Agric: Biol. Cham. 53, 2763-2767, 1989
A; Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
A; Reference number: PQ0008
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C:Date: 17-Jul-i992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
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                   - mouse (fragment)
                                                                                                                                                                                                                           A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Experimental source: newborn thymus, strain BALB/c, clone 120-2K
A;Accession: PT0617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-5 <FE2>
A;Experimental source: day 18 fetal thymus, strain BALB/c, 154-1H
C;Reywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-5 < FEE3>
A;Experimental source: newborn thymus, strain BALB/C, 120-2CA
A;Accession: Pr0694
A;Status: translation not shown
A;Status: DNA
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2.2e+05;
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            receptor beta chain V-D-J region (120-2K)
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66.78;
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A; Residues: 1-6 <MAR>
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Best Local Similarity
Matches 2; Conserv
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Indels

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C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: 178890
R;Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, Oncogene 9, 3437-3448, 1994
A;Title: Two distinct protein isoforms are encoded by ntk, a csk-related tyrosine pro A;Reference number: 158407; MUID:95060800
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C;Species: Periplaneta americana (American cockroach)
C;Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 23-Aug-1996
C;Accession: A01644
R;Starratt, A.N.; Brown, B.E.
Life Sci. 17, 1253-1256, 1975
A;Title: Structure of the pentapeptide proctolin, a proposed neurotransmitter in inse
A;Reference number: A93048; MUID:76074708
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C;Species: Lycopersicon esculentum (tomato)
C;Daceies: Lycopersicon esculentum (tomato)
C;Dacession: S53608
R;Koeck, M.; Loeffler, A.; Abel, S.; Glund, K.
Plann Mol. Biol. 27, 477-485, 1995
A;File: cDNA structure and regulatory properties of a family of starvation-A;Reference number: S53506; MUID:95201242
                                                                          Gaps
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100.0%; Pred. No. 2.2e+05;
tive 0; Mismatches 0;
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A;Molecule type: DNA
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66.7%;
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A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-4 <KOE>
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Matches 2; Conserv
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Best Local Similarity
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3 SDD 5
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                                      RESULT 8
B44787
calliFMRFamide 11 - bluebottle fly (Calliphora vomitoria)
callifmRFamide 11 - bluebottle fly (Calliphora vomitoria)
callifmRFamide 11 - bluebottle fly (Calliphora vomitoria)
c;Species: Calliphora vomitoria
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C;Accession: B44787
Froc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
A;Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi A;Reference number: A41978; MUID:92196111
A;Reference number: A41978; MUID:92196111
A;Accession: B44787
A;Accession: Proctein
A;Accession: Proctein
A;Accession: Calliphora voice and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptide
C;Keywords: amidated carboxyl end; neuropeptide
F;7/Modified site: amidated carboxyl end (Phe) #status experimental
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PT0628
T-cell receptor beta chain V-D-J region (111-1AG) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0628
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N rep. Reference number: PT0629; MUID:91277601
A;Reference number: PT0629
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-7 cFEE.
A;Experimental source: newborn thymus, strain BALB/C
C;Keywords: T-cell receptor
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PT0576
T-cell receptor beta chain V-D-J region (141-1G) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C; Accession: PT0576
R; Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chains have few N ref A; Reference number: PT0579; MUID:91277601
A; Recession: PT0576
A; Status: translation not shown
A; Molecule type: mRNA
A; Residues: 1-7 <FEE>
A; Residues: 1-7 <FEE>
A; Residues: 1-7 <FEE>
A; Experimental source: day 19 fetal thymus, strain BALB/C
C; Keywords: T-cell receptor
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Pred. No. 2.2e+05;
1; Mismatches 0;
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Best Local Similarity 66.7
Matches 2; Conservative
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Matches 2; Conserv
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Search completed: February 21, 2002, 17:01:17 Job time: 110 sec
                                                              Rior Shea, M.; Adams, M.E. Science 213, 567-569, 1981
A;Title: Pentapeptide (proctolin) associated with an identified neuron.
A;Reference number: A94260; WUID:81225865
A;Contents: annotation; biological source
C;Comment: This peptide is found in the lateral white neurons, which occur (in the cockr innervate the striated hindgut muscles in insects and stimulate contraction of these musc; Superfamily: proctolin
C;Superfamily: neuropeptide
                                          A; Note: the synthetic peptide had the same chromatographic, electrophoretic, and pharmad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Groome, J.R.; Tillinghast, E.K.; Townley, M.A.; Vetrovs, A.; Watson III, W.H.; Hunt, Deptides 11, 205-211, 1990
A;Title: Identification of proctolin in the central nervous system of the horseshoe craft A;Reference number: A60411; MUID:90287800
A;Accession: A60411
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A.Residues: 1-5 <GRO>
C.Comment: This neuropeptide stimulates cardiac output and hindgut motility in the horse
C.Keywords: neuropeptide
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C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 02-Jul-1998
C;Accession: PS0324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proctolin - Atlantic horseshoe crab
C;Species: Limulus polyphemus (Atlantic horseshoe crab)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 17-Mar-1999
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Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
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A; Residues: 1-5 <TSU>
A; Experimental source: leaf, chlorophyll
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A; Reference number: PS0206
A; Accession: PS0324
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A; Molecule type: protein
A; Residues: 1-5 <STA>
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              Compugen Ltd
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      GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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                                                          vibrio fisc
achatina fu
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                                                                                              chlamydia t
                                                                                                                                    cydia pomon
                      cal
                                        pinas
                                                                                                                    moniezia ex
                                                                                                                                                                        procambarus
                                                                                                                                                                                               procambarus
                                                                                                                                                                                                                   mus musculu
  carnobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequencing and characterization of trypsin modulating oostatic factor (TMOF) from the ovaries of the grey flashfly, Neobellieria (Sarcophaga) bullata "; (Sarcophaga) bullata "; Regul. Pept. 50:61-72(1994).

- PONCTION: HAS AN OSSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN CONCENTRATION IN THE HEMOLYMPH RESULTING IN INHIBITION OF OCCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Last annotation update)
TRYPSIN-MODULATING OOSTATIC FACTOR (TMOF).
Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycerygota; Oestroidea; Sarcophagidae; Sarcophaga.
                    aplysia
                                                                                                                                                          ascaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                        pinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FELLICOSAR EPITHELIUM AFTER A BLOOD MEAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Ovary;
MEDLINE=94211930; PubMed=8159807;
Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Citrobacter freundii.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Citrobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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01-JAN-1990 (Rel. 13, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE
(EC 2.6.1.62) (7,8-DIAMINO-PELANGONIC ACID AMINOTRANSFERASE)
AMINOTRANSFERASE) (FRAGMENT).
                                    P81675
P24272
P35904
                                                                                          P38005
P41966
P82158
P31889
P38499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61E72451B7642000 CRC64
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Pred. No. 1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                        AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                         ALIGNMENTS
LANC_CARUI
MYOM_APLCA
UN06_PINPS
                                                                          ACH1_ACHFU
UXA4_CHLTR
FARP_MONEX
                                                                                                                                  ALL7_CYDPO
FAR1_ASCSU
                                                                                                                                                                        FAR1_PROCL
FAR2_PROCL
                                                                                                                                                                                                                 UF03_MOUSE
                                                        LUXE_VIBFI
                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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ilarity 75.0%; l
Conservative 1;
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                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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StyGene; SG10026; bioA.
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                                                                                                                                                                                                                                                                                                                 Pyridoxal phosphate.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TDD 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VP19_HSV1K
P23210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TDD 7
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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VP19_HSV1K
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                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifised and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó;
                                                             MEDLIND=89006280; PubMed=2971595;
Shiuan D., Campbell A.;
"Transcriptional regulation and gene arrangement of Escherichia coli,
Citrobacter freundii and Salmonella typhimurium biotin operons.";
Gene 67:203-211(1988).
-!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + 8-AMINO-7-
                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter freundia and Salmonella typhimurium biotin operons."; Gene 67:203-211(1988).
-i- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + 8-AMINO-7-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
20-AGG-2001 (Rel. 40, Last annotation update)
ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE
EC 2.6.1.62) (7, 8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
                                                                                                                                                                                                  OXONONANOATE = S-ADENOSYL-4-METHYLTHIO-2-OXOBUTANOATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OXONONANOATE = S-ADENOSYL-4-METHYLTHIO-2-OXOBUTANOATE 7,8-DIAMINONONANOATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.5%; Score 17; DB 1; Length 5; 100.0%; Pred. No. 1e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000954; Aminotran_3.
PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
Biotin biosynthesis; Transferase; Aminotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M21922; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                           -1- COFACTOR: PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COFACTOR: PYRIDOXAL PHOSPHATE. PATHWAY: BIOTIN BIOSYNTHESIS. SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-89006280; PubMed-2971595;
Shiuan D., Campbell A.;
                                                                                                                                                                                                                         7,8-DIAMINONONANOATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                        SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                   AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pyridoxal phosphate.
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Matches 3; Conserva
                                             SEQUENCE FROM N.A.
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P12677;
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TDD 5
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Analysis of the herpes simplex virus type 1 promoter controlling the expression of UL18, a true late gene involved in capsid assembly."; J. Virol. 65:769-786(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
CAPSID ASSEMBLY AND DAM MATURATION PROTEIN (VIRION PROTEIN UL38)
(CAPSID PROTEIN VP19C) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17; DB 1; Length 5; Pred. No. 1e+05; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=91101287; PubMed=1846198;
Flanagan W.M., Papavassiliou A.G., Rice M., Hecht L.B.,
Silverstein S., Wagner B.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herpes simplex virus (type 1 / strain KOS).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                InterPro: IPR000954; Aminotran_3.
PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
Biotin blosynthesis; Transferase; Aminotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6AAAB1B1A6F00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 AA; 703 MW; 67376451A336F000 CRC64;
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Pred. No. 1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 AA.
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NON_TER 6
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                                                                                                                                                                                                                                                       EMBL; M21923; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.5%; Scc.
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.18;
66.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 AA; 582 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 41.5
Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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CALLIFWRFAMIDE 11.
Calliphora vomitoria (Blue blowfly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Calliphora.
                                                                                                                                                                                                                                                                                                                                                                                 "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2 neuropeptides (designated calliFMRFamides) from the blowfly calliphora vomitoria.", Proc. Natl. Acad. Sci.", 89:2326-2330(1992).
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                  TISSUE-Thoracic ganglion;
BEDILNE-22195111; Pubmed-1549595;
Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I., Rehfeld J.F., Thorpe A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMIDATION.
69D40699C44AB700 CRC64;
                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=P.americana;
MEDLINE=81225865; Pubmed=6113690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=P.americana;
MEDLINE=76074708; PubMed=576;
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Neuropeptide; Amidation.
MOD_RES 7 7 7
SEQUENCE 7 AA; 926 MW;
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Best Local Similarity
Matches 2; Conserv
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                                                                                                   FARB_CALVO
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PRCT_PERAM
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-!- CATALYTIC ACTIVITY: CHOLINE + O(2) = BETAINE ALDEHYDE + H(2)O(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohta-Fukuyama M., Miyake Y., Emi S., Yamano T.; "Identification and properties of the prosthetic group of choline
                                                                                                                                                                                                                                                                                                                                                                              "Isolation and identification of multiple neuropeptides of the allacotatin superfamily in the shore crab Carcinus maenas."; Eur. J. Biochem. 250:727-734(1997).
-!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide; Amidation; Multigene family.
MOD_RES.
7 AMIDATION.
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                                                                                                                                                                                        Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae; Alcaligenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.7%; Score 13; DB 1; Length 7; 100.0%; Pred. No. 1e+05; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                             TISSUE-Cerebral ganglion, and Thoracic ganglion; MEDLINE-98121193; PubMed-9461295;
                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1990 (Rel. 14, Last annotation update)
CHOLINE OXIDASE (EC 1.1.3.17) (FRAGMENT).
                                                                                              7 AA.
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Best Local Similarity
Thes 2; Conserva
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                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Periplaneta americana (American cockroach),
Limulus polyphemus (Atlantic horseshoe crab), and
Carcinus maenas (Common shore crab) (Green crab)
Eukaryota; Medrazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blattoidea; Blattidae; Periplaneta.
                                                                 Indels
31.7%; Score 13; DB 1; Length 7; 66.7%; Pred. No. 1e+05; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
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SEQUENCE

SEQUENCE

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Grimm-Joergensen Y., McKelvy J.F.;
"Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brain in vitro. Isolation and characterization of thyrotropin releasing factor.";
J. Neurochem. 23:471-478(1974).
-!- FUNCTION: TRH FUNCTIONS AS A REGULATOR OF THE BIOSYNTHESIS OF TSH
IN THE ANTERIOR PITUITARY GLAND AND AS A NEUROTRANSMITTER/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The elucidation of the primary structure of the hypothalamic thyroid stimulating hormone releasing factor of ovine origin by means of mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=Pig; MEDLINE=70039904; PubMed=4982117; MEDLINE=70039904; PubMed=4982117; Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.; "The identity of chemical and hormonal properties of the thyrotropin releasing hormone and pyroglutamyl-histidyl-proline amide."; Biochem. Biophys. Res. Commun. 37:705-710(1969).
                                                                                                                                                             Sus scrofa (Pig), Ovis aries (Sheep),

Bombina orientalis (Oriental fire-bellied toad), and

Notophthalmus viridescens (Eastern newt) (Triturus viridescens).

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

NCBI_TaxID=9823, 9940, 8346, 8316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEUROMODULATOR IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=76138399; PubMed=815011;
Yasuhara T., Nakajima T.;
"Letter: Occurrence of Pyr-His-Pro-NH2 in the frog skin.";
Chem. Pharm. Bull. 23:3301-3303(1975).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Characterization of ovine hypothalamic hypophysiotropic
                                                                                                                                                                                                                                                                                                                           SPECIES=Pig; TISSUE=Hypothalamus;
MEDLINE=70136150; PubMed=4984938;
Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;
"Structure of porcine thyrotropin releasing hormone.";
Biochemistry 9:1103-1106(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES-Sheep;
MEDLINE-70163386; PubMed-4985794;
Burgus R., Dunn T.F., Desiderio D.M., Ward D.N., Vale
                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
THYROLIBERIN (THYROTROPIN RELEASING HORMONE) (TRH).
                                            3 AA.
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MEDLINE=75035605; PubMed=4214528;
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Nature 226:321-325(1970).
                                            STANDARD;
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PIR; A92971; A92971.
Amidation.
MOD_RES 1
MOD_RES 3
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PIR; A93750; RHSHT.
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                                          THYL_PIG
P01151;
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                                                                                                                                                                                                                                                                                                  Standier J., Dircksen H., Keller R.;
"Identification and immunocytochemical localization of proctolin in pericardial organs of the shore crab, Carcinus maenas.";
Peptides 7:67-72(1986).
-!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY, MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
-!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN THE CRAB PERICARDIAL ORGANS.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-95009907; PubMed=7523108;
Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
"Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:735-4746(1994).
-1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOW PROTEIN IS: 5.0, ITS MW IS: 46 KDA.
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                                                                                                                                                           "Identification of proctolin in the central nervous system of horseshoe crab, Limulus polyphemus."; Peptides 11:205-211(1990).
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01-OCT-1994 (Rel. 30, Last sequence update)
01-EEB-1995 (Rel. 31, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P46) (FRAGMENT).
                                                        SPECIES-L.polyphemus;
MEDLINE-90287800; PubMed-2356151;
Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A., Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.
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Science 213:567-569(1981).
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MEDLINE=86232789;
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                                                                                                                                          Shabanowitz J.;
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                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                              01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
CARBON MONOXIDE DEHYDROGENASE LARGE CHAIN (EC 1.2.99.2) (FRAGMENT).
                                                                                                                                                                                                                                                                  Kraut M., Hugendieck I., Herwig S., Meyer O.;
Homology and distribution of CO dehydrogenase structural genes in
carboxydotrophic bacteria.";
Arch. Microbiol. 152:335-341(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.; "The characteristics, isolation and synthesis of the phagocytosis stimulating peptide tuftsin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR = CO(2) + REDUCED
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                                  Length 3;
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     7761F6B000000000 CRC64;
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                                19.5%; Score 8; DB 1;
llarity 50.0%; Pred. No. 1e+05;
Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   19.5%; Score 8; DB 1; 50.0%; Pred. No. 1e+05; iive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
20-JUG-2001 (Rel. 40, Last annotation update)
PHAGOCYTOSIS-STIMULATING PEPTIDE (TUFFISIN).
                                                                                                                                              4 AA.
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                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                        MEDLINE=90055678; PubMed=2818128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=68091045; PubMed=4169272; Fidalgo B.V., Najjar V.A.;
                                                                                                                                                                                                      Pseudomonas carboxydohydrogena.
                                                                                                                                                                                                                                                                                                                                                                    Oxidoreductase; Molybdenum
      380 MW;
                                                                                                                                                                                                                 Bacteria; Proteobacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                        -1- COFACTOR: MOLYBDENUM.
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                                                                                                                                                                                                                                                                                                                                                          PL0140; PL0140.
                                  Query Match
Best Local Similarity
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Matches 1; Conserv
      AA;
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                                                                                                                                              DCML_PSECH
P19916:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TUFT_HUMAN P01858;
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SEQUENCE
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2 HP
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TUFT_HUMAN
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DCML_PSECH
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or send an email to license@isb-sib.ch).
"The physiological role of the lymphoid system. VI. The stimulatory effect of leucophilic gamma globulin (leucokinin) on the phagocytic activity of human polymorphonuclear leucocyte.";
Biochemistry 6:3386-3392(1967)
--- MISCELLANEOUS: AN IGG (CALLED LEUCOKININ) BINDS REVERSIBLY TO THE CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD. LEUCOKININASE ON THE MEMBRANE RELEASES THE ACTIVE PEPTIDE TUFTSIN FROM THE GAMMA CHAIN TUFTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC ACTIVITY OF NEUTROPHILS.

PIR; AO2147;
MIM; 191150; --
SEQUENCE 4 AA; 501 MW; 74176321C0000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shiuan D., Campbell A.; "Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter freundii and Salmonella typhimurium biotin operons."; Gene 67:203-211(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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-i- PATHWAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.
-i- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella.
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01-0CT-1989 (Rel. 12, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE) (FRAGMENT).
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Stydene; SG10027; bioB.
Biotin biosynthesis; Iron-sulfur; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.5%; Score 8; DB 1; 33.3%; Pred. No. 1e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89006280; PubMed=2971595;
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                                                                                                                                                                                                                                                         and tray genes of plasmid R100.";
J. Bacteriol. 170:2749-2757(1988).
-!- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION
-!- FUNCTION: TRANSFER GELLS FOR THE EXCHANGE OF PLASMID DNA.
-!- SUBCELLULAR LOCATION. CYTOPLASMIC.
-!- SIMILARITY: TO TRAM PROTEIN OF OTHER PLASMIDS.
                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-88227859; PubMed-2836369;
Inamoto S., Yoshioka Y., Ohtsubo E.;
"Identification and characterization of the products from the traJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
NCBI_TaxID=6550;
                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
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50.0%; Pred. No. 1e+05;
iive 1; Mismatches
                                      01-JAN'1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
115-DEC-1998 (Rel. 37, Last annotation update)
TRAM PROTEIN (FRACMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-DE-1998 (Rel. 37, Last annotation update)
CONTRACTION-INHIBITING PEPTIDE I (MIP I).
                5 AA.
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                PRT;
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                STANDARD;
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Hormone: Amidation.
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Best Local Similarity
Matches 1; Conserv
                                                                                                                Escherichia coli
                                                                                                                                                                        NCBI_TaxID=562;
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P13736;
              TRM3_ECOLI
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CIP1_MYTED
TRM3_ECOLI
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637 MW; 72C9C68775B81000 CRC64;
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                                       Score 8; DB 1;
Pred. No. 1e+09
1; Mismatches
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50.0%;
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Best Local Similarity
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6 AA;
MOD_RES
SEQUENCE
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P92387 herracia p
P92387 herracia p
P92393 hordeam vul
P92425 pseudorcegn
P92427 peridictyon
P92430 aegilops ta
P9244 teaniatheru
P92440 thinopyrum
P92401 lophopyrum
P92461 lophopyrum
P92461 litoria rub
P82065 litoria rub
P82061 litoria rub
P82001 litoria rub
P82001 litoria rub
P82001 litoria rub
P82001 litoria rub
                                                                                                                                                                                                  0613480 rattus norv
055184 rattus norv
067113 influenza a
P82072 litoria rub
P82073 litoria rub
crithopsis
haynaldia v
                   hordeum bra
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STRAIN-PRAGUE C;
MEDLINE-93010967; PubMed=1327749;
DONZE O., Spahr P.E.;
"Role of the open reading frames of Rous sarcoma virus leader RNA in translation and genome packaging.";
EMBO J. 11:3747-3757(1992).
EMBL; X67587; CAA47862.1; -.
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HYPOTHETICAL PROTEIN (FRAGMENT).
ROUS sarcome virus.
Viruses: Retroid viruses; Retroviridae; Alpharetrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       049223 PRELIMINARY; PRT; 7 AA. 049223; 01-JUN-1998 (TrEMBLrel. 06, Created) 01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-NOV-1998 (TrEMBLrel. 08, Last annotation update) HMG-1-LIKE PROTEIN (FRAGMENT).
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Pred. No. 4.7e+05;
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                  P92381
P92387
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P82070
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P82072
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75.0%;
  Query Match 36.6
Best Local Similarity 75.0
Matches 3; Conservative
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4 PSIP 7
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01-NOV-1996
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SEQUENCE
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Q07624;
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049223
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AC 04
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049223 glycine max
p93233 lycopersico
063668 rattus norv
Q65578 bovine herp
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Q28742 oryctolagus
Q99007 hordeum vul
P82096 litoria rub
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050556 actinobacil
047505 escherichia
P92421 psathyrosta
P92385 hordeum mar
P92210 agropyron c
                                                             February 21, 2002, 17:00:42; Search time 22.11 Seconds (without alignments) 46:310 Million cell updates/sec
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amblyopyrum
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P92218
P92221
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                    Compugen Ltd
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                        473505 seqs, 146272329 residues
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                                               OM protein - protein search, using sw model
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Q63668
Q65578
P70804
P82099
Q28742
Q99007
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Gapop 10.0 , Gapext 0.5
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O49223
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Q50556
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P92421
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P92218
P92221
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_vertebrate:*
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sp_bacteria:*
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Matches 2; Conserv
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                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                  NCBI_TaxID=10116;
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Glycine max (Soybean).

Bukaryots, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
                                                                                                                                                                                                                                                           Gaps
                                                                                        Laux T., Goldberg R.B.;
"A plant DNA binding protein shares highly conserved sequence motifs with HMG-box proteins.";
Nucleic Acids Res. 19:4769-4769(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oetiker J.H., Olson D.C., Shiu O.Y., Yang S.F.; 
"Differential induction of seven 1-aminocyclopropane-1-carboxylate 
synthase genes by elicitor in suspension cultures of tomato 
(Lycopersicon esculentum).":
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE (EC 4.4.1.14) (ACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 12; DB 10; Length 7; Pred. No. 4.7e+05; 0; Mismatches 0; Indels
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Pred. No. 4.7e+05;
0; Mismatches 1; Indels
                                                                                                                                                     STRAIN=CV. ESSEX; TISSUE=ROOTS;
Mahalingam R., Knap H.T.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases:
EMBL; AF047050; AAC03556.1; -.
                                                                                                                                                                                             NON_TER 1 1 1
SEQUENCE 7 AA; 850 MW; 6AAAAAB378637810 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 AA; 828 MW; 71B412C7377415D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                  AA.
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                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                     STRAIN-CV. ESSEX; TISSUE-ROOTS;
MEDLINE-91367679; PubMed-1891369;
                                                                                                                                                                                                                             29.3%; Scc.
100.0%; Pre
0;
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MEDLINE=97351561; PubMed=9207843;
                                                                                                                                                                                                                                                                                                                                                                                                                                Lycopersicon esculentum (Tomato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.8%;
66.7%;
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Best Local Similarity
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Best Local Similarity
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                                                            SEQUENCE FROM N.A.
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Inverse PCR-mediated cloning of the promoter for the rat vasopressin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDITNE=93313343; PubMed=7793062; V1ck C., Benes V., Lu Z., Kutish G.F., Paces V., Rock D., Letchworth G.J., Schwyzer M.; Letchworth G.J., Schwyzer M.; Mucleotide sequence analysis of a 30-kb region of the bovine herpesvirus 1 genome which exhibits a colinear gene arrangement with the UL1 to UL4 genes of herpes simplex virus."; EMBL; Z48053; CAA88130.1; ...
                                                                                                                                               Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Alphaherpesvirinae; Varicellovirus.
                                                              Last sequence update)
Last annotation update)
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08, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                              EMBL; X83264; CAA58237.1; -. SEQUENCE 7 AA; 703 MW; 75A767287DC6D6F0 CRC64
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. 4.7e+05;
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Pred. No. 4.7e+05;
7 AA.
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
01-NOV-1998 (TrEMBLrel. 08, Last ann
HYPOTHETICAL PROTEIN (FRAGMENT).
                                           Created)
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                                                                                                                                                                                                                                                                    MEDLINE=95396550; Pubmed=7667072;
                                                                                                                                                                                                                                                                                                                                       V2 receptor gene.";
Pflugers Arch. 430:12-18(1995).
                 Q63668;
01-NOV-1996 (TTEMBLrel. 0
01-NOV-1996 (TTEMBLrel. 0
01-NOV-1998 (TTEMBLrel. 0
vASOPRESSIN V2 RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Conservative
  PRELIMINARY;
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                                                                                                                           Rattus norvegicus (Rat)
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NON_TER 1 1
SEQUENCE 7 AA; 758
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"Characterization of genomic clones specifying rabbit alpha- and beta-
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
ALPHA-MYOSIN HEAVY CHAIN (FRAGMENT).
Oryctolagus cuniculus (Rabbit).
Gutazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                            SEQUENCE FROM N.A.
MEDLINE-84221901; PubMed-6328491;
Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.J., Jokovcic S.,
Rabinowitz M.;
                                                                                                                                                                                                       1 1
7 AA; 916 MW; 6B1B1AA1E69326B0 CRC64;
                                                                                                                                                     ventricular myosin heavy chains.";
Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
EMBL; K01698; AAA31415.1; --
                                                                                                                                                                                                                                                19.5%;
50.0%;
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                                                                       NCBI_TaxID=9986;
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                                                                                                                                                              Rehm B.H.A., Ertesvag H., Valla S.;
Rehm B.H.A., Ertesvag H., Valla S.;
"A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is part of an alg gene cluster physically organized in a manner similar to that in Pseudomonas aeruginosa.";
J. Bacteriol. 178:5884-5889(1996).
EMBL; X87973; CAA61230.1; -.
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wabditz P.A., Bowle J.H., Tyler M.J., Wallace J.C.;
"Peptides from the skin glands of the Australian buzzing tree frog
Litori electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Bufonoidea, Hylidae,
                                                                                                                                                                                                                                                                                                            ;
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                                                                               Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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Pred. No. 4.7e+05;
1; Mismatches 0; Indels
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Pred. No. 4.7e+05;
1; Mismatches 1; Indel.
                        Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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5 AA; 630 MW; 668761F2C9A00000 CRC64;
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                                                                                                                                         STRAIN=E;
MEDLINE=96427318; PubMed=8830682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liveria.";
Aust. J. Chem. 52:0-0(1999).
Amphibian skin; Amidation.
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50.0%;
          01-FEB-1997 (TrEMBLrel. 02, 01-FEB-1997 (TrEMBLrel. 02, 01-NOV-1998 (TrEMBLrel. 08,
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50.0%;
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                                                                      Azotobacter vinelandii
                                              ALGG GENE (FRAGMENT).
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Matches 2; Conserv
                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                   NCBI_TaxID=354;
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4 SSST 7
                                                                                             Azotobacter
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3 HP
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Q28742;
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                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, X54043, CAA38455.1; -.
Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
Calcium; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-HIMALAYA; TISSUE-ALEURONE LAYER;
MEDLINE-91329704; PubMed-1831055;
Jacobsen J.V., Close T.J.;
Jacobsen J.V., Close T.J.;
Jacobsen J.V., Close T.J.;
Jacobsen J.V., Close T.J.;
Toncirol of transient expression of chimaeric genes by gibberellic acid and abscisic acid in protoplasts prepared from mature barley aleurone layers. "
10: Tayers."
1: CATALYTIC ACTYVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINRAGES IN OLIGOSACCHARIDES.
1: COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
1: COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
1: MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
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Score 8; DB 6; Length /;
Pred. No. 4.78+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel: 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
ALPHA-AMTIASE (EC 3.2.1.1) (FRAGMENT)
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Best_Local Similarity
Matches 1; Conserv
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                                                                            NCBI_TaxID=714;
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SEQUENCE
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Q47505;
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                                                                                                                                                              Wabnitz P.A., Bowle J.H., Tyler M.J., Wallace J.C.; "Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces griseus.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Poehling S., Piepersberg W., Wehmeier U.F.,
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, X95915; CAA65160.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.1%; Score 7; DB 2; Length 7; 50.0%; Pred. No. 4.7e+05; tive 1; Mismatches 0; Indel&
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
SECY & ADK GENES (FRAGMENT).
                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
ELECTRIN 1.
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SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;
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                                                                                  Litoria rubella (Desert tree frog).
                          PRT;
                                                                                                                                                                                       Aust. J. Chem. 52:0-0(1999).
Amphiblan skin; Amidation.
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050556 PRELIMINARY;
050556;
01-JUN-1998 (TrEMBLrel. 06,
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                         PRELIMINARY;
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                                                                                                                                                      TISSUE-SKIN SECRETION;
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Best Local Similarity
'-has 1; Conserva
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Matches 1; Conserv
                                                                                                                          NCBI_TaxID=104895;
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P82096;
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"cis Elements and trans factors are both important in strain-specific regulation of the leukotoxin gene in Actinobacillus actinomycetemcomitans.";
Infect. Immun. 64:3451-3460(1996).
EMBL; U51862; AABB8721.1;
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-ATCC 33384;
MEDLINE-96355846; PubMed-8751884;
Kolodrubetz D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,
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MEDLINE=96099297; PubMed=8522520;

Gonzalez-Pastor J.E., San Millan J.L., Castilla M.A., Moreno F.;

"Structure and organization of plasmid genes required to produce the translation inhibitor microcin C7.";
J. Bacteriol. 177:7131-7140(1995).

ENBL, X57583; CAA40808.1; -.
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                             Actinobacillus actinomycetemcomitans (Haemophilus actinomycetemcomitans).
Bactinomycetemcomitans).
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Actinobacillus.
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) GLYA (FRAGMENT).
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-NOV-1998 (TrEMBLrel. 08, Last ann
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Best Local Similarity
Matches 1; Conservat
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                                                                      Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Psathyrostachys.
                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
NCBI_TaxID=4519;
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                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=H4372, AND H917; TISSUE-LEAVES;
Petersen G., Seberg O.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; 277753; CAB01337.1; ...
EMBL; Z77752; CAB01334.1; ...
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SEQUENCE FROM N.A.
STRAIN-H299, AND H801; TISSUE-LEAVES;
Petersen G., Seberg O.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; 277763; CAB01367.1;
EMBL; 277762; CAB01364.1;
01-WAY-1997 (TrEMBLrel. 03, Last sequence update) 01-JAN-1998 (TrEMBLrel. 05, Last annotation update) RIBOSOWAL PROTEIN 11 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JAN-1998 (TrEMBLrel. 05, Last annotation update)
RIBOSOMAL PROTEIN 11 (FRAGMENT).
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Hordeum marinum (Seaside barley).
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NON_TER 1 1 1 SEQUENCE 7 AA; 894 MW; 6734;
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Best Local Similarity 100.v
                                                           Psathyrostachys fragilis.
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Search completed: February 21, 2002, 17:03:44 Job time: 182 sec

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protein search, using sw model

OM protein -

Run on:

522463 seqs, 74073290 residues

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

US-08-753-851-10

Title: Perfect score:

Sequence:

1 PSNPTDD 7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 7

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B. thuringlensis of Scaffold protein S B. thuringlensis of B. thuringlensis of B. thuringlensis of Pentapeptide paral Mimotope peptide # Pentameric mimotop Peptide 83 from 88 Sequence of linker RNA polymerase II RNA polymerase I
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Urokinase peptide
Miscellaneous pept
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Peptide SEQ ID NO:
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Bovine DRADA amino
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Bovine 88 kD DRADA
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polymerase II
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    significance not defined"
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AAB30131
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Misc-difference
 16-SEP-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09306134-A
 AAR34137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR34137
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigenic peptide
B. thuringiensis c
Conserved peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide encoded by Peptide encoded by Ovine Calpha-s pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B. thuringiensis c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Urokinase peptide
Prothrombin/thromb
                                                                                                                                         (without alignments)
22.093 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA polymerase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                      February 21, 2002, 16:58:47; Search time 23.47 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Sides/grodata/geneseq/geneseqp/AA1980.DAT:*
/ Sides/grodata/geneseq/geneseqp/AA1981.DAT:*
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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SUMMARIES

AAE06219 AAW78635 AAW95063 AAW47462 AAR99608

AAX17785 AAX01210 AAY82403 AAU05017 AAU05024

118 128 128 128 128 128 128 128 128

63.4 58.5 58.5 58.5 58.5 56.1 553.7 51.2

AAR34137

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Query Match Length DB

Score

Result Š.

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7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-1999.
                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                       AAY01210;
                                                                                                                                                                                                                                                                                                                                                     AAY01210
                                                                                                                                                                                                                                                                                                                                           RESULT
    δ
                                                                                                                                                                                                                                                                                                         Q
                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                     having an apparent molecular weight of 85,000 daltons, with a prof 4.9 to 5.1. The peptide is antiganic and specifically reacts with a monoclonal antibody obtained by immunising an animal with a monoclonal antibody obtained by immunising an animal with inver epithelial cells, followed by fusing and cloning. The liver cell regulatory factor is localised to the membrane, particularly at the sinusoidal pole, of normal adult hepatocytes.

The proteins of the invention, as well as being expressed by hepatocytes, are expressed by epithelial cells of the biliary ducts, endothelial cells, Ito cells and macrophages, by Sertoli cells, by spermatocytes at a specific developmental stage (end of the leptotene and zygotene), by ovocytes and follicular cells (also at a specific developmental stage), by haematopoietic cells and blood cells. The factors can be used for cell culture and to restore or maintain cell function in culture. See also AAR34137-R34139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus thuringiensis; delta-endotoxin; insecticide; crystal protein; lepidopteran insect; CrylC; genetic engineering; mutagenesis; mutant; caterpillar; beetle; mosquito; toxic; modification.
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                           This peptide fragment is derived from a cell regulation protein
                                                                                                                                                                                                                                                                                                                              ..

    B. thuringiensis crystal protein CrylC mutant peptide fragment.

          Protein(s) useful as cell regulation factor(s) - specifically reactive with antibodies from animal immunised with rat liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New modified delta-endotoxin crystal proteins from Bacillus tâpringiensis are useful in insecticidal compositions
                                                                                                                                                                                                                                                                                                        Length 7;
                                                                                                                                                                                                                                                                                                      Score 26, DB 14; Length 7;
Pred: No. 4.3e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             AAY17785 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 5; Fig 4; 144pp; English
                                                       Claim 11; Page 40; 72pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mettus AL;
                                                                                                                                                                                                                                                                                                       63.4%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0980071
96US-0757536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus thuringiensis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baum JA, Gilmer AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-370510/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ECOG-) ECOGEN INC.
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                 epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAX80016
                                                                                                                                                                                                                                                                                                                                                   NPTDD 7
                                                                                                                                                                                                                                                                                                                                                                       nptde 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY17785;
                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                             Matches
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polypeptide for modified Bacillus funringiensis crystal proteins (Crylc). The polypeptide of the composition is insecticidally-active against Lepidopterans. The composition is toxic to an insect cell and comprised within an insecticidal formulation can be used as a plant protective spray which is toxic to caterpillars, beetles and mosquitoes. The polypeptide of the composition may be used to kill an insect through ingestion of the composition directly or by ingestion of a plant coated with the composition a transgenic plant that expresses the polypeptide composition. The insecticidal proteins produced by B. thuringiensis are harmless to plants and other non-targeted organisms but toxic to their specific target insect. The polypeptides have improved toxicity so a reduced amount of bioinsecticide per unit area of treated crop can be used allowing economic and efficient utilization in the field. The
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The present invention describes a new composition comprising an isolated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-aminocyclopropane-1-carboxylic acid synthase; ACS; EFE; banana; ethylene forming enzyme; ethylene biosynthesis; plant; fruit ripening; transgenic; enzyme; inhibition; flavour; texture; tomato.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present sequence represents a B. thuringiensis CrylC crystal protein mutant peptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated cDNA molecules ((PASC6) and (PACOS7)) encoding l-aminocyclopropane-1-carboxylic acid synthase (ACS) and an ethylene forming enzyme (EFE) - useful for modifying fruit ripening characteristics, especially in bananas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to two isolated cDNA molecules ((pASC6) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 24; DB 20; Length 7; Pred. No. 4.3e+05; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conserved peptide from tomato for designing ACS primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Columns 5-6; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY01210 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.5%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0632598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 80.0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bird CR, Fletcher JD;
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processes involved in fruit ripening (and other ethylene related processes). Vectors comprising the CDNA sequences may be used to produce transgenic bananas with altered fruit ripening characteristics. The orientation of the pASCS and pACOSY used in the construct, will determine how the ripening process is affected. If the genes have a sense orientation, and transcribe mRNA that encodes an active enzyme, the rate of ripening will be increased (up-regulation) (however, full-length sense inhibition). If genes encode antisense mRNA, they will inhibit the expression of the genes involved in fruit ripening and hence slow the process down (down-regulation). In this manner different spatial and
                                                                                                                                                                                                     temporal patterns of genes expression can be produced. Retardation of the rate of ripening will reduce the rate of deterioration of banana fruit after harvest. This helps in production of high quality fruit that has improved flavour and texture. The present sequence represents a conserved peptide from tomato used for designing 3' degenerate primers for PCR amplification of ACS gene fragments from banana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes isolated Bacillus thuringiensis CrylC delta-endotoxin polypeptides having: (i) at least one amino acid (aa) mutation in the loop region between alpha-helices 6 and 7 of domain 1; and (ii) better activity against Lepidoptera than the native CrylC. The polypeptides, possibly after activation in the digestive tract of
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus thuringiensis; CrylC; crystal protein; insecticide; insect; delta-endotoxin; lepidopteran; modification; genetic engineering; resistance; mutant; mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New mutant Bacillus thuringiensis endotoxin, used for controlling lepidopteran pests, has mutated loop region to impart higher insecticidal activity \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B. thuringiensis crystal gene CrylC mutated peptide SEQ ID NO:26.
                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                        58.5%; Score 24; DB 20; Length 7; 100.0%; Pred. No. 4.3e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 4; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY82403 standard; Peptide; 7 AA
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96US-0757536
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                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mettus AL, Baum JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-255697/22.
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ECOG-) ECOGEN INC
                                                                                                                                                                                                                                                                                                                                      7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-NOV-1997;
27-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 PSNP 4
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                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY82403;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY82403
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insects, kills insect cells by formation of pores and disturbing cellular homeostasis. The polypeptides are used to control lepidopteran pests on plants, either: (1) applied as a composition; or (il) expressed in plants from heterologous nucleic acid (generating insect-resistant plants). They are more astive against Lepidoptera than native Crylc. AAAO08144 to AAA08182, and AAY82136 to AAY82432, represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modifying level of ethylene biosynthesis in plant of genus Musa, involves inserting into genome of plant a DNA sequence encoding banana 1-aminocyclopropane-1-carboxylic acid synthase or ethylene-forming
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-aminocyclopropane-1-carboxylic acid synthase; ACS; banana; ethylene biosynthesis; ethylene-forming enzyme; EFE; fruit ripening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide encoded by PCR primers #8-12 used to clone ACS from banana.
                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                   Length 7;
                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                  Score 24; DB 21;
Pred. No. 4.3e+05;
                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Column 6; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    AAU05017 standard; Peptide; 7 AA.
                                                                                                                                                                                                58.5%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0231240.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-OCT-2001 (first entry)
                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lycopersicon esculentum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bird CR, Fletcher JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-450497/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                             7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fruit storage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vigna sp.
Nicotiana sp.
Dianthus sp.
                                                                                                                                                                                                                                                                         1 PSNPT 5
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                                                                                                                                                                                                                                                                                             | ||||
3 phnpt 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US6262346-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Orchideae.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU05017;
                                                                                                                                                 Sequence
                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enzyme
                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                  RESULT
AAU05017
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still have the robustness to withstand handling and transport to reach the consumer in good condition. In this way high quality ripe fruit can be made available to the consumer with reduced requirement for postharvest treatment. High quality fruit will have improved flavour and texture. High quality fruit can be produced consistently over a wide harvest period, and such fruit can be held in store for long periods and ripened to optimal quality by the supply of exogenous ethylene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     involves inserting into genome of plant a DNA sequence encoding banana l-aminocyclopropane-1-carboxylic acid synthase or ethylene-forming
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  1-aminocyclopropane-1-carboxylic acid synthase; ACS; banana; ethylene biosynthesis; ethylene-forming enzyme; EFE; fruit ripening; fruit storage; tomato; squash; peach; melon; avocado; mustard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AASO9917, AASO9918, AASO9919, AASO9920, AASO9921, AASO9922,
AASO9923, AASO9924.
                                                                                                                                                                                                                                                                                                                                                                        Peptide encoded by PCR primers #1-7 used to clone EFE from banana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modifying level of ethylene biosynthesis in plant of genus Musa,
                                                                                                                                                                          ;
0
                                                                                                                                                Length 7;
                                                                                                                                               Score 24; DB 22; Length 7;
Pred. No. 4.3e+05;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Column 8; 23pp; English.
                                                                                                                                     58.5%; Scor.
100.0%; Pre
                                                                                                                                                                                                                                                                                           AAU05024 standard; Peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0231240
                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lycopersicon esculentum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fletcher JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-450497/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ZENE ) ZENECA LTD.
                                                                                                                                                           Similarity
                                                                                                       7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           apple; carnation
                                                                                                                                          Query Match
Best Local Simi
Matches 4; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cucurbita sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US6262346-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JAN-1999;
                                                                                                                                                                                                                                                                                                                                               24-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synapsis sp.
Dianthus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUL-2001.
                                                                                                                                                                                                  1 PSNP 4
                                                                                                                                                                                                                         1 psnp 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prunus sp.
                                                                                                                                                                                                                                                                                                                     AAU05024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Malus sp.
                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bird CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Persea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enzyme
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                                                                                                                                                                                                                                                                  RESULT
 8866666666
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The sequence represents the amino acid sequence encoded by PCR primers (AASO9917-AASO9924) used to clone ethylene-forming enzyme (EFE) from banana, used in the method of the invention. The method involves modifying the level of ethylene blosynthesis in a plant of the genus Mbsa by inserting into the genome of the plant a DNA sequence (I) encoding a banana 1-aminocyclopropane-1-carboxylic acid synthase (ACS) or an ethylene-forming enzyme (EFE), where (I) is in sense or antisense

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configuration, and modifies the level of activity of ACS or EFE. This retards the rate of ripening in banana fruits which reduces the rate of deterioration of banana fruit after harvest. As a result, fruit may be harvested when they have reached partial or full ripeness and still have the robustness to withstand handling and transport to reach the consumer in good condition. In this way high quality ripe fruit can be made available to the consumer with reduced requirement for post-harvest treatment. High quality fruit will have improved flavour and texture. High quality fruit can be produced consistently over a wide harvest period, and such fruit can be held in store for long periods and ripened to optimal quality by the supply of exogenous ethylene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haugen T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel cDNA sequence encoding C alpha-S protein which is a new splice variant of C alpha catalytic subunit of CAMP dependent protein kinase, useful for treating male infertility and for developing male
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human Calpha-s proteins and cDNA molecules encoding them. Calpha-s is a new splice variant of Calpha catalytic subunit of CAMP dependent protein kinases. Human Calpha-s CDNA is useful for the preparation of an antisense drug. Calpha-s protein is useful for the preparation of a pharmaceutical, and a medicament for manipulating the motility in sperm, for use as contraceptive, and for treating male infertility. A kit comprising antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ovine; Calpha-s; antisense drug; sperm motility; contraceptive; cAMP dependent protein kinase catalytic subunit C alpha; therapy; male infertility.
                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tasken K,
                                                                                                                                                                                                                                                             Length 7;
                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skalhegg BS,
                                                                                                                                                                                                                                                          58.5%; Score 24; DB 22; I 100.0%; Pred. No. 4.3e+05; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jahnsen T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE06219 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 1; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-DEC-2000; 2000WO-NO00441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99NO-0006424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                              4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ovine Calpha-s peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Orstavik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (JAHN/) JAHNSEN T.
(SKAL/) SKALHEGG B S
(TASK/) TASKEN K.
(HAUG/) HAUGEN T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-418266/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORSTAVIK S.
                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REINTON N.
                                                                                                                                                                                                          7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200148170-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                 psnp 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2001.
                                                                                                                                                                                                                                                                                                                            1 PSNP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reinton N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE06219;
                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ovis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (REIN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ORST/)
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AAE06219
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PTPases. AAW78524 to AAW78702 represent other peptides given in the present invention, but which are not specifically claimed.
                                                         Sequence
                                                                                                                                                                                                                                                                                        AAW95063
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**HWARLYST*** MEAT*** I, where R1 = phosphotyrosine (pryr) or a
phosphotyrosine analogue having a hydrolysis resistant phosphorous
molety, and R3 = any amino acid. AAM/R501 to AAW/R523 represent
specifically claimed examples of the peptides described. The peptides useful for modulating both cellular growth to control unwanted cell
proliferation in e.g. selected malignancies and for metabolic control in
e.g. diabetes, by inhibiting signal transduction molecules such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A method has been developed of inhibiting a site-specific interaction between a first molecule having an SH2 domain and a second molecule that interacts with the SH2 domain. The method comprises contacting the first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein tyrosine kinases (PTKs) which include growth factor receptors, prote-oncogene and oncogene products and the insulin receptor. The peptides are also useful for treating and for studying the enzymatic mechanisms of PTPase activity and the metabolic and biochemical roles of
                                                                                                                                                                                                                                                                                                                                                                                                                                              SH2 domain; binding; inhibition; interaction; site specific; signal transduction; protein tyrosine kinase; phosphotyrosine; growth factor receptor; oncogene; cellular growth; cell proliferation; metabolic control; diabetes; PTK; proto-oncogene; insulin receptor.
                                                                                                                                            Gaps
against Calpha-s protein is useful for diagnosing non-motile sperm. The present sequence is ovine Calpha-s peptide.
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0
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                                                                                                         Length 7;
                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              SH2 domain binding inhibiting peptide SEQ ID NO:128.
                                                                                                       Score 23; DB 22;
Pred. No. 4.3e+05;
                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Column 85; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "unspecified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                   AAW78635
ID AAW78635 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (JOSL-) JOSLIN DIABETES CENT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95US-0408604.
91US-0722359.
92US-0959949.
93US-0134558.
                                                                                                       56.1%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                            4; Conservative
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                                                                                                   Query Match
Best Local Similarity
                                                 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                               111 |
3 snpnd 7
                                                                                                                                                                             2 SNPTD 6
                                                                                                                                                                                                                                                                                                                                                                           04-NOV-1998
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08-0CT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US5801149-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shoelson S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                     Sequence
                                                                                                                                                                                                                                                                                                                                          AAW78635;
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                                                                                                                                        Matches
                                                                                                                                                                                                                                                                      RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Urokinase; anti-invasive; anti-angiogenic; variant; chemical derivative; affinity ligand; pharmaceutical; inhibition; tumour invasion; metastasis; peptidomimetic; cell migration; proliferation; angiogenesis; fibrosis; atherosclerosis; post-balloon angioplasty vascular restenosis; neointima; vascular trauma; vascular graft restenosis; inflammatory; lung; scarring; wound healing; psoriasis; venous thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMM95057 or a substitution variant, addition variant angivents shown in AMM95057 or a substitution variant, addition variant or other chemical derivative of that peptide. The peptide or its variant or a derivative can be capped or uncapped. The peptides are useful for in vivo or in vitro prognostic and diagnostic applications, e.g. as labelled peptides to detect a binding site for the peptide on a surface or in the interior of a cell (see AMM95057 for detailed uses of the peptide compound, its variants/derivatives). The present sequence represents a urokinase peptide derivative tested for inhibition of angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an anti-invasive and anti-angiogenic peptide
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                         Length 7;
                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 22, DB 20; Length 7;
Pred. No. 4.3e+05;
3; Mismatches 1; Indels
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                                                                         DB 19; L
4.3e+05;
                                                                                                                             Mismatches
                                                                         Score 22;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Page 46; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                    AAW95063 standard; peptide; 7 AA.
                                                                                                                             .;
                                                                      53.7%; £ 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.7%; 9
42.9%; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Urokinase peptide derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US15437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0900327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ANGS-) ANGSTROM PHARM INC
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-142921/12.
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Best Local Similarity
Matches 3; Conserv
                                                                         Query Match
Best Local Similarity
A);
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                                                                                                                             4;
                                                                                                                                                                                                                               3 snpt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                SNPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jones TR,
                                                                                                                                                                                                                                                                                                                                                                                                                        AAW95063;
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                                                                                                                                                                                                                                                                                                                ά
                                                                                                                             Matches
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AAR99602-R99603 are heptad repeat sequences found in the C-terminal of the large subunit of mammalian RNA polymerase II. The peptides all correspond to a consensus heptad repeat sequence (see AAR99601) found not only in mammals but in other ewaryote species e.g. Drosophila. Arabidopsis, C. elegans, S. cerevisiae and plasmodium spp. The heptad repeats are used for the delivery of compounds to the nucleus of a cell. In vivo the C-terminal heptad repeats are phosphorylated and accumulate in discreet subnuclear compartments where pre-mRNA molecules are
                                                                                                                                                                                                                                                                                                                                                        synthesized and spliced. The peptides may be attached to antisense oligonoucleotides, catalytic RNAs, transgenes, drugs or imaging agents. Peptides used for the delivery of agents to the RNA splicing domains within the nucleus are pref. made up of multiple consensus or variable
                                                                                                                                                     Carboxy-terminal RNA polymerase II peptide(s) - used to deliver bioactive agents into discrete compartments in the nucleus of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA polymerase II carboxy-terminus; Pol II CTD; peptide conjugate; bioactive molecule; phosphorylation; serine/arginine motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Ser in consensus motif is replaced by Thr'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 21, DB 17; Length 7; Pred. No. 4.3e+05; 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNA polymerase II carboxy-terminus derived peptide 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW18362 standard; peptide; 7 AA.
                                                                                                                                                                                                     Claim 3; Page 34; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.2%;
60.0%;
 95WO-US15683.
                               94US-0348718.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Conservative
                                                                                                                          WPI; 1996-277787/28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                            (UYYA ) UNIV YALE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    7. AA;
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 01-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 PSNPT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                               02-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 ptspt 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9720031-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUN-1997.
                                                                                            Warren SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Warren SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW18362;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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   δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present peptide is a prothrombin/thrombin ligand, which can be used in an affinity matrix for the purification of prothrombin or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA polymerase II; heptapeptide repeat; nuclear localisation; targetting; delivery; phosphorylation signal.
                                                                                                                                                                                                                                 Prothrombin; thrombin; ligand; affinity matrix; purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide(s) that bind to prothrombin and thrombin - useful in affinity chromatography
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNA polymerase II large subunit C-terminal heptad repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hammond DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 21; DB 19;
Pred. No. 4.3e+05;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dadd CA,
                                                                                                                                                                                                   Prothrombin/thrombin peptide ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 6; 21pp; English.
                                                                                                       AAW47462 standard; peptide; 6 AA.
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75.0%;
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                                                                                                                                                                     (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                     (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 AA;
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| pssppee 7
PSNPTDD
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panp 6
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                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                     . AAW47462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hrombin.
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Gaps

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7 AA;
             Sequence
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This heptapeptide is derived from RNA polymerase II carboxy-terminus

(Pol II CTD) and is a variation of the consensus motif in AAW18356. At least two heptapeptide repeats form a peptide conjugate with a linker and a bioactive molecule. The peptide conjugate can then be used to deliver the bioactive compound, such as a protein, peptide, sugar or nucleic acid sequence (e.g. a ribozyme, external guide sequence for nucleoside, nucleotide, gene, cDNA, mRNA or RNA) to the nucleotide, nucleoside, qene, cDNA, mRNA or RNA) to the nucleus of a nucleoside, nucleotide, gene, cDNA, mRNA or RNA) to the nucleus of a cell. Phosphorylating the peptide alters its association with certain molecules in the nucleus, such as proteins having a serine/arginine molecules in the nuclear ribonucleoprotein (5m snRNP) e.g. phosphorylated Pol II CTD (COOH terminal domain) derived peptides bind to nuclear proteins associated with transcription and splicing. Also, for delivery of molecules which are desired or not desired to be in close association with RNA, it may be desirable to phosphorylate or leave the ე Peptide conjugate for delivery of bioactive compounds to cell nucleus - comprises targetting molecule derived from RNA polymerase II carboxy-terminus and the bioactive molecule peptide unphosphorylated, respectively. Claim 7; Page 46; 51pp; English

; 0 Gaps 0; Score 21; DB 18; Length 7; Pred. No. 4.3e+05; 2; Mismatches 0; Indels Indels 2; Mismatches 51.2%; 60.0%; Query Match 51.2 Best Local Similarity 60.0 Matches 3; Conservative

2 1::11 3 ptspt 7 1 PSNPT

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RESULT 13

AAY40791 standard; peptide; 7 AA. AAY40791 

(first entry) 01-DEC-1999 AAY40791

Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine; Amino acid loop 7 (connects scaffold protein beta strands S1

tumour; chemotherapeutic agent. Synthetic.

EP947582-A1

06-OCT-1999.

98EP-0870065 31-MAR-1998;

98EP-0870065 31-MAR-1998;

(INNO-) INNOGENETICS NV.

Sablon E; Hoodenboom H, Hufton S, Desmet J,

WPI; 1999-542958/46.

New scaffold protein, useful for stabilizing antigens used as vaccines

Sequences AAY40791-Y40799 are examples of amino acid loops that can be used to connect beta strands S1 (AAY40602) and S2 (AAY40603). S1 and S2 are examples of beta strand peptides which form part of a scaffold Disclosure; Page 6; 105pp; English.

protein. Peptides (AAY40601-Y40609) together form a single-chain scaffold protein which contains at least 1 disulfide bond, contains less than 10% alpha helix and contains at least 6 beta-strands. The scaffold protein is constructed of beta strands S1-S6, and may also include beta strands form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to the next by hydrogen bonds, which generate a beta sandwich architecture. If the additional beta strands A1-A3 are included in the structure the scaffold is constructed of two beta sheets, with the structure scaffold is constructed of two beta sheets, with the structure the scaffold is constructed of two beta sheets, with the structure all/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each other via amino acid loops, where at least one of the structures blids to a receptor or antigen. The scaffold may be totheir such as receptors. Or their constraince of the scaffold may be bound to a protein which binds to a tumour antigen. This will target the complex to tumour cells. Another surface may be bound to a cytotoxic molecule or an autoimmune antibody which may then kill the tumour cells. Therefore the scaffold protein may be used to target chemotherapeutic agents to specific cells. It may be used to target chemotherapeutic agents to specific cells. It may be used to target chemotherapeutic agents to specific cells. It may be used in diagnostic techniques, and to stabilize antigens used as ö Bacillus thuringiensis; delta-endotoxin; insecticide; crystal protein; lepidopteran insect; CrylC; genetic engineering; mutagenesis; mutant; caterpillar; beetle; mosquito; toxic; modification. Gaps B. thuringiensis crystal protein CrylC mutant peptide fragment. ; 0 Score 21; DB 20; Length 7; Pred. No. 4.3e+05; 1; Mismatches 1; Indels AAY17818 standard; peptide; 7 AA. Mettus' AL; 51.2%; 66.7%; 97US-0980071. 97US-0980071 96US-0757536 4; Conservative 12-AUG-1999 (first entry) Bacillus thuringiensis. Baum JA, Gilmer AJ, (ECOG-) ECOGEN INC. Query Match Best Local Similarity Matches 4; Conserv 7 AA; 1 PSNPTD 6 2 pshntd 7 26-NOV-1997; 26-NOV-1997; 27-NOV-1996; 22-JUN-1999 US5914318-A Synthetic vaccines. Sequence AAY17818; AAY17818 RESULT QQ δ

The present invention describes a new composition comprising an isolated New modified delta-endotoxin crystal proteins from Bacillus thuringiensis are useful in insecticidal compositions Disclosure; Fig 4; 144pp; English. WPI; 1999-370510/31

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                                                                    spray which is toxic to caterpillars, beetles and mosquitoes. The polypeptide of the composition may be used to kill an insect through ingestion of the composition directly or by ingestion of a plant coated with the composition or a transgenic plant that expresses the polypeptide composition. The insecticidal proteins produced by B. thuringiensis are specific target insect. The polypeptides have improved toxicity so a reduced amount of bioinsecticide per unit area of treated crop can be used allowing economic and efficient utilization in the field. The present sequence represents a B. thuringiensis CrylC crystal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a new composition comprising an isolated polypeptide for modified Bacillus thuringiensis crystal proteins (CrylC). The polypeptide of the composition is insecticidally-active against Lepidopterans. The composition is toxic to an insect cell and comprised within an insecticidal formulation can be used as a plant protective spray which is toxic to caterpillars, beetles and mosquitoes. The polypeptide of the composition may be used to kill an insect through ingestion of the composition directly or by ingestion of a plant coated with the composition at ransgenic plant that expresses the polypeptide
modified Bacillus thuringiensis crystal proteins (Cry1C).
             The polypeptide of the composition is insecticidally-active against Lepidopterans. The composition is toxic to an insect cell and comprised within an insecticidal formulation can be used as a plant protective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus thuringiensis; delta-endotoxin; insecticide; crystal protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lepidopteran insect; CrylC; genetic engineering; mutagenesis; mutant;
caterpillar; beetle; mosquito; toxic; modification.
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                                                                                                                                                                                                                                                                                                                                                            Score 21; DB 20; Length 7;
Pred. No. 4.3e+05;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide SEQ ID NO:28 from US5914318.
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                                                                                                                                                                                                                                                                                                                                                            51.2%;
75.0%;
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96US-0757536
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                                                                                                                                                                                                                                                                  mutant peptide fragment
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Best Local Similarity
Matches 3; Conserv
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27-NOV-1996;
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3 pnnp 6
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                                                                                                                                                                                                                                                                                                       Sequence
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composition. The insecticidal proteins produced by B. thuringiensis are harmless to plants and other non-targeted organisms but toxic to their specific target insect. The polypeptides have improved toxicity so a reduced amount of bioinsecticide per unit area of treated crop can be used allowing economic and efficient utilization in the field. The
                                                                                                                                                                                                                                  Gaps
                                                                                               present sequence represents a peptide from the present invention.
                                                                                                                                                                                                                                ;
                                                                                                                                                                                         Score 21; DB 20; Length 7;
Pred. No. 4.3e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                    Search completed: February 21, 2002, 17:00:39 Job time: 112 sec
                                                                                                                                                                                           51.2%;
75.0%;
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                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 3; Conserv
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5217869

130, App 1, Appli 1, Appli

129, 130,

protein

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Run on:

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TITLE OF INVENTION: FACTORS FOR THE CELLULAR FUNCTIONAL TITLE OF INVENTION: REGULATION AND BIOLOGICAL APPLICATIONS THEREOF NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                  Sequence Sequence 1
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
        US-08-566-190-14
US-08-566-190-15
US-08-566-190-18
US-08-441-871-54
US-08-329-820-190
US-08-329-820-120
US-08-329-820-120
US-08-329-820-120
US-08-192-243-1
US-08-448-059-1
US-08-457-459-34
US-08-329-820-131
US-08-329-820-131
US-08-329-820-131
US-08-329-820-132
US-08-329-820-132
US-08-329-820-132
US-08-329-820-134
                                                                                                                                                                                                 US-08-555-678-34
                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/204,417A FILING DATE: 19-APR-1994 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                             SSEE: NIXON & VANDERHYE P.C.: 1100 NORTH GLEBE ROAD ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 1721-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9111389
FILING DATE: 16-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08204417A Patent No. 5859192
                                                                                                                                                                                                                                                                                                                              CHRISTIANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.4%;
80.0%;
                                                                                                                                                                                                                                                                                                                            APPLICANT: GUILLOUZO, CHRI
APPLICANT: CORLU, ANNE
APPLICANT: KNEIP, BERNARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LECURAL 703-0100 TELEPHONE: 703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-204-417A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: Patentin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 4; Conserv
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CLASSIFICATION:
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ADDRESSEE:
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY:
(without alignments)
12.592 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                             ; Search time 12.51 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep:*
          4.5
Compugen Ltd
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US-08-757-536-26
US-09-1314-093-26
US-09-250-848-26
US-09-231-885-26
US-09-231-40-11
US-08-408-604A-128
US-08-672-805-14
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US-08-980-071-23
US-08-980-071-27
US-08-980-071-55
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-09-314-093-23
-09-314-093-27
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US-09-251-885-55
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         version -
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                                                                            February 21, 2002, 16:59:07
                                                      using sw model
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Gapop 10.0 , Gapext 0.5
         GenCore (c) 1993
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    protein search,

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                   Copyright
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Total number Minimum DB Maximum DB

Database

Result

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Searched:

Sequence

Title: Perfect :

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Gaps

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GENERAL INFORMATION:

APPLICANT: Baum, James A.

APPLICANT: Baum, James A.

APPLICANT: Gilmer, Amy Jelen

APPLICANT: Mettus, Anne-Marie Light

TITLE OF INVENTION: Bacillus thuringlensis CrylC

TITLE OF INVENTION: Compositions Toxic to Lepidopteran Insects and Methods for TITLE OF INVENTION: Making CrylC Mutants

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 7;
                                                                                                                                                                                OURTOILN. 1211 COURTOIL OF PER 1.0 Version #1.30 SOFWHARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,071 FILING DATE: Concurrently Herewith
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Pred. No. 1.6e+05;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/757,536
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PC-DOS/MS-DOS
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                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Kitchell, Barbara S. REGTRATION NUMBER: 33,928 REFERENCE/DOCKET NUMBER: METALECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
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INFORMATION FOR SEQ ID NO: 26:
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ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         512/418-3000
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Best Local Similarity 80.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 amino acids
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TOPOLOGY: linear
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US-08-980-071-26
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                                                                                 COUNTRY:
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APPLICANT: Baum, James A.

APPLICANT: Gilmer, Amy Jelen

APPLICANT: Mettus, Anne-Warie Light

TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING

TITLE OF INVENTION: LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS

NUMBER OF SEQUENCES: 76

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.5%; Score 24; DB 2; Length 7;
                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: BIRD, COLIN R
APPLICANT: ELETCHER, JONATHON D
TITLE OF INVENTION: RIPENING-RELATED GENES FROM BANANA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY AND CUSHMAN
STREET: 1100 NEW YORK AVENUE N.W.
CITY: WASHINGTON
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/632,598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
RESISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 223355/SEE50112/US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER REGISABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                   Sequence 11, Application US/08632598 Patent No. 5886164
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
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20005-3918
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Matches 4; Conserv
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2 NPTDE 6
                   NPTDD 7
                                                                                                                           RESULT 2
US-08-632-598-11
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US-08-980-071-26
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APPLICANT: Baum, James A.
APPLICANT: Gilmer, Amy Jelen
APPLICANT: Gilmer, Amy Jelen
APPLICANT: Mettus, Anne-Marie Light
TITLE OF INVENTION: Bacillus thuringiensis CrylC
TITLE OF INVENTION: Compositions Toxic to Lepidopteran Insects and Methods for TITLE OF INVENTION: Making CrylC Mutants
                                                                                                                                                                                                                                            APPLICANT: Mettus, Anne-Marie Light
TITLE OF INVENTION: Bacillus thurhagiensis CrylC
TITLE OF INVENTION: Compositions Toxic to Lepidopteran Insects and Methods for
TITLE OF INVENTION: Making CrylC Mutants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/250,848
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/757,536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOBT: 023
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; Patent No. 6153814
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80.0%; Pred
0;
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ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOST:
TELECOMUNICATION INFORMATION:
TELEPHONE: (512) 414-7577
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                     APPLICANT: Baum, James A. APPLICANT: Gilmer, Amy Jelen
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                                                                                                                                                                                                                                                                                                                                                                                   STREET: P.O. Box 4433
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                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS: ADDRESSEE: Arnold, W
                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
7TP: 77210-4433
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Best Local Similarity
Matches 4; Conserv
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PHNPT 7
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3 PHNPT 7
  1 PSNPT 5
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US-09-251-885-26
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STATE:
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APPLICANT: Gilmer, Amy Jelen
APPLICANT: Gilmer, Amy Jelen
APPLICANT: Mettus, Anne-Marie Light
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
TITLE OF INVENTION: LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                              Score 24; DB 2; Length 7; Pred. No. 1.6e+05; 0; Mismatches 1; Indels
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Pred. No. 1.6e+05;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE-POCKET NUMBER: MECO:206
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
                    MOBT: 023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26, Application US/09314093 Patent No. 6033874 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/980,071
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
REGISTRATION NUMBER: 33,928
                REFERENCE/DOCKET NUMBER: MC
TELECOMMUNICATION INFORMATION:
                                                 TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 58.5%;
Best Local Similarity 80.0%;
Matches 4; Conservative (
                                                                                                                                                                                                                                                                                58.5%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 512/777
                                                                                                                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
                                                                                                                                                                                                                                                                                                                                                                 1 PSNPT 5
                                                                                                                                                                                                                                                                                                                                                                                        1 | | | | 3 PHNPT 7
                                                                                                                                                                                                   ; TOPOLOGY:
US-08-757-536-26
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                                                                                                                                                                                                                                                                                                                       Matches
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Sequence 128, Application US/08408604A
Patent No. 5801149
GENERAL INPORMATION:
APPLICANT: Shoelson, Steven
TITLE OF INVENTION:
INHIBITION OF SIGNAL TRANSDUCTION MOLECULES
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                     58.5%; Score 24; DB 4; Length 7; 100.0%; Pred. No. 1.6e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,604A
FILING DATE: 21-MAR-1995
CLASSIFICATION: 514
                                            223355/SEE50112/US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROCE APPLICATION DATA:
APPLICATION NUMBER: US 08/134,558
FILING DATE: 08-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/959,949
FILING DATE: 09-0CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/722,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RELECCOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                             ORGANISM: LYCOPERSICON ESCULENTUM IMMEDIATE SOURCE: CLONE: PROBE 3' PRIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
    NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 22.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 128:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                     11
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ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                          TELEFAX: 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                      SEQUENCE CHARACTERISTICS LENGTH: 7 amino acids
                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
                                                                                     TELEPHONE: 861-3000
TELEFAX: 822-0944
                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                amino acid
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ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDAL.
STREET: DV
"MV: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BIRD, COLIN R
APPLICANT: FLETCHER, JONATHON D
TITLE OF INVENTION: RIPENING-RELATED GENES FROM BANANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20005-3918
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,240
                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/251,885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 24; DB 4;
Pred. No. 1.6e+05;
0; Mismatches 1
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CORRESPONDENCE ADDRESS:
ADDRESSE: CUSHMAN DARBY AND CUSHMAN STREET: 1100 NEW YORK AVENUE N.W.
CITY: WASHINGTON
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT:023
RELECOMMUNICATION INFORMATION:
FELEPHONE: (512) 418-3000
TELEFAX: (512) 474-757
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White and Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/757,536
                                                                                                                                                                                                              PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/09231240 Patent No. 6262346 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
PAPPLICATION NUMBER: 08/632,598
                                                                                                    COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO
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80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
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                                                               Houston
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                                                               CITY: 1
STATE:
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APPLICANT: GUILLOUZO, CHRISTIANE
APPLICANT: CORLU, ANNE
APPLICANT: CORLU, ANNE
APPLICANT: KNEIP, BERNARD
TITLE OF INVENTION: FACTORS FOR THE CELLULAR FUNCTIONAL
TITLE OF INVENTION: REGULATION AND BIOLOGICAL APPLICATIONS THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
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APPLICANT: Baum, James A.
APPLICANT: Gilmer, Amy Jelen
APPLICANT: Gitter, Amy Jelen
APPLICANT: Mettus, Anne-Marie Light
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
TITLE OF INVENTION: LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.2%; Score 21; DB 2; Length 7; 60.0%; Pred. No. 1.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,417A
FILING DATE: 19-APR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9111389
FILING DATE: 16-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1721-2
                                                            ; Sequence 6, Application US/08204417A; Patent No. 5859192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: SADOFF, B.J. REGISTRATION NUMBER: 36,663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: P.O. BOX 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                              COUNTRY: U:
ZIP: 22201
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2 NPXDE 6
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STATE:
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APPLICANT: Baumbach, George A.,
APPLICANT: Buettner, Joseph A.,
APPLICANT: Buettner, Joseph A.,
APPLICANT: Hammond, David J.
ITILE OF INVENTION: Peptides Which Bind to Prothrombin and TITLE OF INVENTION: Thrombin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Bayer Corporation
STREET: 800 Dwight Way
STREET: 0. Box 1986
CITY: Berkeley
STATE: California
                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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                                                                                                                    53.7%; Score 22; DB 1; Length 7; 100.0%; Pred. No. 1.6e+05; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94701-1986
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.2%; Score 21; DB 2; Le
75.0%; Pred. No. 1.6e+05;
iive 1; Mismatches 0;
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OPERATING SYSTEM: DOS
SOFTWARE: WORDERfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,805
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSB-7236
                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/08672805
Patent No. 5831003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Giblin, James A. REGISCRATAIN NUMBER: 25772 REFERENCE/DOCKET NUMBER: MITELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (510)705-7904
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (510)705-7910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                  Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                    ; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-408-604A-128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DESCRIPTION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 3; Conserv
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3 PANP 6
TOPOLOGY:
                                                                                                                                                                                                      2 SNPT 5
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US-08-672-805-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Baum, James A.

APPLICANT: Gilmer, Amy Jelen
APPLICANT: Mettus, Anne-Marie Light
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
TITLE OF INVENTION: LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                    Score 21; DB 2; Length 7;
Pred. No. 1.6e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 21; DB 2; Length 7; Pred. No. 1.6e+05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,071
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/757,536
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5: Arnold, White & Durkee P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 55, Application US/08980071 Patent No. 5914318 GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                          27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                      51.2%;
75.0%;
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Best Local Similarity 75.0%;
Matches 3; Conservative
                                TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                            Conservative
        TELEPHONE: 512/474-7577
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INFORMATION FOR SEQ ID NO:
                                                                                                7 amino acids
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                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy
                                                                                                                                                     linear
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Best Local Similarity
Matches 3; Conserv
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US-08-980-071-27
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3 PNNP 6
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US-08-980-071-55
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                                                                                              LENGTH:
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APPLICANT: Baum, James A.
APPLICANT: Gilmer, Amy Jelen
APPLICANT: Mettus, Anne-Marie Light
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
TITLE OF INVENTION: LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 7;
                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA 105/08/80,071 FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 21; DB 2;
Pred. No. 1.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/757,536
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: KİLCHBLI, BATDARA S.
REGISTRATION NUMBER: MECO: 206
                                                                                                                                                 APPLICATION NUMBER: US/08/980,071 FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: Concurrently Herewith CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/757,536
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arnold, White & Durkee
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5914318
                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION TELEPHONE: 512/418-3000
                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 512/4/4-7577
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.2%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.0
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, W
STREET: P.O. Box 4433
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MEDIUM TYPE: Floppy
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STATE: Texas
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US-08-980-071-27
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3 PNNP 6

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RESULT 15
US-08-75-56-23
Sequence 23, Application US/08757536
APPLICANT: Glimer, Amy Jelen
APPLICANT: Glimer, Amy Jelen
APPLICANT: Glimer, Anne Marie Light
TITLE OF INVENTION: Bacilius thuringiensis Crylc
TITLE OF INVENTION: Geometric Compositions Toxic to Lepidopteran Insects and Methods for TITLE OF INVENTION: Making Crylc Mutants
NUMBER OF SECUENCES.
ADDRESSEE: Arold Milte and Durkee
STREET: ADJ0-4433
COUNTRY: USA
COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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Best Local Similarity
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3 PNNP 6
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 21, 2002, 17:03:19; Search time 12.74 Seconds (without alignments) 59.792 Million cell updates/sec Run on:

US-08-753-851-11 56 1 TSGCYIFYTF 10 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 segs, 76174552 residues Searched:

1098 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

PIR\_68:\* Database :

pir1:\* pir2:\* pir3:\* pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	T-cell receptor be	Ig heavy chain CRD	T-cell receptor be	. hypothetical prote	neuropeptide Grb-A	3-oxoacid CoA-tran	Leu-enkephalin - b	T-cell receptor be	T-cell receptor be	60K Ca binding pro	ᅩ	sperm-activating p	sperm-activating p				sperm-activating p		sperm-activating p	T-cell receptor be	Met-enkephalin - b	T-cell receptor be	T-cell receptor be	lipopeptide WS1279	T-cell receptor be	T-cell receptor be	T-cell receptor be	hypothalamic hepta	Met-enkephalin-Arg
SUMMARIES	QI	PT0215	PT0243	PH0944	G85802	C57444	PD0443	B61445	C53284	PT0717	PT0080	A60410	н60787	D60788	B60787	A60788	C60589	E60589	в60589	D60588	PT0706	A61445	PT0669	PT0707	JU0355	PT0514	PT0512	PT0727	NY PG7	A60224
	DB	5	7	7	7	7	N	~	7	~	~	7	7	~	7	7	7	~	7	7	~	7	Ċ	~	~	~	~	~	_	7
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æ	Query	42	33	33	32	32	32	30	30	30	30.4	30	3	ĕ	30	ž	ĕ	ĕ	30	30	28	28	3	28	28	2	28	28		28
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T-cell receptor be capsid protein VP-	leucokinin VIII - telomeric and tetr	c-rel protein - ch sperm-activating p	sperm-activating p	sperm-activating p	sperm-activating p	sperm-activating p	lectin GNL1 alpha	neomyosuppressin -	cocoonase (EC 3.4.	neuropeptide Grb-A	neuropeptide Grb-A	. Ig heavy chain CDR
PT0542 PL0184	JS0318 PC4373	I50633 F60787	E39572	F60589	D60589	A60588	S38304	A56633	B61168	A57444 .	B57444	PT0231
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30 31	35 33 3	34 35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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T-cell receptor beta chain V-J region (4-1-K.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C;Accession: Pr0215
R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
T. Exp. Med. 173, 1091-1097, 1991
A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not rest A;Reference number: Pr0209; MuID:9127621
A;Accession: Pr0215
A;Accession: Pr0215
A;Molecule type: mRNA
A;Residues: 1-10 <NAK>
C;Keywords: T-cell receptor
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3 SGGYEQY 9
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PTG243

PT0243

PT0243

PT0243

PT0243

C; Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

B; Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991

A; Title: Preferential utilization of specific immunoglobulin heavy chain diversity an A; Residues: PT0222; MUID: 91108337

A; Molecule type: DNA

A; Residues: 1-10 < YAM>
A; Residues: immunoglobulin

0; Gaps h 33.9%; Score 19; DB 2; Length 10; Similarity 60.0%; Pred. No. 1.3e+03; 3; Conservative 1; Mismatches 1; Indels Query Match Best Local Similarity 2 SGGYI 6 Matches Qγ

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| ||: |6 SSGYL 10

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RESULT

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C;Accession: B61445
R;Leung, M.K.; Stefano, G.B.
R;Leung, M.K.; Stefano, G.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
A;Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edul A;Reference number: A61445; MUID:84144823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A; Title: Evolutionarily conserved organization and sequences of germline diversity an A; Reference number. 453284; MuID:91342695
A; Accession: C52884
A; Status: preliminary
A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                C:Species: Mus musculus (house mouse)
C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 05-Feb-1999
C:Accession: PD0443
R:Kawakami, T: Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A. submitted to JIPID, August 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Mytilus edulis (blue mussel)
C;Date: 07-Oct_1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
                                      Gaps
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Pred. No. 2.2e+05;
.--.tohes 0; Indels
                                      Indels
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                                                                                                                                                                                                                                                                                                             3-oxoacid CoA-transferase (EC 2.8.3.5) - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ore 18; DB 2; Le
pred. No. 2.2e+05;
Mismatches 0;
      Pred. No. 2.2e+05;
L; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Description: Proteome analysis of mouse brain. A; Reference number: PD0441
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100.0%; Pred. No.
:ive 0; Mismatch
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C; Keywords: neuropeptide; opioid peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.4%;
50.0%;
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                                Conservative
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A,Residues: 1-9 <KAW>
C,Keywords: CoA-transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein A; Residues: 1-5 <LEU>
Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 2; Conserv
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                                                                                                                                III:
SGGW 9
                                                                                             SGGY 5
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                                            C; Species: Rattus norvegicus (Norway rat)
C; Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C; Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C; Accession: PH0944
B; Cold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
A; Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergin A; Reference number: PH0844
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-10 GGDL>
A; Residues: 1-10 GGDL>
A; Residues: 1-10 cGDL>
A;
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A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cr i
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J. Biol. Chem. 270, 21103-21108, 1995
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the
A;Reference number: A57444; MUID:95403341
A;Accession: C57444
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
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C;Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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C:Species: Escherichia coli
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                         receptor beta chain V-D-J region (clone 15) - rat (fragment)
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Best Local Similarity 100.0
Matches 3; Conservative
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Best Local Similarity 100..
3; Conservative
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A;Molecule type: DNA
A;Residues: 1-9 <STO>
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3 YTF 5
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R;Suzuki, N.; Kajiura, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka Comp. Biochem. Physiol. B 89, 687-693, 1988
A;Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocen A;Reference number: A60787; MUID:88242184
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A.Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocer A.Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocer A. Reference number: A6787; MUID:88242184
A. Reference number: A60788
A. Molecule type: protein
A. Residues: 1-10 < SUZ>
C.; Comment: This oligopeptide from egg jelly is one of several from this species, all at shows some, but not absolute, species restriction.
C.; Superfamily: unassigned animal peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of several from this species, all
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C;Species: Pseudocentrotus depressus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Aug-2000
                                         Deta-neoendorphin / dynorphin precursor - guinea pig
WiAlternate names: alpha-neoendorphin; proenkephalin B precursor
C;Species: Cavia porcellus (guinea pig)
C;Dacies: Oavia porcellus (guinea pig)
C;Date: 03-Reb-1993 #sequence_revision 03-Feb-1993 #text_change 21-Jan-2000
C;Date: 03-Reb-1993 #sequence_revision 03-Feb-1993 #text_change 21-Jan-2000
C;Accession: A60410
R;Murphy, R.; Turner, C.A.
Peptides 11, 65-68, 1990
A;Title: Isolation and microsequence analysis of guinea pig alpha-neo-endorphin.
A;Title: Isolation and microsequence analysis of guinea pig alpha-neo-endorphin.
A;Reference number: A60410; MUID:90259864
A;Residues: 1-10 MUID:
C;Superfamily: proenkephalin
C;Superfamily: proenkephalin
C;Keywords: neuropeptide; opioid peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sperm-activating peptide (Thr-5 speract) - sea urchin (Anthocidaris crassispina)
C.Species: Anthocidaris crassispina
C.Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000
C.Accession: #60787
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A;Residues: 1-10 <SUZ>
C;Comment: This oligopeptide from egg jelly is one of
at shows some, but not absolute, species restriction.
C;Superfamily: unassigned animal peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17; DB 2;
Pred. No. 3e+03;
2; Mismatches
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Pred. No. 3e+03;
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75.0%;
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50.0%;
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75.0%;
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
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2 GGFL 5
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R;Treveso, S.; Zorzato, F.; Chiozzi, P.; Melandri, P.; Volpe, P.; Pozzan, T.
Biochem. Biophys. Res. Commun. 175, 44-450, 1991
A;Title: Frog brain expresses a 60 kDa G2++ binding protein similar to mammalian calreti A;Reference number: PT0080; MUID:91207333
A;Accession: PT0080
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <TRE>
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A;Reference number: PT0509; MUID:91277601
A;Reference number: PT0509; MUID:91277601
A;Reference number: PT0509; MUID:91277601
A;Residues: 1-5 <FEE>
A;Residues: 1-5 <FEE>
A;Residues: 1-5 <FEE>
A;Residues: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-5 <FE2>
A;Residues: 1-5 <FE2
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C;Accession: PT0717; PT0681
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C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
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A;Residue's: 1-5 <HAR>
A;Cross-references: GB:S60737; NID:g233916; PIDN:AAB19519.1; PID:g233919
A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60740)
C;Keywords: T-cell receptor
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Pred. No. 2.2e+05;
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Pred. No. 2.2e+05;
1; Mismatches 0;
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Pred. No. 2.2e+05;
2; Mismatches 1;
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C;Date: 17-Jul-1992 #sequence_revision
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Best Local Similarity
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R;Suzuki, N.; Kajiura, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H. Comp. Biochem. Physiol. B 89, 687-693, 1988
A;Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentrd A;Reference number: A60787; MUID:88242184
A;Accession: A60788
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R.Suzuki, N.; Kajiura, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, F. Comp. Biochem. Physiol. B 89, 687-693, 1988
A.Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentro A; Reference number: A60787; MUID:88242184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Wolecule type: protein A; Molecule type: protein A; Molecule type: protein C; Molecules: 1-10 < SUZ>. C: Comment: This oligopeptide from egg jelly is one of several from this species, all of at shows some, but not absolute, species restriction. C; Superfamily: unassigned animal peptides
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A; Residues: 1-10 <SU2>
C; Comment: This oligopeptide from egg jelly is one of several from this species. Unlike
of the repeats in the known precursor (see PIR:A34543).
C; Superfamily: unassigned animal peptides
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C;Speries: Strongylocentrotus purpuratus (purple urchin)
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000
C;Accession: A60788
                                                                                                                                                                                                                                  sperm-activating peptide (Thr-5 speract) - sea urchin (Hemicentrotus pulcherrimus)
C.Species: Hemicentrotus pulcherrimus
C.Spacies: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000
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llarity 75.0%; Pred. No. 3e+03;
Conservative 0; Mismatches 1; Indels
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GenCore version 4.5 Coryright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

February 21, 2002, 17:04:54 ; Search time 10.03 Seconds
(without alignments)
36.555 Million cell updates/sec

US-08-753-851-11 56 Title:

1 TSGGYIFYTF 10 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 segs, 36664827 residues Searched:

334 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 10

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P81012 schizaphis	P81820 carcinus ma	P11735 locusta mig	P81811 carcinus ma	P81814 carcinus ma	P24816 nephrops no	P01153 sus scrofa	P81818 carcinus ma	P82156 cydia pomon	P81812 carcinus ma	P19990 leucophaea	P34966 cavia porce	_	4	P81179 diaprepes a		P21144 leucophaea	P81817 carcinus ma	P58261 daucus caro	P41966 moniezia ex		4	0	n	P43170 ascaris suu	P80159 treponema h	P82691 periplaneta	P16223 locusta mig	P81822 carcinus ma	P42560 mytilus edu	P16224 locusta mig		P81805 carcinus ma
SUMMARIES	QI	ESTA_SCHGA	AL17_CARMA	CU30_LOCMI	ALL8_CARMA	AL11_CARMA	D1_NEPNO	HY7_PIG	AL15_CARMA	ALL5_CYDPO	ALL9_CARMA	LCK8_LEUMA	NEUU_CAVPO	NEMS_DROME	PAP2_PARMA	PGLR_DIAAB	FARP_LOCMI	LCMS_LEUMA	AL14_CARMA	PSK_DAUCA	FARP_MONEX	AL18_CARMA	ALL3_CYDPO	ALL4_CALVO	ALL4_CYDPO	FAR5_ASCSU	FLA2_TREHY	PPK1_PERAM	TKL1_LOCMI	AL19_CARMA	FARP_MYTED	TKL2_LOCMI	UC22_MAIZE	ALL2_CARMA
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RESULT 2
AL17\_CARMA STANDARD; PRT; 8 AA.

ID AL17\_CARMA STANDARD; PRT; 8 AA.

AC PR1820;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence crab)
DE CARCINUSTATIN 17.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Cumalacostraca; Bucarida; Decapoda; Pleccyemata; Brachyura; OC Eubrachyura; Portunoidea; Portunidae; Carcinus.

OX NCBI\_TaxID=6759;

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d d d d d O O d M Z d 5	ENTS 10 AA.	odate) update) (CARBOXYLIC-	(Aphid). Arthropoda; Tracheata; Hexapoda; Paraneoptera; Hemiptera; Sternor idea; Aphididae; Aphidini; Schiza	a carboxyle greenbug,	Omopuera: Apintologe); ch. Insect Biochem. Physiol. 36:229-240(1997). CATALYTIC ACTIVITY: A CARBOXYLIC ESTER + H(2)O	CARBOXYLEST B. 1; PARTIAL. 2; PARTIAL.	865A2C0 C	DB 1;
ALL3_CARMA ALL5_CARMA ALL2_CARMA AL12_CARMA ALL1_CYDPO ALL6_CYDPO ALL6_CYDPO ALL6_CARMA BUF06_MOUSE UPAA_HUMAN AL10_CARMA	ALIGNMENTS PRT; 10	ed) sequence unnotation	oda; Trache optera; Hen phididae; <i>l</i>	[1] SEQUENCE. SEQUENE—97468499; PubMed—9327586; SLegfried B.D., Ono M., Swanson J.J.; Purification and characterization of a	.ol. 36:229	CARBOXILIC ANION1 - SUBCELLULAR LOCATION: CYTOPLASMIC1 - SIMILARITY: BELONGS TO THE TYPE-B C. InterPro; IPRO02018; Carboxylesterase_B PROSITE; PSO0122; CARBOXYLESTERASE_B_1; PROSITE; PSO0941; CARBOXYLESTERASE_B_1; Hydrolase; Serine esterase.		Score 26;
	STANDARD;	35, 35, 36, UBUNI	num (Aphid). va; Arthropo vra; Paraneo nidoidea; Ap	[1] SEQUENCE. SEQUENCE. SIGGITHE—97468499; PubMed—9327586; Siggitied B.D., Ono M., Swanson J., "Purification and characterization with organophosphate resistance in	(HOMIOPLEFIA: APHIBAIDABE); Arch. Insect Biochem. Physiol.	CARBOXLLC ANION. SUBCELLULAR LOCATION: C SIMILARITY: BELONGS TO rPro: JPR002018: CARBOXVLE TTE; PS00122; CARBOXVLE TTE; PS00941; CARBOXVLE olase; Serine esterase.	101	46.4%; V 83.3%;
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Eubrachyura; Portunoidea; Portunidae; Carcinus.
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-!- FUNCTION: MAY AGT AS A NEUROFRANSMITTER OR NEUROMODULATOR.-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
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                                                       TISSUE-Cerebral ganglion, and Thoracic ganglion;
MEDLINE-98121193; PubMed-9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Locusta migratoria (Migratory locust).
Eukaryota: Metazoa; Arthropoda: Tracheata; Hexapoda: Insecta;
Pteryota: Neoptera: Orthopteroidea: Orthoptera; Caelifera;
NCBI_TaxID=7004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 daenas (Common shore crab) (Green crab).
A: Metazoa; Arthropoda; Crustacea; Malacostraca;
Straca; Eucarida; Decapoda; Pleocyemata; Brachyura;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.9%; Score 19; DB 1; Length 10; 100.0%; Pred. No. 8.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.9%; Score 19; DB 1; Length 8; 66.7%; Pred. No. 1e+05;
                                                                                                                                                                                                                                                                                                                             Neuropeptide; Amidation; Multigene family.

MOD_RES 8 8 AMIDATION (POTENTIAL).

SEQUENCE 8 AA; 858 MW; C82879D5AB46D865 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
CUTICLE PROTEIN 30 (LM-30) (LM-ACP 30) (FRAGMENT).
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CACAMATIN 8.
Ca. Jaenas (Common shore crab) (Green crabulation and Arthropoda; Crustace; Malamalae, Straca; Butcarida; Decapoda; Pleocyemat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 AA.
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Mismatches
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Matches 4; Conservative
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P11735;
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P81811;
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                                                                                                                          "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas."; Eur. J. Blochem. 250:727-734(1997).

-! FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.

-! SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
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TISSUE-Cerebral ganglion, and Thoracic ganglion;
MEDLINE-98121193; PubMed-9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas."; Eur. J. Biochem. 250:727-734(1997).
-!- FUNCTION: MAY AGT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.4%; Score 17; DB 1; Length 8; 50.0%; Pred. No. 1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
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                                                                                                                                                                                                                                                                                                                          8 8 AMIDATION. 8 AMIDATION. 922879CDCB47687D CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 AA.
                                                                                                                                                                                                                                                                                            Neuropeptide; Amidation; Multigene family.
MOD RES 8 AMIDATION
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MOD_RES 9 AMIDATION
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SEQUENCE

Hormone

SEQUENCE

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Cydia pomonella (Codling moth).
Bukaryota, Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricoidea; Tortricidae; Olethreutinae; Cydia.
                                                                                                                                                     "Isolation and identification of multiple neuropeptides of the
                                                                                                                                                                    allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Biochem. 250:727-734(1997).
-- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
-- I- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide; Amidation; Multigene family.
                                                                                                          Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P., Thorpe A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley Davey M., East P.D., Thorpe A.; "Lepidopteran peptides of the allatostatin superfamily."; Peptides 18:1301-1309(1997).

-: SIMILARITY: BELONG TO THE ALLATOSTATIN FAMILY.
Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                               2; Indels
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Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
                                                                                                                                                                                                                                                                                                                                          Score 16; DB 1; Length 8; Pred. No. 1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16; DB 1; Length 8; Pred. No. 1e+05;
                                                                                                                                                                                                                                                                   8 8 AMIDATION.
8 AA; 811 MW; 922879D5AB47687D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      922879CABB58640D CRC64;
                                                                           TISSUE-Cerebral ganglion, and Thoracic ganglion; MEDLINE-98121193; PubMed-9461295;
   Eubrachyura; Portunoidea; Portunidae; Carcinus.
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                            28.68;
50.08;
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                               3; Conservative
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Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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Best Local Similarity
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                   NCBI_TaxID=6759;
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1 AGPYSF
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P81812;
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P82156;
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SEQUENCE
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Chang R.C.C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H.,
Saffran M., Kong A., Hamilton J.W., Cohn D.V., Schally A.V.;
"Isolation, structure and synthesis of a heptapeptide with in vitro
                                                                                                                                                 MEDLINE-92082847; PubMed-1747388; Favrel P., Kegel G., Sedlmeier D., Keller R., van Wormhoudt A.; Structure and blological activity of crustacean gastrointestinal peptides identified with antibodies to gastrin/cholecystokinin."; Biochimie 73:1233-1239(1991).
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Sus.
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-i- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
Nephrops norvegicus (Norway lobster).
Melazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
Nephropoidea; Nephropidae; Nephrops.
NCBI_TaxID=6829;
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Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
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Horm. Metab. Res. 13:228-232(1981).
PIR; A01417; NPG7.
SEQUENCE 7 AA: 957 MW; 632845B1FB5059A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                         9 AA; 1038 MW; 60EC79CAB6D8787B CRC64;
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Pred. No. 1e+05;
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16.7%; Pred. No. 1e+05;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1986 (Rel. 01, Last annotation update)
HYPOTHALAMIC HEPTAPEFTIDE.
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Best Local Similarity 37.5.
37. Conservative
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Best Local Similarity
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1 SEGGQDFW 8
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HY7\_PIG P01153;

HY7\_PIG RESULT

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P41494;
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-!- FUNCTION: THIS CEPHALOWYORNOPIC EPPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
                                                                                                                                                                                                                   .,
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                                                                                          "Isolation and identification of multiple neuropeptides of the
                                                                                                             Eur. J. Biochem. 250:727-734(1997).
-!- FUNCTION: MAY ACT AS A NEGROTRANSMITTER OR NEUROMODULATOR.
-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.

MOUNTOPEPTIDE: Amidation; Multigene family.

MOD_RES

MAIDARTON.
                                                                       Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                     allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Biochem. 250:727-734(1997).
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Trachéata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
NCBL_TaxID=6759;
                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                             Score 16; DB 1; Length 8;
Pred. No. 1e+05;
); Mismatches 2; Indels
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Pred. No. 1e+05;
2; Mismatches 2; Indels
                                                                                                                                                                8 AA; 781 MW; 7C2879CDCB476878 CRC64;
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                                               TISSUE-Cerebral ganglion, and Thoracic ganglion; MEDLINE-98121193; PubMed-9461295;
                                                                                                                                                                                                                                                                                                                           01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                           8 AA.
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Leucophaea maderae (Madeira cockroach).
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42.98;
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                                                                                                                                                                                                                   3; Conservative
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MOD_RES 8 8
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Matches 3; Conserv
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Matches 3; Conserv
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GADFYSW 7
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LCK8_LEUMA
ID LCK8_LEUMA
AC P19990;
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NEUU_CAVPO
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MEDLINE=90341105; PubMed=2381877;
Murphy R., Turner C.A., Furness J.B., Parker L., Giraud A.;
Murphy R., Turner C.A., Furness J.B., Parker L., Giraud A.;
Murphy R., Turner C.A., Furness J.B., Parker L., Giraud A.;
Murphy R., Turner C.A., Furness J.B., Parker L., Giraud A.;
from guinea pig small intestine.";
Peptides 11:613-617(1990).
-!- FUNCTION: STIMULATES UTERINE SMOOTH MUSCLE CONTRACTION AND CAUSES SELECTIVE VASOCONSTRICTION.
-!- SIMILARITY: BELONGS TO THE NMU FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly), and Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata). Eukaryota; Metazoa; Arthropoda; Tracheatu; Hexapoda; Insecta; Pteryota; Neoptera; Endopterygota; Diptera; Brachycerygota; Diptera; Endopterygota; Diptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                            Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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Pred. No. 1e+05;
1; Mismatches 2; Inde
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1ECF177409C729DB CRC64;
15-DEC-1998 (Rel. 37, Last annotation update)
NEUROMEDIN U-9 (NMU-9).
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01-FEB-1996 (Rel. 33, Last annotation update)
NEOMYOSUPPRESSIN (NEB-MS).
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-!- FUNCTION: MYOINHIBITING NEUROPEPTIDE.
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01-FEB-1996 (Rel. 33, Last ann
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40.0%;
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PROSITE; PS00967; NMU; 1.
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Best Local Similarity 40.0
Matches 2; Conservative
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MOD_RES 10 10
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abbreviatus L.) larvae.";
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MEDLINE=87057369; PubMed=3782138;
Lazarovici P., Primor N., Loew L.M.;
"Purification and pore-formity of two hydrophobic polypeptides from the secretion of the Red sea moses sole (Pardachirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Doostdar H., McCollum T.G., Mayer R.T.; "Purification and characterization of an endo-polygalacturonase from the gut of West Indies sugarcane rootstalk borer weevil (Diaprepes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYSIS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. BIOJ. Chem. 261:16704-16713(1986).

-!- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT PROPERTIES: FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYS SUBUNIT: MONOMER. IN AQUEDUS SOLUTION EXISTS AS A TETRAMER.
-!- SUBCELLULAR LOCATION: SECRETED.
-!- SIMILARITY: BELONGS TO THE PARBAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
8DNO-POLYGALACTURONANSE (PG) (EC 3.2.1.15) (FRAGMENT).
Diaprepes abbreviatus (Sugarcane rootstalk borer weevil).
Eukaryota; Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Cucujiformia; Phytophaga; Curculionidae; Entimina;
                    Score 16; DB 1; Length 10;
Pred. No. 2.9e+03;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15; DB 1; Length 5; Pred. No. 1e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 5 AA; 614 MW; 7769C9C9C8100000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAX-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PATRAPAKIN II (PXII) (FRRGMENT).
Pardachirus marmoratus (Red sea moses sole).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 AA.
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50.0%;
                    28.6%;
30.0%;
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                                                                               3; Conservative
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                    Query Match
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Matches 3; Conserv
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P81179;
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P81864;
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SEQUENCE
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RL Comp. Biochem. Physiol. 118B:861-867(1997).

CC -!- CATALYTIC ACTIVITY: RANDOM HYDROLYSIS OF 1,4-ALPHA-D-CC GALACTOSIDHORIC LINKAGES IN PECTATE AND OTHER GALACTURONAS.

CC -!- INDUCTION: INHIBITED BY CITRUS PGIP.

CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:

CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:

CC -!- SIMILARITY: WEAK TO OTHER POLYGALACTURONASES.

KW Hydrolase; Glycosidase; Cell wall.

FT NON TER 9

SQ SEQUENCE 9 AA; 1041 MW; 1F49087042DB41BB CRC64;

Autches 2; Conservative 1; Mismatches 0; Indels 0; Gaps

QY 8 YTF 10

QY 8 YTF 10

| |: Db 2 YTY 4

Search completed: February 21, 2002, 17:07:52
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Tue Feb 26 05:51:57 2002
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

February 21, 2002, 17:04:34; Search time 22.09 Seconds (without alignments) 66.217 Million cell updates/sec

US-08-753-851-11 56 1 TSGCXIFYTF 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

473505 seqs, 146272329 residues Searched:

996 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 10

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL\_17:\* Database :

sp\_arches:\*
sp\_bacteria:\*
sp\_fungi:\*
sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\*
sp\_mhc:\* sp\_organelle:\* sp\_phage:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_unclassified:\*

sp\_virus:\*
sp\_vertebrate:\*

sp\_plant:\* sp\_rodent:\*

### SUMMARIES

	Description	P82445 nicotiana t	O9h3v3 homo sapien	09s8i8 orvza sativ	P82923 bos taurus	09tq68 gerrhonotus	P87225 saccharomyc	092009 gallus gall	052837 rhizobium 1			09ta80 ophiodes st	09tq65 abronia oax		09tq59 elgaria coe	09tq56 elqaria kin	elgaria	elgaria	P82072 litoria rub	P82073 litoria rub
	ID	P82445	09нзүз	0958J8	P82923	Q9TG68	P87225	092009	052837	051812	079924	091680	Q9TG65	Q9TG62	Q9TG59	Q9TG56	Q9TG53	Q9TG50	P82072	P82073
	gth DB	7 10	9	9 10	10 6	10 8	8	9 13	10 2	10 2	10 8	10 8	10 8	10 8	10 8	10 8	10 8	10 8	5 13	5 13
æ	Query Match Length DB	30.4	30.4	30.4	30.4	30.4	28.6	28.6	26.8	26.8	26.8	26.8	26.8	26.8	26.8	26.8	26.8	26.8	25.0	25.0
	Score	17	17	17	17	17	16	16	15	15	15	15	15	15	15	. 15	15	15	14	14
,	Result No.	П	7	3	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19

	8 699		030790 erwinia amy Q9byf9 homo sapien Q9trs0 oryctolagus Q44693 bacillus am 09x334 lecleria a		P92774 xantusia vi 07988B basiliscus 079897 hoplocercus 079915 leiolepis b
4 11 8	8 10 13 7	8 2 095443 8 2 097572 8 5 097WH6 8 7 095213	9 2 030790 9 4 09BYF9 9 6 09TRS0 10 2 044693 10 2 09X534	0.0100	10 8 P92774 10 8 079888 10 8 079897 10 8 079915
	14 25.0 14 25.0 14 25.0 13 25.0		, , , , , , , , , , , , , , , , , , ,	23. 23. 23.	13 23.2 13 23.2 13 23.2 13 23.2
20 22 23 23	4 2 2 2 2 2 4 4 5 4 4 5 4 4 5 6 5 6 5 6 6 6 6 6 6 6	9 9 9 8 6 9 9 9 9 9 6	. 4 R B B . 4 R D C V	38 39 11	4 4 4 4 7 6 4 7

# ALIGNMENTS

RESULT 1 198445 10 P8445 10 P8445 10 P82445; 11 P8CPCELWALL PROTEIN (FRACHEN) 10 P8CPCELWALL PROTEIN (FRACHEN) 10 P8CPCC ENGRACY (COMMON LODACCO) 10 P8CPCC ENGRACY (COMMON LODACCO) 10 P8CPCC ENGRACY (COMMON LOCACE) 11 PROTECHIA PANA, Mitchell G.P., Robertson D., Slabas A.R., 11 PROTECHIA LOCATION: CELL WALL. 12 PROTECHIA LOCATION: CELL WALL. 13 PROTECHIA LOCATION: CELL WALL. 14 Planta 0.0-0(2000). 15 PROTECHIA LOCATION: CELL WALL. 15 Planta 0.0-0(2000). 16 P8245 PROTE PROTEIN PROTEI

9 AA. RESULT 2
09H3Y3
ID 09H3Y3; PRELIMINARY; PRT;
AC 09H3Y3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created) 4 GYIF 7 |::| 4 GHVF 7 B S

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10 AA.
                                                                                                             Pfan; PF00318; Ribosomal S2; PARTIAL.
PRINTS; PR00395; RIBOSOMALS2; PARTIAL.
PROSITE; PS00962; RIBOSOMAL_S2_1; PARTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                    Ribosomal protein; Mitochondrion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P87225;
01-JUL-1997 (TrEMBLrel. 04, 01-NOV-1999 (TrEMBLrel. 12, 01-UNN-2001 (TrEMBLrel. 17, GIN11 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 AA; 1213 MW;
                                                                                                                                                                                                                           Query Match 30.4
Best Local Similarity 100.
Matches 3; Conservative
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Best Local Similarity 33.3
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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2 TTARWLFST 10
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                IISSUE=LIVER;
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NON_TER
SEQUENCE
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Takahashi M., Moriguchi S., Yoshikawa M., Sasaki R.;
"Isolation and characterization of oryzatensin: a novel bioactive
peptide with ileum-contracting and immunomodulating activities derived
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinee; Bos
                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DJ839B11.1 (CONTINUES AS DJ461P17.1 IN EM:AL031663) (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MITOCHONDRIAL 28S RIBOSOMAL PROTEIN S2 (MRP-S2) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
30.4%; Score 17; DB 10; Length 9;
Best Local Similarity 60.0%; Pred. No. 4.7e+05;
Matches 3; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                             Score 17; DB 4; Length 9; Pred. No. 4.7e+05; 0; Mismatches 1; Indels
                                                                                                                       Lloyd D.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL121778; CAB76844.1; -.
NON_TER 9 9
SEQUENCE 9 AA; 1036 MW; 2C417B01B412D1B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                          09SBJB;
01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
ORYZATENSIN-BIOACTIVE PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from rice albumin.";
Blochem. Mol. Biol. Int. 33:1151-1158(1994).
SEQUENCE 9 AA; 1093 MW; 0E8C67377B56877B CRC64;
                                                                                                                                                                                                                                                                                                                                                9 AA.
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75.0%;
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Best Local Similarity 75.0
Matches 3; Conservative
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                                                                                                             SEQUENCE FROM N.A.
                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9913;
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                                      DJ839B11.1.
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Koc E.C., Burkhart W., Blackburn K., Moseley A., Spremulli L.L.; "Small subunit of the mammalian mitochondrial ribosome. Identification of the full complement ribosomal proteins present."; Submitted (DEC-2000) to the SWISS-PROT data bank.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL.
-!- SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.
-!- Interpro, IPR001865; Ribosomal_S2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular Phylogenetics, tRNA evolution, and historical biogeography in anguid lizards and related taxonomic families.";
EMBE: AF085614; AAD51532.1; -. Mitchondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Anguidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDILTRE-99343613; PubMed=10413621;
Macey J.R., Schulte J.A. II, Larson A., Tuniyev B.S., Orlov N.,
Papenfuss T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.4%; Score 17; DB 6; Length 10; 100.0%; Pred. No. 6.2e+03; Live 0; Mismatches 0; Indels
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Pred. No. 6.2e+03;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      10 AA; 1246 MW; 6A7A6679C04B476B CRC64;
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U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2000 (TrEMBLrel. 13, Last annotation update)
CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
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Last annotation update)
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Cram D.S., Loh S.M., Chean K.C.C., Skurray R.A.;
"Sequence and conservation of genes at the distal end of the transfer region on plasmids F and R6-5.";
Gene 104:85-90(1991).
EMBL; M38047; AAA98090.1; -.
                                                                                                                                   MEDIINE-90136072; PubMed=2693897;
Roelvink P.W., Hontelez J.G.J., Van Kammen A., van den Bos R.C.;
"Nucleotide sequence of the regulatory nifA gene of Rhizobium
leguminosarum PRE: transcriptional control sites and expression in
Escherichia coli.";
Mol. Microbiol. 3:1441-1447(1989).
EMBL: X17073; CAA34923.1; -.
FIXX PROTEIN (10 AA) (FRAGMENT).
Rhizobium leguminosarum.
Bacteria: Proteobacteria: alpha subdivision; Rhizobiaceae group;
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Escherichia
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
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MEDLINE=92009201; PubMed=1916281;
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                                                  Rhizobiaceae; Rhizobium.
NCBI_TaxID=384;
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Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
Matches 3; Conserv
                                                                                                        SEQUENCE FROM N.A.
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6 TLGG 9
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2 GGF 4
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
C-REL PROTEIN (FRAGMENT).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                       Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; Z73169; CAA97518.2; -
SGD; SO003988; GIN11.
NON.TER. 1 1
                                                                                                    SEQUENCE FROM N.A.
Wedler H., Wedler E., Scharfe M., Wambutt R.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91133738; PubMed=2284104; Hannink M., Temin H.M.; "Structure and autoregulation of the c-rel promoter."; Oncogene 5:1843-1850(1990).
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Last annotation update)
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Oncogene 0:0-0(1990).
EMBL; X5640; CAA3982.1; -.
EMBL; X56515; CAA39866.1; -.
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
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NCBI_TaxID=9031;
 GIN11 OR YLL065W.
                                                                      NCBI_TaxID=4932;
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Mitochondrion.
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Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Anguidae; Ophiodes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Papenfuss T.J.;
"Molecular phylogenetics, tRNA evolution, and historical biogeography in anguid lizards and related taxonomic families.";
Mol. Phylogenet. Evol. 12:250-272(1999).
EMBL; AF085610; AAD51520.1;
                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Anguidae; Elgaria.
NCBI_TaxID=52222;
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in Anguid Lizards and Related Taxonomic Families.";
MMOl. Phylogenet. Evol. 0:0-0(1998).
EMBL: U82692; AAC622780.1; -.
                                                                                                                                           SEQUENCE FROM N.A.
Macey J.R., Schulte J.A. II, Larson A., Tuniyev B.S., Orlov N.,
Papenfuss T.J.;
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MEDLINE=99343613; PubMed=10413621;
Macey J.S., Orlote J.A. II, Larson A., Tuniyev B.S., Orlov N.,
Papenfuss T.J.;
                                                                         MEDLINE-97315309; PubMed-9169559;
Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
"Evolutionary shifts in three major structural features of the
mitochondrial genome among iguanian lizards.";
J. Mol. Evol. 44:660-674(1997).
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Pred. No. 1.4e+04;
3; Mismatches 3; Indels
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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33.3%;
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Best Local Similarity 33.3
Matches 3; Conservative
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 panamintina.
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2 TTTRWLFST 10
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Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Anguidae; Mesaspis.
NCBL_TaxID=102187;
                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular phylogenetics, tRNA evolution, and historical biogeography in anguld lizards and related taxonomic families."; Mol. Phylogenet. Evol. 12:250-272(1999).

EMBL: AF085615; AAD51535.1.
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EMBL: AF085616; AAD151538.1.
                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Anguidae; Abronia.
NCBI_TaxID=102176;
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Maccy J.R., Schulte J.A. II, Larson A., Tuniyev B.S., Orlov N.,
Papenfuss T.J.;
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MEDLINE=99343613; PubMed=10413621;
Macey J.R., Schulte J.A. II, Larson A., Tuniyev B.S., Orlov N.,
Papenfuss T.J.;
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Pred. No. 1.4e+04;
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                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
  10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                              CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.8%;
33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.8%;
33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 10
10 AA; 1243 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 AA; 1243 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Conservative
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14

RESULT

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                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Anguidae; Elgaria.
NCBI_TaxID=102184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
MEDLINE-9943613; PubMed=10413621;
Macey J.R., Schulte J.A. II, Larson A., Tuniyev B.S., Orlov N.,
Papenkius T.J.,
"Molecular phylogenetics, tRNA evolution, and historical biogeography
in anguid lizards and related taxonomic families.";
Mol. Phylogenet. Evol. 12:250-272(1999).
EMBL: AR095618; AAD51544.1;
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                     "Molecular phylogenetics, tRNA evolution, and historical biogeography in anguld lizards and related taxonomic families.";
MMOL. Phylogenet. Evol. 12:56-272(1999).
EMBL; AF085617; AAD51541.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Elgaria kingii.
Mitochondrion.
Mitochondrion.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Anguidae; Elgaria.
NCBI_TaxID=102185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=99343613; PubMed=10413621;
Macey J.R., Schulte J.A. II, Larson A., Tuniyev B.S., Orlov N., Papenfuss T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .<u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.8%; Score 15; DB 8; Length 10; 33.3%; Pred. No. 1.4e+04; Ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.8%; Score 15; DB 8; Length 10; 33.3%; Pred. No. 1.4e+04; Live 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER 10 10 10 SECUENCE 10 AA; 1243 MW; 85EE80C7336411B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER 10 10 10 SEQUENCE 10 AA; 1243 MW; 85EE80C7336411B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09TG56 PRELIMINARY; PRT; 10 AA.
09TG56;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 26.8°
Best Local Similarity 33.3°
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 26.8
Best Local Similarity 33.3
Matches 3; Conservative
                     PRELIMINARY;
                                                                                                                                                   Elgaria coerulea.
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1: :: | f
2 TTTRWLFST 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TSGGYIFYT 9
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                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrion.
Q9TG59
ID Q9TG59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
Q9TG56
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|: ::| | 2 TTTRWLFST 10

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Search completed: February 21, 2002, 17:07:35 Job time: 181 sec
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February 21, 2002, 17:01:23; Search time 23.61 Seconds (without alignments) 31.374 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                           Run on:
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522463 seqs, 74073290 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 US-08-753-851-11 56 1 TSGGYIFYTF 10 Perfect score: Scoring table: Sequence: Searched: Title:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 10

121109

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_1101:\* Database

/SIDS8/ggdatca/geneseq/geneseqp/An1989.DAT:
/SIDS8/ggdatca/geneseqgpAneseqp/An1989.DAT:
/SIDS8/gcgdatca/geneseqgpeneseqp/An1991.DAT:
/SIDS8/gcgdatca/geneseqgpeneseqp/An1991.DAT:
/SIDS8/gcgdatca/geneseqgpeneseqp/An1991.DAT:
/SIDS8/gcgdatca/geneseqgpeneseqp/An1991.DAT:
/SIDS8/gcgdatca/geneseqgpeneseqpyAn1995.DAT:
/SIDS8/gcgdatca/geneseqgpeneseqpyAn1995.DAT:
/SIDS8/gcgdatca/geneseqgpeneseqpyAn1995.DAT:
/SIDS8/gcgdatca/geneseqgpeneseqpyAn1995.DAT:
/SIDS8/gcgdatca/geneseqgpeneseqpyAn1999.DAT:
/SIDS8/gcgdatca/geneseqgpeneseqpyAn1999.DAT:
/SIDS8/gcgdatca/geneseqgpeneseqpyAn1999.DAT:
/SIDS8/gcgdatca/geneseqgpeneseqpyAn1999.DAT:
/SIDS8/gcgdatca/geneseqgpeneseqpyAn1999.DAT: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:\* /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:\* /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:\* /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:\* /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA1986.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:\* 14: 115: 116: 117: 118: 220: 221: 12::

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:\*

# SUMMARIES

	Description	Arabidopsis thalia	Human urokinase-tv	Peptide linker #1	Urokinase-type pla	HLA class I bindin	Synthetic pentapep	Synthetic heptapep	Cyclic pseudosteli	Pseudostellarin F	Human urokinase-ty	Human ADAMTS-1 pep
	ΩI	AAG83483	AAW12680	AAB37492	AAY81791	AAB75680	AAU05475	AAU05547	AAB11894	AAB11896	AAW12681	AAW78436
	DB	22	18	21	21	22	22	22	21	21	1.8	20
	Query Match Length DB ID	10	10	10	10	10	2	7	80	80	10	10
æ	Query Match	48.2	46.4	46.4	46.4	46.4	44.6	44.6	44.6	44.6	44.6	44.6
	Score	27	26	26	26	26	25	25	25	25	25	25
	Result No.		2	٣	4	2	9	7	80	6	10	11

Urokinase-type pla	ypiro itoantiqen	an insulin an	Gluconobacter subo	Anti-IqE antibody	Beta-1 integrin ce	Bacterial HsdM sub	Amino acid sequenc	Amino acid sequenc	Human urokinase-ty	Preferred decapept	Peptide used as hy	Urokinase-type pla	Human complementar	Human complementar	Human complementar		Human complementar	Saccharomyces cere	N-terminally disub		Cyclic peptide use	Xa	Factor Xa inhibiti	Interleukin-4 inhi	Brucella antigen t	a)	T cell epitope/MHC	Protein encoded by				
AAY81792	AAR82627	AAW94602	AAY49914	AAB30601	AAY28528	AAY 04 64 9	AAB19060	AAB19064	AAW12683	AAW44251	AAW45526	AAY81794	AAG93846	AAG93848	AAG93850	AAG95676	AAG95684	AAG96676	AAG96688	AAG96702	AAG96704	AAG87087	AAP30581	AAW08626	AAR98865	AAY28119	AAY28052	AAB13825	AAR97227	AAY07314	AAY10309	AAB67562
0 21	16	8 17	7	3 21	C	3 20	7	21	-	7	7		7	7	N	7	7		7	~	7		4	Н	5 17	3 20	6 20	7	17	3 20	3 20	22
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9.6	2.9		2.9			2.9	٠.	٠	5.9	5.9	2.9	2.9	5.9	2.9	2.9		•	5.9	5.9	5.9	5.9	5.9	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1
4.4	. 4	4	4	4	4	1 . 4	1 4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	3	3	3	3	3	3	3	3	3	3
25	Ñ	Ñ	ñ	7	5	7	5	5	ñ	5	5	Ñ	5	5	Ñ	7	Ö	5	7	5	Ö	5	7	7	2	2	7	2	7	7	7	7
12	14	15	16	17	18	19	20	21	22	23	24	25	26	27	. 28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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Plant; peptide pesticide; peptide herbicide; agricultural research.
                                                      Arabidopsis thaliana peptide ligand #123.
            AAG83483 standard; Peptide; 10 AA.
                                                                                                                          13-DEC-2000; 2000WO-GB04781.
                                                                                                                                        99GB-0029469.
                                        (first entry)
                                                                                 Arabidopsis thaliana.
                                                                                                                                                     (PROT-) PROTEOM LID.
                                                                                               WO200142279-A2.
                                                                                                                                       13-DEC-1999;
                                        11-SEP-2001
                                                                                                             14-JUN-2001.
                          AAG83483;
      AAG83483
RESULT
```

Roberts GW, Heal JR; WPI; 2001-381629/40. A set of peptide ligands for agricultural research and development of therapeutic agents comprise specific complementary peptides to proteins encoded by genes of plant genomes

Example 4; Page 48; 201pp; English

The present invention relates to a set of peptide ligands consisting of

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Human, fibrinogengamma, tissue targeting, ionising radiation, GPIIb, platelet membrane glycoprotein IIb; platelet membrane glycoprotein IIIa; IIIa; platelet activation; tumour; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Targeting agents, e.g. therapeutic agents and imaging agents, to target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissues, e.g. neoplasms, using ionizing radiation
                                                                                                                                                       Peptide linker #1 used as a control peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 10; Page 94; 135pp; English.
                                                   AAB37492 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                        28-APR-2000; 2000WO-US11485
                                                                                                                                                                                                                                                                                                                                                                                           99US-0302456.
                                                                                                                     26-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                          (UYVA-) UNIV VANDERBILT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-687452/67.
                                                                                                                                                                                                                                                                                         WO200066182-A1.
                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                         29-APR-1999;
                                                                                                                                                                                                                                                                                                                           09-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hallahan DE;
                                                                                      AAB37492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                  RESULT
AAB37492
                                                                      ;
0
specific complementary peptides to proteins encoded by genes of plant denomes. The present sequence is one such peptide from Arabidopsis thaliana. The peptides of the present invention are useful in an assay to identify a peptide, especially a peptide pesticide or herbicide. The peptides are also useful for tools for agricultural research and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antagonist; human; urokinase-type plasminogen activator receptor; huPAR; treat; metastasis; anglogenesis; chronic inflammation; Kaposi's sarcoma; diabetic retinopathy; rheumatoid arthritis; inhibit; proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW12680-90 are peptide antagonists of the human urokinase-type plasminogen activator receptor (huPAR) and are used to treat disorders involving huPAA, especially metastasis, inappropriate angiogenesis, chronic inflammation, Kaposi's sarcoma, diabetic retinopathy and rheumatoid arthritis. They may also inhibit proliferation of
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptide antagonists of huPAR - useful for treating uPA-mediated diseases, e.g. chronic inflammation or metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human urokinase-type plasminogen activator receptor antagonist 1.
                                                                                                                                                                                                        0;
                                                                                                                                                                     Length 10;
                                                                                                                                                                   Score 27; DB 22; Length 10
Pred. No. 1.3e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Valerio R;
                                                                                                                                                                                                                                                                                                                                                       AAW12680 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spear KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 21; 28pp; English.
                                                                                                                                                                  48.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nuPA-activated tumour cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-US12044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-0509208
                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosenberg S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-145694/13.
                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                     2 SGGYIFYTF 10
                                                                                                                     Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 AA;
                                                                                                                                                                                                                                                                  1 agglfyylf 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JUL-1995;
                                                                                    development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09705257-A1
                                                                                                                                                                                                                                                                                                                                                                                                                        06-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                         AAW12680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bray A,
                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                     AAW12680
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The present invention relates to a method for targeting a tissue in a vertebrate for delivery of an active agent. The method comprises exposing the tissue to ionising radiation before, after and/or during administration of a delivery vehicle comprising the active agent. The ionising radiation targets the delivery vehicle to the tissue. The carboxyl-terminal segment of the gamma chain of human fibrinogen (see ABB37480) can be used as a delivery vehicle in the present invention. Human fibrinogengamma peptide binds to platelet membrane glycoprotein III (IIIa) following platelet activation, and can be used for site-specific localisation to irradiated tumours. The methods of the present invention may be used for irradiated tumours. The methods of the present invention may be used for cargeting therapeutic agents and imaging agents to target tissues. Cargeting theoplasms, e.g. benign intracranial melanomas, arteriovenous maccination and can entity and the activation and can be used to active the active tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               malignant glioma, prostatic carcinoma, kidney carcinoma, bladder carcinoma, pancreatic carcinoma, thyroid carcinoma, lung carcinoma, colon carcinoma, rectal carcinoma, solid tumours, solid tumour metastases, angiofibromas, retrolental fibroplasia, haemangiomas and/or Kaposi's sarcomas. The present sequence is a peptide linker. This sequence was used as a control peptide in assays for determining the effects of the carboxyl-terminal segment of the gamma chain of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.4%; Score 26; DB 21; Length 10; 57.1%; Pred. No. 1.9e+02; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 57.1%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fibrinogen (AAB37480)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 SGGYIFY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGSYYYY
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Gaps

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Length 10;

h 46.4%; Score 26; DB 18; Length 10 Similarity 57.1%; Pred. No. 1.9e+02; 4; Conservative 2; Mismatches 1; Indels

Best Local Similarity

Matches

δλ

Query Match

AAY81791;

AAY81791

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characterised by expression of a human cancer associated antigen (CAA) precursor (I) coded by a NA Group 1 nucleic acid molecule (NI) comprising contacting the biological sample with an agent (A) that specifically binds to NI, (I) or its fragment, complexed with an human leukocyte antigen (HLA) molecule and determining the interaction between the agent and NI or (I), (I) has cytostatic activity and can be used in gene therapy and vaccine production. The method can be used for treating a subject with a condition characterised by expression of (I) in cells of a subject AAB75607 and AAB75608 represent proteins from human cancer associated antigen precursors, and AAB75609 to AAB75802 represent HLA class I binding motifs in human cancer associated antigen precursors and precursors given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pentapeptide ligand; drug design; high throughput screening; HTS; MQSAR; Multivariate Quantitative Structure Activity relationships.
                                                                                                                                                                                                                                                   Diagnosing a disorder characterized by expression of a human cancer associated antigen precursor, comprises detecting interaction of an agent with a nucleic acid molecule encoding the antigen precursor
                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method for diagnosing a disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 26; DB 22; Length 10
Pred. No. 1.9e+02;
1; Mismatches 0; Indels
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                                                                                                                                                                          Pfreundschuh'M;
                                                                                                                                                                                                                                                                                                                           Example 10; Page 63; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU05475 standard; Peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic pentapeptide ligand 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MELA-) MELACURE THERAPEUTICS AB
                                                                                                                                    (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.4%;
80.0%;
                                                        23-JUN-2000; 2000WO-US17207.
                                                                                              99US-0346498.
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                                                                                                                                                                          Sahin U, Tureci O,
                                                                                                                                                                                                               WPI; 2001-112465/12
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Best Local Similarity
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5 gyiff 9
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                                                                                              30-JUN-1999;
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                  04-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human urokinase-type plasminogen activator (huPA) receptor. The antagonists are used for treating huPA-mediated disorders, such as metastasis, inappropriate anglogenesis e.g. Kaposi's sarcoma and diabetic retinopathy and chronic inflammation e.g. rheumatoid arthritis.
                                                                                                                                                                    Antagonist; urokinase-type plasminogen activator receptor; human; huPA receptor; huPA-mediated disorder; metastasis; Kaposi's sarcoma; inappropriate anglogenesis; diabetic retinopathy; chronic inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cancer associated antigen precursor; cancer associated antigen; seminoma; HLA; human leukocyte antigen; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptides are urokinase-type plasminogen activator receptor (uPAR) antagonists useful for treating urokinase-type plasminogen activator-mediated diseases such as metastasis and inappropriate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                  Urokinase-type plasminogen activator receptor antagonist peptide #1
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Pred. No. 1.9e+02;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spear KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Column 19; 11pp; English.
                AAY81791 standard; peptide; 10 AA.
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                                                                                                                                                                                                                               rheumatoid arthritis; therapy.
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heptapeptide ligand; drug design; high throughput screening; HTS; MQSAR; Multivariate Quantitative Structure Activity relationships.
                         A novel method for identifying the interaction site, binding site or active site in a macromolecule, using of informative combinatorial chemistry, informative peptide libraries and Multivariate Quantitative Structure Activity Relationships
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5;
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Pred. No. 4.3e+05;
0; Mismatches 1; Indels
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                                                                                          Example 6; Fig 28; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU05547 standard; Peptide; 7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  44.6%;
80.0%;
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WPI; 2001-432565/46.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of type X/or artificial ligands of type Y, analysis and/or in the engineering of regions and/or parts of targets of type X and/or ligands of type Y, design of organic compound, catalyst, pharmaceutical, drug,
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active site in a macromolecule, using of informative combinatorial chemistry, informative peptide libraries and Multivariate Quantitative
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Pred. No. 4.3e+05;
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                                                                                                                                                                                                                                                                                                                               Example 8; Fig 30; 131pp; English.
                                                                                        chemistry, informative peptide in Structure Activity Relationships
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99US-0158077.
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Scott CP, Abel-Santos EV;

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                                                                                                                                                              The invention relates to methods of producing cyclic peptides which utilise the trans splicing ability of split inteins to catalyse cyclisation of a peptide from a precursor peptide. The precursor peptide has a target peptide interposed between two portions of a split intein. The interaction of the two portions of the split intein creates a catalytically active intein, and also forces the target peptide into a loop configuration that stabilises the ester isomer of the amino acid at the junction between one of the intein portions and the target peptide. To form a cyclic ester intermediate. The ester isomer of the amino acid at form a cyclic ester intermediate. The active intein catalyses the commation of an aminosuccinimide that liberates a cyclised form of the target peptide, which spontaneously rearranges to form the terrapt peptide, which spontaneously rearranges to form the creater peptide, which spontaneously rearranges to form the creative peptide flanked by the two portions of the split intein), also discloses nucleic acids encoding the precursor peptide (i.e. the cyclised peptide product or a splicing intermediate thereof (e.g., a thicester or a lariat intermediate), methods of generating peptide cyclised peptides or a splicing intermediates. The methods can be used for screening the cyclic peptides, for identifying molecules that bind to the target peptides and cyclic peptides. The methods can be used for screening the cyclic peptides, to detect the presence of a predetermined characteristic in a peptide ce.g., the ability to specifically bind a target molecule. The present sequence represents cyclic pseudostalarin F which was generated
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                                                  Non-naturally occurring nucleic acid molecule encodes a target peptide produced in a host system in a cyclized form or as a splicing intermediate of the cyclized form -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Split intein, peptide cyclisation; trans splicing; peptide library; peptide screening; cyclic ester intermediate; Ssp DnaE C-intein; plasmid pARCP-p; plasmid pARCBD-p; pseudostellarin F.
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Pred. No. 4.3e+05;
1; Mismatches 0; Indels
                                                                                                                                   Examples; Page 44; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB11896 standard; Protein; 8 AA.
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80.08;
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              WPI; 2000-431582/37
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Best Local Similarity
Matches 4; Conserv
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| sggyl 5
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07-OCT-1999;
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The invention relates to methods of producing cyclic peptides which

utilise the trains splicing ability of split inteins to catalyse

cyclisation of a peptide from a precursor peptide. The precursor peptide

thas a target peptide interposed between two portions of a split intein.

The interaction of the two portions of the split intein creates a

catalytically active intein, and also forces the target peptide into a

configuration that stabilises the ester isomer of the amino acid at

the junction between one of the intein portions and the target peptide.

A heteroatom from the other intein portion then reacts with the ester to

configuration of an aminosuccinimide that liberates a cyclised form of the

target peptide, which spontaneously rearranges to form the

ctarget peptide, which spontaneously rearranges to form the

thermodynamically favoured backbone cyclic peptide product. The

curvention also discloses nucleic acids encoding the precursor peptide

(i.e. the target peptide flanked by the two portions of the split

intein), expression vectors and host cells comprising the nucleic acid,

the cyclised peptide product or a splicing intermediate thereof (e.g., a

thloester or a lariat intermediate), methods of generating peptide

continees and methods of screening peptides and peptide

contines, and methods of screening peptides and peptides

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contines of the presence of a predetermined characteristic in a peptide

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                                                                                                                                                      Non-naturally occurring nucleic acid molecule encodes a target peptide produced in a host system in a cyclized form or as a splicing intermediate of the cyclized form -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence represents pseudostellarin F in its linear form. Plasmids pARCP-p and pARCBD-p encode pseudostellarin F. Expression of these plasmids generates cyclic pseudostellarin F (AAB11894).
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Pred. No. 4.3e+05;
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                                              Benkovic SJ, Scott CP, Abel-Santos EV;
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(PENN-) PENN STATE RES FOUND.
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80.0%;
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Best Local Similarity
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                                                                                         WPI; 2000-431582/37.
                                                                                                              N-PSDB; AAA61909
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| sggy|| 5
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leukocyte and thrombocyte blood count and increasing the erythrocyte blood count, e.g. for treatment of inflammatory diseases such as rheumatoid arthritis, hepatitis, nephritis, Crohn's disease, asthma and
            metalloproteinase disintegrin protein with a thrombospondin domain (ADAWTS-1). The peptide was used to generate a primer (AAAXT991) order to isolate the coding sequence (AAXT7990). The protein may be used in drug compositions and foodstuffs, as an agent for decreasing the
This sequence represents a peptide fragment of a human
                                                                                                                                                                                Query Match
Best Local Similarity 55.v
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Metalloproteinase-disintegrin protein with a thrombospondin domain, ARDS; ADAWTS-1; drug composition; foodstuff; leukocyte; thrombocyte; hepatitis; blood; erythrocyte; inflammatory disease; rheumatoid arthritis; asthma;
                                                                                                                                                                                                                                         AAW12680-90 are peptide antagonists of the human urokinase-type plasminogen activator receptor (huPAR) and are used to treat disorders involving huPA, especially metastasis, inappropriate angiogenesis, chronic inflammation, Kaposi's sarcoma; diabetic retinopathy and rhematoid arthritis. They may also inhibit proliferation of huPA-activated tumour cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                 New peptide antagonists of huPAR - useful for treating uPA-mediated diseases, e.g. chronic inflammation or metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human metalloproteinase-disintegrin protein with thrombospondin domain - useful as leukocyte and thrombocyte decreasing and egythrocyte increasing agent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nephritis; Crohn's disease; acute respiratory disease syndrome
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                                                                                                                                                                                                                                                                                                                                                                                                  Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 25; DB 18; Le
Pred. No. 2.9e+02;
2; Mismatches 1;
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                                                                                                       Valerio R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 30; 82pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW78436 standard; peptide; 10 AA.
                                                                                                       Spear KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ADAMTS-1 peptide fragment.
                                                                                                                                                                                                              Claim 1; Page 21; 28pp; English
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57.18;
            96WO-US12044.
                                          95US-0509208
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                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
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Kuno K, Matsushima K;
                                                                                                     Rosenberg S,
                                                                       CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-070277/06
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                   10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGYIFYT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9855643-A1
                                         31-JUL-1995;
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                                                                                                     Bray A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents an antagonist of the invention, and targets human urokinase-type plasminogen activator (huPA) receptor. The antagonists are used for treating huPA-mediated disorders, such as metastasis, inappropriate angiogenesis e.g. Kaposi's sarcoma and diabetic retinopathy and chronic inflammation e.g. rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antagonist; urokinase-type plasminogen activator receptor; human; huPA receptor; huPA-mediated disorder; metastasis; Kaposi's sarcoma; inappropriate angiogenesis; diabetic retinopathy; chronic inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptides are urokinase-type plasminogen activator receptor (uPAR) antagonists useful for treating urokinase-type plasminogen activator-mediated diseases such as metastasis and inappropriate
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Urokinase-type plasminogen activator receptor antagonist peptide #2
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     Length 10;
  Score 25; DB 20; Length 10
Pred. No. 2.9e+02;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                AAY81792 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rheumatoid arthritis; therapy
44.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0800213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHIR ) CHIRON CORP.
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AAR62161;

AAR62161

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important for antibody recognition. These structures include the A and B domains as well as scattered hydrophilic sequences. Domain B encompasses a consensus binding sequence of 8 amino acids that is necessary and sufficient for binding to UI RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ribonucleo- protein (snRNP) complex and is immunologically homologous to the HIV-1 envelope glycoprotein, gpl20/41. The 70K autoantigen can be used for diagnosing HIV-1 infection in a subject by identifying the presence of anti-HIV-1 antibodies that react with it. The 70K autoantigen has a relatively hydrophobic amino terminus and a hydrophilic carboxy terminus. Three structures within the 70K autoantigen are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR82609-28 are regions of the 70K autoantigen that are immunologically homologous to HIV-1 regions with the major neutralising epitopes of gpl20/41. The 70K autoantigen is part of the UI small nuclear
                                                                         70K autoantigen; Ul small nuclear ribonucleoprotein; snRNP; HIV-1; Human immunodeficiency virus type 1; infection; anti-HIV antibody; diagnosis; neutralising epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70k auto:antigen immunologically homologous to {\tt HIV}{-1} - useful for diagnosis and therapeutic treatment of {\tt HIV}{-1} in a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human insulin analogue construction synthetic octapeptide #15.
                                       70K autoantigen peptide immunologically homologous to HIV-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 24; DB 16; Length 8;
Pred. No. 4.3e+05;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insulin; human; hyperglycaemia; modified
                                                                                                                                                                                                                                                                                                                                                                                                        Takehana Y;
                                                                                                                                                                                                                                                                                                                                                             (UYSC-) UNIV SOUTHERN CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW94602 standard; peptide; 8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 55; 66pp; English.
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57.1%;
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01-MAY-1996 (first entry)
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Best Local Similarity
The 4; Conserv?
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1 gfafvtf 7
                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                        Douvas A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW94602;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          previous immunological analyses of the V3 loop of HIV-1 (AAR62159) have localised the main neutralising domains. The target of more than 80% of neutralising antibodies in HIV-1 infected sera from AIDS patients has now been found to overly the consensus binding sequence and domain A epitopes of the U1 snRNP 70% protein. In AIDS, antibody Litres are too low to arrest the disease, however, the homologous sequences in 70% are immunodominant targets of autoantibodies in the systemic rheumatoid disorder of mixed connective tissue disease. The liters of such autoantibodies exceed HIV-1 epitopes and are useful for treating HIV infection.
                                                                                                                                                                                                                                                                                                                epitope; autoantibody; immunoinfective cluster virus; nuclear protein antigen; systemic rheumatic disorder; human immunodeficiency virus; HIV-1; systemic lupus erythematosus; mixed connective tissue disease; scleroderma; glycoprotein 120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methods for treating immunoinfective cluster virus infections -
utilise antibodies or fragments characteristic of auto antibodies
produced by patients with rheumatic disorders
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                                                                                                                                                                                                                                                                           HIV-1 gp120 v3 loop neutralising domain.
                                                                                                                                                                                                                                                                                                                                                                                                                      Human Immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takehana Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 61; 106pp; English.
                                                                                                                                                      AAR62161 standard; peptide; 8 AA.
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ilarity 57.1%;
Conservative
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                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-302689/37
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Best Local Similarity
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                  GGYIFYT 9
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2 gfafvtf
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Gaps

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Sequence

Matches

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AAR82627

Length 8;

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The present invention describes analogues of human insulin modified at position 29 of the B chain, and optionally at other positions. The insulin analogues have modified physico-chemical and pharmacokinetic properties and are useful in the treatment of hyperglycaemia. They are less prone to dimerisation or self-association to higher molecular weight forms and so possess a comparatively more trapid onset of activity while retaining the biological activity of native human insulin. The present sequence represents a synthetic octapeptide used in the preparation of human insulin analogues in an example from the present invention.
                                                                                                                                                                                                                                                        New insulin analogues modified at B-chain position 28 - showing reduced self-association and more rapid onset of activity, used for
                                                                                                                                                                                              Frank BH, Shields JE;
                                                                                                                                                                                                                                                                                                                          Example 19; Column 17; 51pp; English
                               91US-0686632.
89US-0308352.
89US-0388201.
93US-0057201.
 93US-0057201
                                                                                                                                                                                              Chance RE, DiMarchi RD,
                                                                                                                                                                                                                                                                                          treating hyperglycaemia
                                                                                                            (CHAN/) CHANCE R E. (DIMA/) DIMARCHI R D.
                                                                                                                                             (FRAN/) FRANK B H.
(SHIE/) SHIELDS J E.
                                                                                                                                                                                                                          WPI; 1996-238795/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 AA;
                               17-APR-1991;
09-FEB-1989;
04-AUG-1989;
05-MAY-1993;
05-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                             (DIMA/)
(FRAN/)
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Query Match 42.9%; Score 24; DB 17; Length 8; Best Local Similarity 100.0%; Pred. No. 4.3e+05; Matches 4; Conservative 0; Mismatches 0; Indels Qy 7 FYTF 10

Db 3 fytf 6

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Gaps

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> Search completed: February 21, 2002, 17:04:31 Job time: 188 sec

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Perfect score:

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Sequence 28,
Sequence 142,
Sequence 7, A
Sequence 8, A
Sequence 9, A
Sequence 15,
Sequence 14,
Sequence 14,
Patent No. 551
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Sequence 13,
Sequence 5,
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Sequence 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Steven Rosenberg, Kerry L. Spear, Robert Valerio, APPLICANT: and Andrew Bray TITLE OF INVENTION: Peptide Analog Inhibitors of Urokinase TITLE OF INVENTION: Receptor Activity NUMBER OF SEQUENCES: 11 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
           US-08-257-782-16
US-08-577-846-16
US-08-079-144-16
US-09-411-531A-4
PCT-US95-03236-28
US-09-139-802-142
US-08-279-906A-7
US-08-279-906A-8
US-08-279-906A-8
US-08-279-906A-9
US-08-279-906A-9
US-08-279-906A-9
US-08-279-906A-15
US-08-1429-15
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US-08-102-738-13
US-08-486-013-5
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Pred. No. 71;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                           5514646-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08800213A Patent No. 6030940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         February 12, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Fujita, Sharon
REGISTRATION NUMBER: 38,459
REFRERNCE/POCKET NUMBER: 1118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510 923 2706
TELEPHONE: 510 655 3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Chiron Corporati
STREET: 4560 Horton Street
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 510 655 3542 INFORMATION FOR SEQ ID NO: 1:
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57.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6030940 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: Fe
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US-08-800-213A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-800-213A-1
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Sequence 12, Appl
Sequence 67, Appl
Sequence 19, Appl
Patent No. 5514646
                                                                                                                       Search time 12.47 Seconds
(without alignments)
18.046 Million cell updates/sec
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Sequence 2,
Sequence 67,
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Sequence 4,
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/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                                  Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-282-758B-35
US-08-374-652C-14
US-08-800-213A-5
US-08-800-213A-9
                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                               212252 seqs, 22503292 residues
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                                                                                                                           2002, 17:02:58
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Listing first 45 summaries
                                                                                       OM protein - protein search, using sw model
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                                                                                                                           February 21,
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Match Length
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Maximum DB seq length: 10
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Score

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Gaps

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APPLICANT: Douvas, Angeline
APPLICANT: Takehana, Yoshi
APPLICANT: Takehana, Yoshi
APPLICANT: Ehresmann, Glenn
ATILE OF INVENTION: THERAPEUTIC STRATEGIES FOR
TITLE OF INVENTION: IMMUNOINFECTIVE CLUSTER VIRUS INFECTIONS
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 No. 5707626th Figueroa Street, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
      PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 25; DB 3;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/029,850
FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Spitals, JOHN P.
REGISTRATION NUMBER: 29,215
                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,213A
FILING DATE: February 12, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 1920-331
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 977-1001
TELEFAX: (213) 977-1003
IFORMATION FOR SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/704,170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-704-170-67; Sequence 67, Application US/08704170; Patent No. 5707626
                                                                                                                                 NAME: Fujita, Sharon
REGISTRATION NUMBER: 38,459
REFRENCE/DOCKET NUMBER: 1118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510 923 2706
TELEPHONE: 510 655 3542
                                                                                                               ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 57.13
امر 4; Conservative
                                                                                                                                                                                                                                                                                                              10 amino acids
                                                                                                                                                                                                                                          TELEFAX: 510 655 3542 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Los Angeles
California
                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                    FILING DATE: Fe CLASSIFICATION:
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COUNTRY: U.
ZIP: 90012
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US-08-800-213A-2
                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                              LENGTH:
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                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Valmori, Danila, Cerottini, Jean-Charles
TITLE OF INVENTION: Isolated No. 6025470a-and Decapeptides Which Bind To
TITLE OF INVENTION: HA Molecules, And The Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Patent No. 6030940
GENERAL INFORMATION:
APPLICANT: Steven Rosenberg, Kerry L. Spear, Robert Valerio, APPLICANT: and Andrew Bray
TITLE OF INVENTION: Peptide Analog Inhibitors of Urokinase TITLE OF INVENTION: Receptor Activity
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.6%; Score 25; DB 3;
60.0%; Pred. No. 1.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COPRATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,963
FILING DATE: 23-June-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Hanson, No. 6025470man D. REGISTRATION UNMBER: 30,946
REFERRUCE/DOCKET NUMBER: LUD 548
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                             Sequence 17, Application US/08880963 Patent No. 6025470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                 ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 3; Conserv
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4 GQYLWYT 10
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4 GFVFY 8
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APPLICANT: Ehresmann, Glenn
TITLE OF INVENTION: THERAPEUTIC STRATEGIES FOR
TITLE OF INVENTION: IMMUNOINFECTIVE CLUSTER VIRUS INFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Methods to Diagnose and Treat HIV-1 TITLE OF INVENTION: Methods to Diagnose and Treat HIV-1 TITLE OF INVENTION: Infection NUMBER OF SEQUENCES: 66 CORRESPONDENCE ADDRESS: ADDRESSE: Campbell STREFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.9%; Score 24; DB 5; Length 8; 57.1%; Pred. No. 1.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                               ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 North Figueroa Street, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/029,850
FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US95-03236-19; Sequence 19, Application PC/TUS9503236; GENERAL INFORMATION:
                                                                                                                                   Sequence 67, Application PC/TUS9402631 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 90012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Spitals, John P.
REGISTRATION NUMBER: 29,215
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                         Douvas, Angeline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (213) 977-1001
TELEFAX: (213) 977-1003
INFORMATION FOR SEQ ID NO: 67
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US94-02631-67
                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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Best Local Similarity
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  5 YIFYTF 10
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2 FLFHTF 7
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ZIP: 90012
                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Pred. No. 1.6e+05;
3; Mismatches 0; Indels
                                                                                               Score 24; DB 1; Length o, Pred. No. 1.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation - Corporate
ADDRESSEE: Patents
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Miller, Timothy J.
APPLICANT: Klepfer, Sharon
APPLICANT: Reed, Albert Paul
APPLICANT: Jones, Elaine V.
TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,625A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/880,194
FILING DATE: 08-MAY-1992
PRIOR APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Schreck, Patricia A.
REGISTRATION NUMBER: 33,777
REPERDENCE/DOCKET NUMBER: SBC H85010-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/08331625A Patent No. 6057436 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (215) 270-5015
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 12:
SEGUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.98;
50.08;
                                                                                                               42.98;
57.18;
                                                                                            Ouery Match
Best Local Similarity 57.1.
---- 4; Conservative
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Best Local Similarity 50.0
Matches 3; Conservative
                                , MOLECULE TYPE: peptide US-08-704-170-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19406-2799
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
amino acid
                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                            4 GYIFYTF 10
                                                                                                                                                                                                                                  2 GFAFVTF 8
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                                                                                                                                                                                                                                                                                                               US-08-331-625A-12
                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
TYPE:
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APPLICANT: Steven Rosenberg, Kerry L. Spear, Robert Valerio, APPLICANT: and Andrew Bray TITLE OF INVENTION: Peptide Analog Inhibitors of Urokinase NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
   IMMUNO-POTENTIATING SYSTEMS FOR PREPARATION OF IMMUNOGENIC MATERIALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 10;
                                                                                                                                                                                                                                               OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,213A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .... 1.6e+02;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 24;
Pred. No. 1
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/143,365A FILING DATE: 29-OCT-1993 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: Lowell-2 TELECOMMUNICATION INFORMATION:
           TILLE OF INVENTION.

TITLE OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
CORRESPONDENCE Hendricks and Assoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08800213A Patent No. 6030940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               February 12, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Chiron Corporation 4560 Horton Street
                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna M
REGISTRATION NUMBER: 32,535
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (703) 425-4250
TELEFAX: (703) 425-2767
INPORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 42.9%;
Similarity 80.0%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                       COMPUTER READABLE FORM:
     TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FRAGMENT TYPE:
US-08-143-365A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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1 GGYCF 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-800-213A-4
                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ## APPLICANT: CHANCE, RONALD E.; DIMARCHI, RICHARD D.; FRANK, BRUCE H.; SHIELDS, JAMES E.
### TITLE OF INVENTION: INSULIN ANALOGS MODIFIED AT POSITION FOR THE B CHAIN B CHAIN.
### CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CARRENT APPLICATION DATA:
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Pred. No. 1.6e+05;
l; Mismatches 2;
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                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Imbra, Richard J.
REGISTRATION NUMBER: 37,643
REFERENCE/DOCKET NUMBER: FP-SI 1394
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFHONE: (619) 535-9049
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                 тиныя: PCT/US95/03236
13-МАR-1995
N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/57,201
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 686,632
FILING DATE: 17-APR-1991
APPLICATION NUMBER: 388,201
FILING DATE: 04-AUG-1889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequegce 11, Application US/08143365A
Patent'No. 5726292
GENERAL INFORMATION:
APPLICANT: LOWELL, George H
           COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOC 20TRAPHE: PATTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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FILING DATE: 09-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 42.9%;
Best Local Similarity 57.1%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                             8 amino acids
ZIP: 92122
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                  FILING DATE: 1. CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 GYIFYTF 10
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                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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; Patent No.
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Gaps

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APPLICANT: Lang, John M.
APPLICANT: Lang, John M.
APPLICANT: Lang, John M.
TITE OF E INVENTYO: Alpha-1 Proteinase Inhibitor Binding Peptides
FILE REFERENCE: MSB-7248
CURRENT APPLICATION NUMBER: US/09/127,574
CURRENT FILING DATE: 1998-07-31
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 6
TAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-127-574-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 35, Application US/08273474
Patent No. 5691134
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
OF DETECTION UTILIZING THE SAME
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS;
ADDRESSEE:
ADDRESSEE:
SUITE 1200, The Candler Building, 127
STREET:
PRACTICE OF INVENTION:
STREET:
PRACTICE OF SEQUENCES
STREET:
SUITE 1200, The Candler Building, 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.3%; Score 22; DB 1; Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,474
FILING DATE: 13-JUL-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 22; DB 2;
Pred. No. 1.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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13-JUL-1993
NN: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 30303-1811
COMPUTER REALABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Perryman, David G.
REGISTRATION NUMBER: 33,438
REFERNCE/DOCKET NUMBER: 141
FELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             39.3%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Perryman, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (404) 688-9880 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 YIFYT 9
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2 FIYYT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: INNOGENETICS N.V.
TITLE OF INVENTION: NEW 17 kDa BRUCELLA ABORTUS ANTIGEN, RECOMBINANT
TITLE OF INVENTION: POLYPEPTIDES, NUCLEIC ACIDS CODING FOR THE SAME AND USE
TITLE OF INVENTION: THEREOF IN DIAGNOSTIC AND PROPHYLACTIC METHODS AND KITS
FILE REFERENCE: INNSO06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.1%; Score 23; DB 4; Length 9; 100.0%; Pred. No. 1.6e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "OTHER"
/label= Xaa
/note= "1-naphthylalanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: INNSOME CURRENT APPLICATION NUMBER: US/08/849,634B CURRENT FILING DATE: 1997-12-01 NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (7)..(9)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-08-849-634B-7
                                                                                                                  1118.002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08849634B Patent No. 6296855
                                                                         NAME: Fujita, Sharon
REGIZTRATION NUMBER: 38,459
REFRENCE/DOCKET NUMBER: 1118
TELECOMMUNICATION INFORMATION:
TELEPAN: 510 923 2706
TELEPAN: 510 655 3542
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09127574 Patent No. 5985836
                                     CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Ver. 2.1
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                                                                                                                                                                                                                                 LENGTH: 10 amino acids
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Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                         single
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OTHER INFORMATION:
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OTHER INFORMATION:
                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | |: ||
4 GQYLXYT 10
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2 GYIF 5
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SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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  NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: Suite 1200, The Candler Building,
STREET: 127 Peachtree Street NE
CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: February 21, 2002, 17:04:50 Job time: 112 sec
                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US94/07881
FILING DATE: 13 July 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/092,110
FILING DATE: 13 July 1993
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                        COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                7 amino acids
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Best Local Similarity
Local 4; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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                                                                                                                                        COUNTRY: USA
ZIP: 30303-1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                          MEDIUM TYPE:
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APPLICANT: Kilpatrick, David R.
TITLE OF INVENTION: POLIOVIRUS SPECIFIC PRIMERS AND METHODS
TITLE OF INVENTION: OF DETECTION UTILIZING THE SAME
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
100.0%; Pred. No. 1.6e+05;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 7;
1.6e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Government of the United States of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,100
                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: Suite 1200, The Candler Building, 127
STREET: Peachtree Street, NE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION DATA:
APPLICATION UNBER:
FILING DATE: 13-JUL-1993
ATTORNEY/AGENŢ INFORMATION:
NAME: PETYWAN, DAVIÐ G.
REGISTRATION NUMBER: 33,438
REFERBNCE/DOCKET NUMBER: 1414.617
TELECOMMUNICATION INFORMATION:
TELEFHONE: (404) 688-0970
TELEFAN: (404) 688-9880
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
FCT-US94-07881-35
Sequence 35, Application PC/TUS9407881
GENERAL INFORMATION:
                                                                                                                                                                           US-08-935-100-35; Sequence 35, Application US/08935100; Patent No. 6143494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.3%; Scc.
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
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Best Local Similarity
Best Local Similarity
Matches 4; Conserve
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ZIP: 30303-1811
                                                                                                                                                                                                                                                                                                                                                                                                                                            Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Atlanta
STATE: Georgia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||||
4 IFYT 7
                                                           IFYT 9
                                                                                                 4 IFYT 7
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APPLICANT:
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Length 7;

77

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 21, 2002, 17:07:09 ; Search time 12.69 Seconds (without alignments) 186.084 Million cell updates/sec Run on:

US-08-753-851-12 164 Perfect score: Title:

1 LCLVPLSLAQIDLNITCRFAGVFHVEKNGRY 31 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues

Searched:

6512 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 31 Minimum DB : Maximum DB :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

pIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### STIMMARTES

SUMMARIES	Description	CD44SP - human	hypothetical prote		omol	olfactory glycopro		dnaK-type molecula	hypothetical prote	┙	hypothetical prote	O	hypothetical prote		hypothetical prote	beta-lactoglobulin	hypothetical prote	. beta-lactoglobulin	plastoquinolplas	tissue kallikrein	dihydropyrimidine	Ψ	major fecal allerg	lysosomal acid lip	NADH dehydrogenase	kallikrein rK8 (pK	T-cell receptor al	hypothetical prote	hypothetical prote	
SUMM	ID	177372	878310	800579	F44957	A60889	S10052	A43826	H64711	145911	B82233	S31613	A83698	A81078	D82348	B61525	A35121	D61590	T07337	S06660	A44626	S12502	B31657	155596	T12250	S46211	E53480	T08489	F64121	
	DB	. 7	7	7	7	~	7	7	7	7	7	7	7	~	7	7	7	7	7	~	~	7	7	~	~	7	~	~	7	
	Length	29	29	26	22	17	28	18	18	28	30	19	23	29	31	26	29	56	31	23	23	23	23	28	29	29	31	31	21	
de	Query Match	32.3	20.7	19.5	18.9		18.3	17.7		17.7	17.7	17.1	17.1	17.1	17.1								ď.	5.	Š.	δ.	δ.	15.9		•
	Score	53	34	32	31	30	30	29	29	29	29	28	28	28	S	27.5	$\sim$	26.5		26	26	26	56					56	25.5	
	Result No.	1	2	e	4	2	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	. 22	23	24	25	26	27	28	•

Ig kappa chain V r NADH dehydrogenase	Ig light chain V r	ig Kappa Chain V i probable flagellar	DNA primase (EC 2.	PEB1 5'-region hyp	gamma-crystallin I	phospholipase A2 (	phospholipase A2 (	alpha-glucosidase	H+-transporting AT	hypothetical prote	insulin chain B -	formylmethanofuran	serine proteinase
A32248 T13836	PC1001	A61144	PQ0710	D48518	A25865	A34280	B44180	PC2361	S21815	D72276	S15778	A58946	S71592
2.2	77	7 (7	7	7	7	7	7	7	~	7	~	7	7
25	28	7 6	20	21	25	26	27	30	30	30	17	17	18
15.5	15.5	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	14.6	14.6	14.6
25.5	25.5	25.2	25	25	25	25	25	25	25	25	24	24	24

# ALIGNMENTS

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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Saccession: 177372
R; Tanabbe, K. K.; Nishi, T.; Saya, H.
Mol. Carcinog. 7, 212-220, 1993
A; Title: Novel variants of CD44 arising from alternative splicing: changes in the CD4
A; Feference number: 157483; MUID:93356912
A; Reference number: 157483; MUID:93356912
A; Reference number: 15737
A; Reference number: 157483; MUID:935697; PIDN:AAB27917.1; PID:9435698
A; Residues: 1-29 < RES>
A; Residues: 1-29 < RES>
A; CGenetics:
A; Genetics:
A; G
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0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.3%; Score 53; DB 100.0%; Pred. No. 0.2 iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GDB:120739; OMIM:107269
A;Map position: 11pter-11p13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 32.3
Best Local Similarity 100.
Matches 11; Conservative
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I77372
CD44SP - human
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12 LCLVPLSLAQI 22 Dp

hypothetical protein 29a - Odontella sinensis chloroplast
C;Species: chloroplast Odontella sinensis
C;Date: 17-Feb-1998 #sequence\_revision 26-Feb-1998 #text\_change 24-Apr-1998
C;Accession: S78310
B;Kowallik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U.
Plant Mol. Biol. Rep. 13, 336-342, 1995
A;Title: The Chloroplast Genome of a chlorophyll a+c- containing Alga, Odontella sine
A;Reference number: S7838
A;Accession: S78310
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-29 <KOW>
A;Rooss-references: EMBL: Z67753; NID: 91185127; PID: e211861; PID: 91185200
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995

C;Genetics:
A;Genome: chloroplast
C;Keywords: chloroplast

; 0

Gaps

us-08-753-851-12.rpr

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C;Species: Schizosaccharomyces pombe
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 30-Sep-1993
C;Accession: S10052
R;Otaka, E.; Higo, K.I.; Itoh, T.
Mol. Gen. Genet. 191, 519-524, 1993
A;Title: Yeast ribosomal proteins: VII. Cytoplasmic ribosomal proteins from Schizosac A;Reference number: S07293; MuID:84038947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dnaK-type molecular chaperone - Ajellomyces capsulata (fragment)
N;Alternate names: 80K heat shock protein 70 homolog
C;Species: Ajellomyces capsulata, Histoplasma capsulatum
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 17-Mar-1999
C;Accession: A43826
R;Gomez, F.J.; Gomez, A.M.; Deepe Jr., G.S.
Infect. Immun. 60, 256-2571, 1992
A;Title: An 80-kilodalton antigen from Histoplasma capsulatum that has homology to he A;Reference number: A43826; MUID:92307875
   A;Residues: 1-17 <SCH>
A;Note: this protein was purified from whole brain
C;Comment: The monoclonal antibody RB-8 blads this integral membrane glycoprotein on C;Keywords: glycoprotein; membrane protein; olfaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ribosomal protein L37 e – fission yeast (Schizosaccharomyces pombe) (fragment) N;Alternate names: ribosomal protein SP-L27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description: involved in protein folding and assembling/disassembling of C; Superfamily: heat shock protein 70
C; Keywords: ATP; heat shock; molecular chaperone; stress-induced protein
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                                                                                                                                                                                                                                                                   3; Indels
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                                                                                                                                                                                                 Score 30; DB 2;
Pred. No. 4.4e+02;
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Pred. No. 7.2e+02;
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A; Residues: 1-28 <OTA>
C; Superfamily: rat ribosomal protein L37
C; Keywords: protein blosynthesis; ribosome
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60.0%;
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Best Local Similarity 46.2%;
Matches 6; Conservative
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33.3%;
                                                                                                                                                                                                                                                                   5; Conservative
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1 LLXVTISLSKVELSV 15
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IDLGTTYSVVGIF 18
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A;Molecule type: protein
A;Residues: 1-18 <GOM>
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 6; Conserv
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RRKGKFHVQK 28
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S10052
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                                                                                                                                                                                                                                                                                                                                                  hypothetical protein 547 (hisA 5' region) - Methanococcus vannielii (fragment) (5/pecies: Methanococcus vannielii (5/peci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Schwob, J.E.; Gottlieb, D.I.
J. Neurosci. 8, 3470-3480, 1988
A;Title: Purification and characterization of an antigen that is spatially segregated in A;Reference number: A60889; MUID:89010968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Takeda, S.; Sato, F.; Ida, K.; Yamada, Y.
Plant Cell Physiol. 31, 215-221, 1990
A;Title: Characterization of polypeptides that accumulate in cultured Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·;
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C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 12-Apr-1995
C;Accession: F44957
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: A60889
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                                                                        Gaps
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      Length 29;
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Pred. No. 3.3e+02;
0; Mismatches 1; Indels
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Score 34; DB 2; 1
Pred. No. 1.9e+02;
2; Mismatches 5,
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Pred. No. 4e+02;
; Mismatches
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20.7%;
50.0%;
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85.7%;
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50.0%;
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                 Conservative
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A; Accession: F44957
A; Status: preliminary
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A, Residues: 1-22 <TAK>
C, Superfamily: thaumatin I
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Query Match
Best Local Similarity
Matches 7; Conserv
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Length 30;

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A;Cross-references: GB:AE004197; GB:AE003852; NID:g9655642; PIDN:AAF94334.1; GSPDB:GN
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RiHird, D.; Worrall, D.; Hodge, R.; Paul, W.; Smartt, S.; Draper, J.; Scott, R. submitted to the EMBL Data Library, December 1992
A; Description: The anther-specific protein encoded by the Brassica napus and Arabidop A; Reference number: $31612
A; Accession: $31613
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A;Experimental source: strain C-125
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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.;
Nucleic, Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Brassica napus (rape)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Nov-2000
C;Accession: S31613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein BH0385 [imported] - Bacillus halodurans (strain C-125) C; Species: Bacillus halodurans C; Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          beta-1,3-glucanase homolog (clone A28) - rape (fragment)
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A,Residues: 1-19 <HIR>
A,Cross-references: EMBL:X69890; NID:g17735; PID:g17736
A,Experimental source: clone A28
C,Superfamily: beta-1,3-glucanase
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Pred. No. 9.7e+02;
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ilarity 100.0%; Pred. No. 1.2e+03;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                  Score 29; DB 2; Pred. No. 1.1e+03;
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A; Accession: A83698
                                                                                                                                                                                                                                                                                                                  17.78;
46.28;
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55.6%;
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Best Local Similarity 55.0.
                                                                                                                                                                                                                                                                                                                  Query Match 17.7
Best Local Similarity 46.2
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | ||:
5 FIGFFHLSLLFRY 17
                                                                                                                                                                                                                                                                                                                                                                                                                                    19 FAGVFHVEKNGRY 31
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Best Local Similarity
Matches 5; Conserv
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A; Residues: 1-23 <STO>
                                                   A; Molecule type: DNA
A; Residues: 1-30 <HEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 NDRCKFPGV 17
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                                 A;Status: preliminary
A; Accession: B82233
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                                                                                                                                                                                                   A; Gene: VC1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11
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                                                                                                                                 Riromb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: Bos primigenius taurus (cattle)
C; Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Aug-1999
C; Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Aug-1999
C; Date: 16-Aug-1999
R; Kowalski, J; Gilbert, S.A.; van Drunen-Littel-van den Hurk, S.; van den Hurk, J.; Bat Vaccine 11, 1100-1107, 1993
A; Title: Heat-Shock Promoter-Driven Synthesis of Secreted Herpesvirus Glycoproteins in TA; Reference number: 145911; MUID:94070117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Description: involved in protein folding and assembling/disassembling of protein compl
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein VC1175 [imported] - Vibrio cholerae (strain N16961 serogroup O1) C; Species: Vibrio cholerae C; Species: Vibrio cholerae C; Species: Vibrio cholerae C; Species: Us. 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C; Accession: B8233 R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000 A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A; Reference number: A802035; MUID: 20406833
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE000651; GB:AE000511; NID:92314708; PIDN:AAD08578.1; PID:9231471
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                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: 145911
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-28 <KOM>A;Csoss-references: GB:M98823; NID:g409185; PIDN:AAA30568.1; PID:g409186
C;Genetics:
C;Genetics:
C;Function:
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0
                           - Helicobacter pylori (strain 26695)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 29; DB 2; Le
Pred. No. 6.5e+02;
2; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 9
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: 1e+03;
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Pred. No. 1
0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N; Alternate names: heat shock protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.7%;
40.0%;
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Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 CRFAGVFHVEKNGRY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein HP1536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-18 <TOM>
                                                                                                      C; Accession: H64711
R; Tomb, J.F.; White
                     hypothetical
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Length 26; Indels

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Comp. Biochen. Physiol. B 99, 917-921, 1991
A;Title: Identification of alpha-lactalbumin and beta-lactoglobulin in cynomolgus mon A;Reference number: A61525; MUID:92164307
A;Recession: B61525
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-26 <AZUS
C;Superfamily: lipocalin; lipocalin homology
                                                                                                                                                                                                                                                                                                                          16.8%; Score 27.5; DB 2; 30.0%; Pred. No. 1.6e+03; iive 5; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: February 21, 2002, 17:09:01
Job time: 112 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                           5 PLSLAQIDLNITCRFAGVFH 24
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                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
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Best Local Similarity
           R; Azuma, N.; Yamauchi, K.
                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                        protein NMB1491 [imported] - Neisseria meningitidis (strain MC58 serogroup
                                                                                                                                                                                                                                                   Rifettelin, H.: Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; T., H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A.Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A.Title: Complete genome sequence of Nelsseria meningitidis serogroup B strain MC58.
A.Reference number: A81000; MUID:20175755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Cross-references: GB:AE002498; GB:AE002098; NID:g7226724; PIDN:AAF41847.1; PID:g72267:
A:Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Cross-references: GB:AE004112; GB:AE003852; NID:99654625; PIDN:AAF93402.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype E1 Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: D82348
R; Heidelberg, J.F.; Elsen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.
Achardson, D.; Ermolaeva, M.D.; Vanathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUID: 20406833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein VC0226 [imported] - Vibrio cholerae (strain N16961 serogroup O1) C;Species: Vibrio cholerae C;Date: 18-Aug_2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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                                                                                                                                                                      C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: A81078
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C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 15-Oct_1994 #sequence_revision 15-Oct-1994 #text_change 11-May-2000
C;Accession: B61525
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Pred. No. 1.5e+03;
1; Mismatches 1
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71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 17.1
Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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A;Molecule type: DNA
A;Residues: 1-31 <HEI>
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LCLMPAS 15
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3 GVFHV
                                                                                                                                           hypothetical
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                             anabaena sp
azotobacter
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                                                                                                         sus scrofa
                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
HYPOTHETICAL 3.5 KDA PROTEIN IN YCF33-TRNY INTERGENIC REGION (ORF29A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                      Kowallik K.V., Stoebe B., Schaffran I., Kroth-Pancic P., Freier U.,
"The chloroplast genome of a chlorophyll a+c-containing alga,
Odontella sinensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                            Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
Biddulphiophycidae; Eupodiscales; Eupodiscaceae; Odontella.
NCBL_TaxID=2839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
P19343
P31144
P80640
Q44507
P23002
P42022
Q09148
P24365
P52964
Q38199
                                                                                             P80158
P34964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               c; Hypothetical protein.
29 AA; 3481 MW; 4960F2ACA72ACBA2 CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                  ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34; D
Pred. No. 67
FIBB_PAPHA
UKA2_HUMAN
UC34_MAIZE
                                              YPE4_LACLC
COOT_SARBU
PTHP_STRSA
FLAW_AZOVI
DNIV_BPD10
FLB1_TREHY
NEUU_PIG
                                                                                                                                                                                                                                                                                                                                      Plant Mol. Biol. Rep. 13:336-342(1995).
                            NIS1_ANASQ
FLAW_AZOCH
                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 267753; CAA91683.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
 1 LCLVPLSLAQIDLN 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||| :: ||| |
12 LCLFCTNIDQIDFN 25
                                                                                                                                                                                                                                          Odontella sinensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
112.8
112.8
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112.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Chloroplast;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEF2_MACMU P82317;
                                                                                                                                                                                 YCX4_ODOSI
P49830;
 SEQUENCE
                                                                                                                                                               YCX4_ODOSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEF2_MACMU
334
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112.983 Million cell updates/sec
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P82317 macaca mula
P56306 chlorella v
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pseudechis
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aspergillus
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chlorella v
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escherichia
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                                                                 February 21, 2002, 17:08:44; Search time 10.06 Seconds
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P31230
P56738
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Q04238
P14471
O96810
P56708
P19187
P80744
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P80526
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P81440
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P56314
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                         1 LCLVPLSLAQIDLNITCRFAGVFHVEKNGRY 31
                                                                                                                                                                                          hits satisfying chosen parameters:
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DIUX_DIPPU
PETN_CYACA
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PETL_CHLVU
UC29_MAIZE
EMA2_MOUSE
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CXMA_CONMR
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LE05_BIOGL
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NEJ2_FASHE
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Y073_ARCFU
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FIBB_HORSE
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                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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Maximum DB
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Result Š. ö

and for commercial

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Gaps

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(See http://www.isb-sib.ch/announce/
                                                                        Electron transport; Chloroplast; Respiratory chain; Transmembrane;
                                                                                                                                                       Score 26.5; DB 1; Length 31;
Pred. No. 1e+03;
                                                                                                                                                                                  Indels
     Usage by
                                                                                                 POTENTIAL. FEE39CBC6F911C9B CRC64;
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8
    modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                        15 AA
                                                                                                                                                                                  9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                            8 IALLISALVITLTC-YIGLLKIK 29
                                                                                                                                                                                                           4 VPLSLAQIDLNITCRFAGVFHVE 26
                                                                                                                                                       16.2%;
21.7%;
                                                                                                4 24
31 AA; 3441 MW;
                                                         EMBL; AB001684; BAA57985.1;
                                                                                                                                      genome analysis program."
                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MaizeDB; 123960; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Coleoptile;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 VPLSLAQID 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4577;
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P31230;
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P80635;
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                                                                                    Thylakoid.
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NON_TER
SEQUENCE
                                                                                                               SEQUENCE.
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                                                                                                TRÂNSMEM
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EMA2_MOUSE
    οy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wakasugi T., Nagai T., Kapoor M., Sugita M., Ito M., Ito S.,
A Tsudzuki T., Nagai T., Kapoor M., Sugita M., Ito M., Ito S.,
A Tsudzuki T., Nakashima K., Tsudzuki T., Suzuki Y., Hamada A., Ohta T.,
Inamura A., Yoshinaga K., Sugiura M.;
Inamura I., Ashina K., Sugiura M.;
Inamura A., Yoshinaga K., Sugiura M.;
Is Important For Potoautotropelic Growth As Well As For Electron
Is Important For Photoautotropelic Growth As Well As For Electron
Is Important Location: Thyladolib Membrane-Associated.
                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chloroplast.
Bukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales; Chlorellaceae; Chlorella.
NCBL_TaxID=3077;
                        MEDLINE=20002603; PubMed=10531277;
Tang Y.Q., Yuan J., Miller C.J., Selsted M.E.;
"Isolation, characterization, cDNA cloning, and antimicrobial
properties of two distinct subfamilies of alpha-defensins from rhesus
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-ANG-2001 (Rel. 40, Last annotation update)
CYTOCHROME B6-F COMPLEX SUBUNIT VI (CYTOCHROME B6F COMPLEX SUBUNIT
                                                                                          Infect. Immun. 67:6139-6144(1999).
-1- FUNCTION: HAS BACTERIOSTATIC ACTIVITY AGAINST L.MONOCYTOGENES,
E.COLI AND S.AUREUS, MICROBICIDIAL ACTIVITY AGAINST
L.MONOCYTOGENES AND S.AUREUS AND ANTIFUNGAL ACTIVITY AGAINST
                                                                                                                                                               -!- MASS SPECTROMETRY: MW-3465.9; METHOD-MALDI.
-!- SIMILARITY: BELONGS TO THE FAMILY OF CORTICOSTATIN/DEFENSIN
                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                          Score 27; DB 1; Length 30;
Pred. No. 8.2e+02;
2; Mismatches 11; Indels
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BY SIMILARITY.
BY SIMILARITY.
D617D04085E7E09F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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MEDLINE=97303241; PubMed=9159184;
                                                                                                                                                                                                                                                              Defensin; Antibiotic; Fungicide.
                                                                                                                                                                                                       InterPro; IPR001271; Defensin. Pfam; PF00323; defensins; 1. SMART; SMO048; DEFSN; 1. PROSITE; PS00269; DEFENSIN; 1.
                                                                                                                                                                                                                                                                                                                                                          Similarity 35.0%; 7; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                 CLVPLSLAQIDLNITCRFAG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                           4 CRIPACLAGERRYGTCFYMG 23
                                                                                                                                                                                                                                                                                                                    3471 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                macaque leukocytes."
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30 AA;
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               TISSUE=Leukocyte;
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P56306;
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Best Local
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Pernollet J.-C., Zivy M., de Vienne D.;
"The maize two dimensional gel protein database: towards an integrated
                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
ENDOTHELIAL MONOCYTE-ACTIVATING POLYPEPTIDE II (EMAP II) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Theor. Appl. Genet. 93:997-1005(1996).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 4.9, ITS MW IS: 37.6 KDA.
Maize-2DPAGE: P80635; COLEOPTILE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 45)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.9%; Score 26; DB 1; Length 15; 55.6%; Pred. No. 5.6e+02;
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15 15
15 AA; 1679 MW; 3D53086B16018BC1 CRC64;
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us-08-753-851-12.rsp

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NCBI_TaxID=3258;
                                                                                         NCBI_TaxID=727;
                                                                                                                                                                                                                                                              influenzae Rd
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VAA2_EQUAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              You Y., Elmore S., Colton L.L., Mackenzie C., Stoops J.K.,
Weinstock G.M., Noris S.J.;
Weinstock G.M., Noris S.J.;
"Characterization of the cytoplasmic filament protein gene (cfpA) of
Treponema pallidum subsp. pallidum";
J. Bacteriol. 178:3177-3187(1996).
-!- FUNCTION: COMPONENT OF THE CYTOPLASMIC FILAMENTS THAT RUN THE
LENGTH OF THE ORGANISM JUST UNDERNEATH THE CYTOPLASMIC MEMBRANE.
-!- SUBCELLULAR LOCATION: AN ARRAY OF 4 TO 6 FILAMENTS LIE IN CLOSE
APPOSITION TO THE INNER MEMBRANE AND ARE ALWAYS LOCALIZED DIRECTLY
                   Kao J., Ryan J., Brett G., Chen J., Shen H., Fan Y.-G., Godman G., Familletti P.C., Wang F., Pan Y.-C.E., Stern D., Clauss M.; Endithelial monocyte-activating polypeptide II. A novel tumor-derived polypeptide that activates host-response mechanisms."; J. Biol. Chem. 267:20239-20247(1992).

-!- FUNCTION: ALTERS ENDOTHELIAL AND MONOCYTE FUNCTIONS; INDUCES THE MIGRATION OF MONOCYTES AND GRANULOCYTES, AND INDUCES AN INFLAMMATORY RESPONSE IN THE MOUSE FOOTPAD MODEL. EMAP II ELICITS A PHLOGOGENIC RESPONSE AND, POTENTIALLY, AUGMENTS THE EFFECTS OF THE OTHER TUMOR-DERIVED CYTOKINES.

-!- SUBUNIT: MONOMER.
PIR; A44032; A44032.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNDERNEATH THE CORRESPONDING GROUP OF PERIPLASMIC FLAGELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.9%; Score 26; DB 1; Length 21; 83.3%; Pred. No. 8e+02;
                                                                                                                                                                                                                           Score 26; DB 1; Length 20;
Pred. No. 7.6e+02;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                     S -> G (IN SOME MOLECULES).
                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
NCBI_TaxID=162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 AA; 2231 MW; 574604B4FFC2D017 CRC64;
                                                                                                                                                                                          018E08BBED066721 CRC64;
                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
0.MAY-2000 (Rel. 39, Last annotation update)
CYTOPLASMIC FILAMENT PROTEIN A (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
          MEDLINE=93015897; PubMed=1400342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96236033; PubMed=8655496;
                                                                                                                                                                                                                           15.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Structural protein; Antigen.
                                                                                                                                                                     1 1
20 20
20 AA; 2164 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Treponema phagedenis.
                                                                                                                                                                                                                                                                         5 PLSLAQIDLNI 15
                                                                                                                                                                                                                                                                                              3 PIDASRLDLRI 13
                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-KAZAN 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 VFHPEK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 VFHVEK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
                                                                                                                                                                                                                                                                                                                                                     CFPA_TREPH
P56738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YD90_HAEIN
P45194;
                                                                                                                                                          Cytokine.
                                                                                                                                                                    VARIANT
NON_TER
SEQUENCE
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                               RESULT 6
CFPA_TREPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YD90_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                         CFPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                             q
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Finetchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, ISOFORM 2 (EC 3.6.1.34)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Equisetum arvense (Field horsetail) (Common horsetail).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Equisetophyta; Sphenopsida; Equisetales; Equisetaceae; Equisetum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-93138084; PubMed-8422915;
Starke T., Gogarten J.P.;
"A conserved intron in the V-ATPase A subunit genes of plants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OF
FOR
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                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEBS Lett. 315:252-258(1993).
-!- FUNCTION: CATALYTIC SUBUNIT OF THE PERIPHERAL VI COMPLEX
VACUOLAR ATPASE. V-ATPASE VACUOLAR ATPASE IS RESPONSIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001109; HupF_HypC.
PROSTIE; PS01097; HUPF_HXPC; UNKNOWN_1.
Hypothetical protein; Complete proteome.
SEQUENCE 21 AA; 2387 MW; 2A63C08B47C2ED3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.5%; Score 25.5; DB 1; 41.7%; Pred. No. 9.5e+02;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN HI1390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=RD / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed-7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U32819; AAC23037.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                 Haemophilus influenzae
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1 MCLGVPIKLSKL 12
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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921A2B02D5F6891D CRC64;

2296 MW;

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Blood coagulation; Plasma; Sulfation.
                                      19
19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                Chloroplast.
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SCK2_TITSE
ID SCK2_TITSE
AC POB816;
DT 01-NOV-1988
DT 01-NOV-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1988
01-NOV-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                              Skeletonema
                                                                                                                                                                                                                                                               PETM_SKECO 096810;
                        MOD_RES
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                  RESULT 10
PETM_SKECO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
          FT
                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                               Qγ
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                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blomback B., Blomback M., Grondahl N.J., Holmberg E.;
"Structure of fibrinopeptides-its relation to enzyme specificity and phylogeny and classification of species.";
Ark. Kemi 25:411-428(1966).
-!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SÜBÜNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA, 6 GAMMA), LINKED TO EACH OTHER BY DISULEIDE BONDS.
-1- MISCELLANEOUS: CONVERSION OF FIBRINGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOBEPTIDES A AND B FROM ALPHA 6 BETA A.—CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
INCEPPO: IPRO02181; Fibrinogen_C.
PROSITE; PSO0514; FIBRIN_AG_C_DOMAIN; PARTIAL.
    ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC
                              SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A PERIPHERAL CATALYTIC VI COMPLEX (MAIN COMPONENTS: SUBUNITS A, B, C, D, E, AND F) ATTACHED TO AN INTEGRAL MEMBRANE VO PROTON PORE COMPLEX (MAIN COMPONENT: THE PROTECLIPID PROTEIN).
MISCELLANEOUS: TWO SEPRARTE GENES ENCODE THE CATALYTIC 70 KDA V-ATPASE SUBUNIT IN PSILOTUM AND EQUISETUM.
SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebráta; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796, 9793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                   InterPro; IPR000194; ATPase_alpha_beta,
PROSITE; PS00152; ATPASE_ALPHA_BETA; PARTIAL.
ATP synthesis; Hydrogen ion transport; Hydrolase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                       15.2%; Score 25; DB 1; Length 30; 33.3%; Pred. No. 1.6e+03; tive 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                             30 30 30
30 AA; 3372 MW; 51CCA4A3DA9E5D84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-JAN-1990 (Rel. 13, Last annotation update)
01-JAN-1990 (Rel. 13, Last annotation update)
FRRINGOPEPTIDE B.
Equus caballus (Horse), and Equus asinus (Donkey).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=Horse;
Blomback B., Blomback M., Grondahl N.J.;
"Studies on fibrinopeptides from mammals.";
Acta Chem. Scand. 19:1789-1791(1965).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                         EMBL; X56984; CAA40302.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 VPLSLAQIDLNI 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 VPMPLRQLTMTL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=E.asinus;
                                                                                                                                                                                                                                                                                                                                 Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGREGATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIBB_HORSE
P14471;
                                                                                                                                                                                                                                                                                                                                                              NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE.
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    QQ
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                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                    20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CYTOCHROME B6-F COMPLEX SUBUNIT VII (CYTOCHROME B6F COMPLEX SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae; Thalassiosirophycidae; Thalassiosirales; Skeletonemataceae;
                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 24; DB 1; Length 25; Pred. No. 1.9e+03;
                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
99ECF1B6CA3113AA CRC64;
                    Score 24; DB 1; 1
Pred. No. 1.4e+03;
2; Mismatches 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 09, Created)
(Rel. 09, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                    25
                    14.68;
57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 44.48;
4; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1
22
2630 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ132266; CAA10631.1;
Query Match
Best Local Similarity 5/...
4; Conservative
                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                             Skeletonema costatum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                       PETM) (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=NIES-323;
                                                                                                24 HVEKNGR 30
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5 HEEEDGR 11
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Gaps

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Indels

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                 Storey C.C., Lusher M., Richmond S.J.;
"Analysis of the complete nuclectide sequence of Chp1, a phage which infects a avian Chlamydia psittaci.";
J. Gen. Virol. 70:3381-3390(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biomphalaria glabrata (Bloodfluke planorb).
Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
Planorbidae; Biomphalaria.
NCBI_TaxID=6526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=M-LINE; TISSUE-Hemolymph;
MEDLINE=97385165; PubMed=9238039;
Adema C.M., Hertel L.A., Miller R.D., Loker E.S.;
Afamily of fibrinogen-related proteins that precipitates parasitederived molecules is produced by an invertebrate after infection.";
Proc. Natl. Acad. Sci. U.S.A. 94:8691-8696(1997).
-!- FUNCTION: BINDS AND PRECIPITATES ANTIGENS OF THE PARASITE
ECHINOSTOMA PARABNSEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.6%; Score 24; DB 1; Length 31; 22.2%; Pred. No. 2.4e+03; ive 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; JU0351; JU0351.
Hypothetical protein.
SEQUENCE 31 AA; 3575 MW; 2F52D99439F181D3 CRC64;
  60.0%; Pred. No. 2.4e+03; ive 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
HYPOTHETICAL 3.6 KDA PROTEIN (ORF7).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LCLVPLSLAQIDLNITCR 18
  Best Local Similarity 60.0
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                  Bacteriophage Chpl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=12367;
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9 CIVPI 13
                                                            2 CLVPL 6
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Р19187;
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LE05_BIOGL
ID LE05_BIOGL
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-!- FUNCTION: BLOCKER FOR CALCIUM-ACTIVATED POTASSIUM CHANNELS.
-!- SIMILARITY: BELONGS TO THE SHORT SCORPION TOXIN FAMILY. POTASSIUM
CHANNEL INHIBITORS SUBFAMILY.
HSSP: P24662; IKTX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                         Possani L.D., Martin B.M., Svendsen I.; "The primary structure of noxiustoxin. A K channel blocking peptide,
                  TOXIN II-9 (FRAGMENT).
Tityus serrulatus (Brazilian scorpion).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Tityus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     channels.";
J. Blol. Chem. 270:16796-16802(1995).
-!- FUNCTION: MJ-CONOTOXINS ACT ON MUSCLE MEMBRANES. THEY BLOCK MUSCLE CONTRACTION BY BINDING TO THE VOLTAGE-ACTIVATED SODIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Venom;
MEDLINE=95348106; PubMed=7622492;
McIntosh J.M., Hasson A., Spira M.E., Gray W.R., Li W., Marsh M.,
Hillyard D.R., Olivera B.M.;
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                                                                                                                                                                                                               purified from the venom of the scorpion Centruroides noxius Hoffmann.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conus marmoreus (Marble cone).
Eukaryota, Metazoa, Mollusca, Gastropoda, Caenogastropoda,
Neogastropoda, Conoidea, Conidae, Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 24; DB 1; Length 30;
Pred. No. 2.3e+03;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 31;
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741FA610E6F9D289 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001947; Charybdotoxin.
Pfam; PF00451; toxin.22; 1.
SOSTE: PS01138; SCORP. SHORT_TOXIN; PARTIAL.
Neurotoxin; Potassium channel inhibitor.
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BY SIMILARITY.
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50.0%;
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Best Local Similarity 50.0
Matches 3; Conservative
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                                                                                                NCBI_TaxID=6887;
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                                                                                                                                                           TISSUE-Venom;
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3 INVKCR
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"Isolation of a peptide structurally related to mammalian corticostatins from the lamprev Petronyzon marinus.";

Comp. Biochem. Physiol. 1148.133-137(1996).

-I- FUNCTION: MAY HAVE MICROBICIDAL ACTIVITIES. MAY INHIBIT CONTICOPROPIN (ACTH) STIMULATED STEROIDOGENESIS AND THE MICROBIAL ACTIONS OF THE CORTICOSTATINS.

-I- MASS SPECTROMETRY: MW-2201; MW_ERR-0.4; METHOD-ELECTROSPRAY.

-I- SIMILARITY: BELONGS TO THE FAMILY OF CORTICOSTATIN/DEFENSIN PEPTIDES.
                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                Petromyzon marinus (Sea lamprey).
Edkaryota: Metazoa: Chordata: Craniata: Vertebrata: Hyperoartia;
Petromyzontiformes: Petromyzontidae: Petromyzon.
NCBI_TaxID=7757;
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                                                                                                               Score 23; DB 1; Length 16; Pred. No. 1.7e+03; 3; Mismatches 3; Indels
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Pred. No. 2e+03;
1; Mismatches 2; Indels
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BY SIMILARITY.
BY SIMILARITY.
8D9CEDC71A199AE5 CRC64;
                                           1 1
16 16
16 AA; 1790 MW; 57489ABFZEEDAA94 CRC64;
-!- SUBCELLULAR LOCATION: SECRETED IN THE HEMOLYMPH.
                                                                                                                                                                                                                                           LCRP_PETMA

ID LCRP_PETMA

AC Q1095

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-1998 (Rel. 36, Last annotation update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE CORTICOSTATIN-RELATED PROFEIN LCRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Skin;
MEDLINE-96321324; PubMed-8759287;
                                                                                                               Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
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Similarity 57.1%;
4; Conservative
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19 AA; 2209 MW;
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6 LAQYVVDLTAR 16
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Best Local Similarity
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Search completed: February 21, 2002, 17:11:46 Job time: 182 sec

13 LNVYCCF 19

Sequence:

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Database

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099684 chelosania
099681 ctocryptis
099681 accarthosaur
096062 helicobacte
P82928 bos taurus
099352 laudakia st
099352 laudakia sa
094811 vibrio chol
051321 escherichia
05131 escherichia
050131 escherichia
05014 brassica na
077225 helix asper
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P92626 dinodon sem
0917pl neisseria m
09624 salea horsf
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099kvc0 vibrio chol
099mc7 rattus norv
P97330 mus musculu
92577 hos anserva
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otocryptis
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pseudotrape
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Ahring B.K.;
"The genes coding for the hsp70 (dnaK) molecular chaperone machine
occur in the moderate thermophilic archaeon Methanosarcina thermophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                  P92577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 238:387-395(1999).

EMBL, AJ010568; CAB54853.1; -.

Hypothetical protein.

SEQUENCE 28 AA; 3258 MW; DD06179D9973A945 CRC64;
                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
HYPOTHETICAL 3.3 KDA PROTEIN.
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        P97330
P92577
Q9G684
Q9G651
Q9G364
Q9G364
P82928
Q9G5W1
Q9G352
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Q52321
Q9UJI8
Q06914
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Q9AJG0
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P92626
09JYP1
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Methanosarcina thermophila
                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2210;
                                                                                                                                                                                                                                                                                                                                                                           Methanosarcina
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Q9UXR3;
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RESULT
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Q9qh74 hepatitis c
Q9twg8 aedes aegyp
Q50835 methanococc
Q9s8k5 nicotiana t
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                                                          February 21, 2002, 17:08:24; Search time 22.15 Seconds (without alignments) 204.715 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                1 LCLVPLSLAQIDLNITCRFAGVFHVEKNGRY 31
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                                                                                                                                                              473505 seqs, 146272329 residues
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                                          OM protein - protein search, using sw model
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Q90H85
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Q9QH70
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Gapop 10.0 , Gapext 0.5
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sp_mammal:*
sp_mhc:*
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sp_unclassified:*
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sp_bacteria:*
sp_fungi:*
sp_human:*
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length: 31
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Nicotiana tabacum (Common tobacco).

Beraryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE-88124191; PubMed=2829115; Brown J.W., Thomm M., Beckler G.S., Frey G., Stetter K.O., Reeve C. Brown J.W., Thomm M., Beckler Brown J.W. Thomm M., Beckler G.S., Frey G., Stetter K.O., Reeve C. "An archaebacterial RNA polymerase binding site and transcription initiation of the hish gene in Methanococcus vannielii."; Nucleic Acids Res. 16:135-150(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Koiwa H., Sato F., Yamada Y.;
"Characterization of accumulation of tobacco PR-5 proteins by IEF-
                                                                                                                                                                                                 Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 26;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GROUP 5 NEUTRAL PATHOGENESIS-RELATED PROTEIN (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                26 AA; 3073 MW; 307BF49A6549F6A0 CRC64;
                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1996 (TrEMBLrel. 01, Last annotation update) VANNIELLI ORF547-HISA INTERGENIC REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31; DB 10; I
Pred. No. 7.5e+02;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 5.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32; DB 1;
                                                               26 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunoblot analysis.";
Plant Cell Physiol. 35:821-827(1994)
                                                                                                    01, Created)
                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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50.0%;
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85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                               PRELIMINARY;
                                                                                                                                                                               Methanococcus vannielii.
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Best Local Similarity
'`^a 6; Conserv?
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Matches 6; Conserv
                                                                                                                                                                                                                                      NCBI_TaxID=2187;
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CONTAINED WITHIN THE GENOME POLYPROTEIN THAT CONTAINS: CAPSID
PROTEIN C; THE ENVELOPE GLYCOPROTEIN E1; ENVELOPE GLYCOPROTEIN
E2/NS1; NONSTRUCTURAL PROTEINS NS2, NS3, NS4A, NS5A AND
NS5B. THE VIRION OF THE VIRUS IS COVERED BY A LIPOPROTEIN ENVELOPE
THAT CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E (BY
                                                                                                                                                    SEQUENCE FROM N.A.
Sandres K., Dubois M., Pasquier C., Izopet J.;
"The genetic heterogeneity of the hypervariable region 1 of the viral genome and the sensitivity of hepatitis C virus to interferon alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aedes aegypti (Yellowfever mosquito).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dunkov B.C., Zhang D., Choumarov K., Winzerling J.J., Law J.H.; "Isolation and characterization of mosquito ferritin and cloning of
                                                                              no DNA stage; Flaviviridae;
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2/NS1 (GP68)]
                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: TO HEPATITIS C VIRUS NON-STRUCTURAL PROTEIN E2/NS1
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Pred. No. 4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                    Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA that encodes one subunit.";
Arch. Insect Biochem. Physiol. 29:293-307(1995).
SEQUENCE 20 AA; 2126 MW; 102824B243316BFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D43859586668B361 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2000 (TrEMBLrel. 14, Last annotation update)
28 KDA FERRIIN SUBUNIT (FRAGMENT).
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Pred. No. 2.6e+02;
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                                                                          Viruses; ssRNA positive-strand viruses,
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InterPro; IPR002531; HCV_NS1.
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33.3%;
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Best Local Similarity 30.8%;
Matches 4; Conservative
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NON_TER 27 27

SEQUENCE 27 AA; 2740 MW;
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Best Local Similarity 33.3
Matches 8; Conservative
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                                                       Hepatitis C virus
                                                                                                                NCBI_TaxID=11103;
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                                                                                                Hepacivirus
                                         FRAGMENT
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EMBL; AF167046; AAD53679.1;
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Best Local Similarity
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SEQUENCE
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CONTAINED WITHIN THE GENOME POLYPROTEIN THY CONTAINS: CAPSID
PROTEIN C; THE ENVELOPE GLYCOPROTEIN E1; ENVELOPE GLYCOPROTEIN
E2/NS1; NONSTRUCTURAL PROTEINS NS2, NS3, NS4A, NS5A AND
NS5B. THE VIRUSION OF THE VIRUS IS COVERED BY A LIPOPROȚEIN ENVELOPE
THAT CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E (BY
                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E2/NSF1 IS
CONTAINED WITHIN THE GENOME POLYPROTEIN THAT CONTAINS: CAPSID
PROTEIR C; THE ENVELOPE GLYCOPROTEIN B1; ENVELOPE GLYCOPROTEIN
E2/NS1; NONSTRUCTURAL PROTEINS NS2, NS3, NS4A, NS5A AND
NS5B. THE VIRION OF THE VIRUS IS COVERED BY A LIPOPROTEIN ENVELOPE
THAT CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E (BY
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                                                                                                                                                                                                                                                 Sandres K., Dubois M., Pasquier C., Izopet J.; "The genetic heterogeneity of the hypervariable region 1 of the viral genome and the sensitivity of hepatitis C virus to interferon alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           no DNA stage; Flaviviridae;
               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2/NS1 (GP68)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2/NS1 (GP68)]
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SIMILARITY: TO HEPATITIS C VIRUS NON-STRUCTURAL PROTEIN E2/NS1
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Pred. No. 7.8e+02;
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                                                                                                                                            Viruses; ssRNA positive-strand viruses,
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29.2%;
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                        Hepatitis C virus
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                                                                                                                                                                                        NCBI_TaxID=11103;
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                                                                                                                                                                  Hepacivirus,
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090н83;
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SUBDUIT: HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E2/NSF1 IS
CONTAINED WITHIN THE GRNOME POLYPROTEIN THAT CONTAINS: CAPSID
PROTEIN C; THE ENVELOPE GLYCOPROTEIN E1; ENVELOPE GLYCOPROTEIN
E2/NS1; NONSTRUCTURRAL PROTEINS NS2, NS3, NS4A, NS4B, NS5A AND
NS5B. THE VIRION OF THE VIRUS IS COVERED BY A LIPOPROTEIN ENVELOPE
THAT CONSISTS OF TWO PROTEINS: PROTEIN AND GLYCOPROTEIN E (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sandres K., Dubois M., Pasquier C., Izopet J.; "The genetic heterogeneity of the hypervariable region 1 of the viral genome and the sensitivity of hepatitis C virus to interferon alpha
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InterPro; IPR002531; HCV_NS1.
Pfan, PF01666; HCV_NS1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
NON_TER 1 1 2 2 2 2 SEQUENCE 27 AA; 2754 MW; D4385958667D5361 CRC64;
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Pfam; PF01560; HCV_NS1; 1
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
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U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2/NS1 (GP68)]
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Pred. No. 7.8e+02;
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Pred. No. 7.8e+02;
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01-MAY-2000 (TrEMBLrel. 13, Created)
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29.2%;
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29.2%;
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Best Local Similarity 29.2
Matches 7; Conservative
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InterPro; IPR002531; HCV_NS1.
Pfam; PF01560; HCV_NS1; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
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01-MAY-2000 (
01-MAY-2000 (
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SEQUENCE
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-!- SUBUNIT: HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E2/NSF1 IS
CONTAINED WITHIN THE GENOME POLYEROTEIN THAT CONTAINS: CAPSID
PROTEIN C; THE ENVELOPE GLYCOPROTEIN E1: ENVELOPE GLYCOPROTEIN
E2/NS1; NONSTRUCTURAL PROTEINS NS2, NS3, NS4A, NS4B, NS5A AND
NS5B. THE VIRION OF THE VIRUS IS COVERED BY A LIPOPROTEIN ENVELOPE
THAT CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E (BY
                                                                                                                                                    Sandres K., Dubois M., Pasquier C., Izopet J.;
The genetic heterogeneity of the hypervariable region 1 of the viral
genome and the sensitivity of hepatitis C virus to interferon alpha
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InterPro; IPR002531; HCV_NS1.
Pfam; PF01560; HCV_NS1; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
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                                                                                      Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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                 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GENOME POLYPROFEIN (CONTAINS: ENVELOPE GLYCOPROTEIN E2/NS1 (GP68))
                                                                                                                                                                                                                                                                                                            SIMILARITY).
SIMILARITY: TO HEPATITIS C VIRUS NON-STRUCTURAL PROTEIN E2/NS1
                                                                                                                                                                                                             Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBUNIT: HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E2/NSF1 IS CONTAINED WITHIN THE GENOME POLYPROTEIN THAT CONTAINS: CAPSID
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2/NS1 (GP68)]
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Pred. No. 7.8e+02;
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29.2%;
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NON_TER 27 27
NON_TER 27 27
SEQUENCE 27 AA; 2754 MW;
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                                                                        Hepatitis C virus
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CONTAINED WITHIN THE GENOME POLYPROTEIN THAT CONTAINS: CAPSID
PROTEIN C; THE ENVELOPE GLYCOPROTEIN B1; ENVELOPE GLYCOPROTEIN
E2/NS1: NONSTRUCTURAL PROTEINS NS2, NS3, NS4A, NS4B, NS5A AND
NS5B. THE VIRION OF THE VIRUS IS COVERED BY A LIPOPROTEIN ENVELOPE
THAT CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sandres K., Dubois M., Pasquier C., Izopet J.; "The genetic heterogeneity of the hypervariable region 1 of the viral genome and the sensitivity of hepatitis C virus to interferon alpha
                                                                                                                                          Gaps
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Pfam; PF01560; HCV_NS1; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; NoN_TER
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Hepatitis C virus.
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepativirus.
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2/NS1 (GP68)]
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-!- SIMILARITY: TO HEPATITIS C VIRUS NON-STRUCTURAL PROTEIN E2/NS1
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                     D4385958667D5361 CRC64;
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Last annotation update)
                                                                                         Score 31; DB 12;
Pred. No. 7.8e+02;
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Pred. No. 7.8e+02;
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                                                                                                                                        4; Mismatches
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                                                                                                                                                                                7 SLAQIDLNITCRFAGVFHVEKNGR 30
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                                                                                         18.9%;
29.2%;
27
2754 MW;
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(TrEMBLrel. 13, I
(TrEMBLrel. 17, I
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29.2%;
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                                                                                                              Best Local Similarity 29.2
Matches 7; Conservative
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Best Local Similarity 29.27
Matches 7; Conservative
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Envelope protein; Glycoprotein; Nonstructural protein;

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-!- SUBUNIT: HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E2/NSF1 IS
CONTAINED WITHIN THE GENOME POLYPROTEIN THAT CONTAINS: CARSID
PROTEIN C; THE ENVELOPE GLYCOPROTEIN B1; ENVELOPE GLYCOPROTEIN
E2/NS1; NONSTRUCTURAL PROTEINS NS2, NS3, NS4A, NS5A AND
NS5B. THE VIRION OF THE VIRUS IS COVERED BY A LIPOPROTEIN ENVELOPE
THAT CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E (BY
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CONTAINED WITHIN THE GENOME POLYPROTEIN THAT CONTAINS: CAPSID
PROTEIN C: THE ENVELOPE GLYCOPROTEIN B1; ENVELOPE GLYCOPROTEIN
E2/NS1; NONSTRUCTURAL PROTEINS NS2, NS3, NS4A, NS5A AND
NS5B. THE VIRION OF THE VIRUS IS COVERED BY A LIPOPROTEIN ENVELOPE
THAT CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E (BY
                                                                                                                                                  Sandres K., Dubois M., Pasquier C., Izopet J.; "The genetic heterogeneity of the hypervariable region 1 of the viral genome and the sensitivity of hepatitis C virus to interferon alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Sandres K., Dubois M., Pasquier C., Izopet J.; Sandres K., Dubois M., Pasquier C., Izopet J.; "The genetic heterogeneity of the hypervariable region 1 of the viral genome and the sensitivity of hepatitis C virus to interferon alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01560; HCV_NS1; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
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                                                        Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae,
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GENOME POLYPROTEIN (CONTAINS: ENVELOPE GLYCOPROTEIN E2/NSI (GP68))
                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: TO HEPATITIS C VIRUS NON-STRUCTURAL PROTEIN E2/NS1
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GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2/NS1 (GP68)]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Indels
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 AA; 2754 MW; D4385958667D5361 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002531; HCV_NS1.
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Pfam; PF01560; HCV_NS1; 1.
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Best Local Similarity 29.2%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polyprotein; Transmembrane.
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                                                                                                                                SEQUENCE FROM N.A.
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Hepatitis C virus.
                   (FRAGMENT).
Hepatitis C virus.
                                                                                         NCBI_TaxID=11103;
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SUBUNIT: HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E2/NSF1 IS CONTAINED WITHIN THE GENOME POLYPROTEIN THAT CONTAINS: CAPSID. PROTEIN C; THE ENVELOPE GLYCOPROTEIN E1; ENVELOPE GLYCOPROTEIN E2/NS1; NOSTRUCTURAL PROTEINS NS2, NS3, NS4A, NS4B, NS5A AND NS5B, THE VIRION OF THE VIRUS IS COVERED BY A LIPOPROTEIN ENVELOPE THAT CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E (BY
                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002531; HCV_NS1.
Pfam; PF01560; HCV_NS1; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2/NS1 (GP68)]
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U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2/NS1 (GP68)]
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                                                                                                     Length 27;
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                                                                                                                                  13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D4385958667D5361 CRC64;
                                                           D4385958667D5361 CRC64;
                                                                                                     Score 31; DB 12;
Pred. No. 7.8e+02;
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29.2%;
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2754 MW;
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NON_TER 27 27
SEQUENCE 27 AA; 2754 MW:
Coat protein; Envelope prot
Polyprotein; Transmembrane.
NON_TER 1 1 1
NON_TER 27 SEQUENCE 27 AA; 2754 MW;
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Best Local Similarity 29.2.
Best Tocal 7; Conservative
                                                                                                                                    Conservative
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Best Local Similarity
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                                                        27 AA;
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!-SUBUNIT: HERATITIS C VIRUS ENVELOPE GLYCOPROTEIN E2/NSF1 IS
CONTAINED WITHIN THE GRNOME POLYPROTEIN THAT CONTAINS: CAPPSID
PROTEIN C; THE ENVELOPE GLYCOPROTEIN E1; ENVELOPE GLYCOPROTEIN
E2/NS1; NONSTRUCTURAL PROTEINS NS3, NS4A, NS4B, NS5A AND
NS5B. THE VIRION OF THE VIRUS IS COVERED BY A LIPOPROTEIN ENVELOPE
THAT CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E (BY
                                                                                                 SEQUENCE FROM N.A.
Sandres K., Dubois M., Pasquier C., Izopet J.;
"The genetic heterogeneity of the hypervariable region 1 of the viral genome and the sensitivity of hepatitis C virus to interferon alpha
                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF167055; AAD53688.1; --
InterPro; IPR00251; HCV_NS1.
Pfam; PF01560; HCV_NS1; 1
Coat protein; Ervelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
NON_TER 1 1 1
NON_TER 27 27
SEQUENCE 27 AA; 2754 MW; D4385958667D5361 CRC64;
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Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
                                                                                                                                                                                                                                                                                                                                SIMILARITY).
SIMILARITY: TO HEPATITIS C VIRUS NON-STRUCTURAL PROTEIN E2/NS1
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Best Local Similarity 29.2'
Matches 7; Conservative
                                                             NCBI_TaxID=11103;
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Search completed: February 21, 2002, 17:11:30 Job time: 186 sec

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Laminin peptide an Alpha D peptide an Alpha D peptide de EMAPLI active pept Laminin A chain de Laminin peptide R3 Laminin peptide R3 Laminin peptide R3 Laminin alpha chail HIV 9p120 protein Human interleukin-Peptide #5663 enco Human 5' EST secre
                      Antigenic peptide
SEQ ID NO 409 from
EGF-like domain #5
Laminin peptide an
CD44 peptide CD44
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Alpha D peptide de
Laminin peptide an
Mouse liver growth
Mouse anti-human I
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Laminin peptide an
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Peptide #6344, der
Atrial natriuretic
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Staphylococcal/str
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Product from plasm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell adhesion molecule; CD44; antiinflammatory; rheumatoid; arthritis; tumor cell metastasis; autoimmune disease;
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                                                                                                                                                                         AAW67047
AAB89238
AAB8826
AAM31626
AAY11616
AAB20363
AAW67061
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AAY97840
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AAY72178
AAP81297
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AAW67059
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AAR72579
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AAW67042
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AAY98296
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AAR25295
AAP82918
AAW67044
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                      AAB8464]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR53482 standard; peptide; 31 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD44 peptide CD44-9
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Homo sapiens
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AAR53482;
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AAR53482
 African green monk
Product from plasm
Product from plasm
Clone CC397-19. H
Clone CC397-11 pro
Human secreted pro
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Human secreted pro
Human alphal-antit
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Human CD44H N-term
                                                                                          (without alignments) 97.672 Million cell updates/sec
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                                                                             February 21, 2002, 17:05:14; Search time 23.51 Seconds
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                                                                                                                                                                                                                                                                                                                                                **SIDSB*/gcgdata/geneseqp/aa1980.DAT:**
SIDSB*/gcgdata/geneseq/geneseqp/Aa1981.DAT:**
SIDSB*/gcgdata/geneseq/geneseqp/Aa1981.DAT:**
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SIDSB*/gcgdata/geneseqy/geneseqp/Aa1983.DAT:**
SIDSB*/gcgdata/geneseqy/geneseqp/Aa1984.DAT:**
SIDSB*/gcgdata/geneseqy/geneseqp/Aa1985.DAT:**
SIDSB*/gcgdata/geneseqy/geneseqp/Aa1986.DAT:**
SIDSB*/gcgdata/geneseqy/geneseqp/Aa1980.DAT:**
SIDSB*/gcgdata/geneseqy/geneseqp/Aa1980.DAT:**
SIDSB*/gcgdata/geneseqy/geneseqp/Aa1990.DAT:**
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SIDSB*/gcgdata/geneseqy/geneseqp/Aa1999.DAT:**
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                     Compugen Ltd
                                                                                                                                                  1 LCLVPLSLAQIDLNITCRFAGVFHVEKNGRY 31
                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
            GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                          522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR53482
AAR53496
AAR82919
AAP82917
AAW47362
AAW47362
AAY08628
AAY08628
AAF07319
AAF07319
AAF07319
                                                        protein search, using sw model
                                                                                                                                                                                                                                                                                                                   Listing first 45 summaries
                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                           US-08-753-851-12
                                                                                                                                                                                                                                                                                                                                         A_Geneseq_1101:*
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Match Length DB
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225
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length: 31
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442.1
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Score

Result . 02 164 69 58 43 42.5 38 38 38 38 38

Minimum DB seq Maximum DB seq

Database :

Perfect score:

Title:

Sequence:

OM protein -

Run on:

Scoring table:

Searched:

Sequence

8 X C C C C C C X & S

Query Match Best Local 8

Best Loca Matches

us-08-753-851-12.rag

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The peptide from which this N-terminal sequence is taken can be used for treating inflammation and immune-mediated tissue damage such as occurs in the course of autoimmune diseases. e.g. Theumatoid arthritis. It can also be used for determining metastatic potential or to treat or prevent tumor cell metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hirudin expression vectors; signal sequence cleavage site; pTG2906; thrombin inhibitor; anticoagulant; alpha-antitrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of CD44 protein and new peptide derivs - for developing prods for inflammation, immune-mediated tissue damage and tumour cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasmid pTG2906 for extracellular hirudin expression,
                                                                                                                                                                                              Cell adhesion molecule; CD44; antiinflammatory; rheumatoid; arthritis; tumor cell metastasis; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 58; DB 15; Length 25; Pred. No. 0.066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Telen MJ;
                                                                                                                                                                  African green monkey CD44 N-terminal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patton KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1..24
/label=signal_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 47; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                         AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA.
                                                                  AAR53495 standard; peptide; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAP82919
ID AAP82919 standard; protein; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liao H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                signal sequence cleavage site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.4%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                            93WO-US10412.
                                                                                                                                                                                                                                                                                                                                                                                           92US-0973339
                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 lcllqlslaqidln 25
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                                                                                                                                                                                                                                                               African green monkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hale LP, Haynes BF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-167121/20
                                                                                                                                                                                                                               immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                          (UYDU-) UNIV DUKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 AA;
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                                                                                                                                                                                                                                                                                                                                                         29-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-NOV-1990
                                                                                                                                  01-DEC-1994
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                                                                                                   AAR53495;
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Peptide
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                                                     AAR53495
                                       RESULT
                                                                                      Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The peptide from which this N-terminal sequence is taken can be used
                                                                                   cell
                              The peptide can be used for treating inflammation and immunemediated tissue damage such as occurs in the course of autoimmune diseases, e.g. rheumatoid arthritis. It can also be used for determining metastatic potential or to treat or prevent tumor cell metastasis. This peptide corresponds to AA 12-42 of the CD44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of CD44 protein and new peptide derivs - for developing prods for inflammation, immune-mediated tissue damage and tumour cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for treating inflammation and immune-mediated tissue damage such occurs in the course of autoimmune diseases, e.g. rheumatoid arthritis. It can also be used for determining metastatic potential or to treat or prevent tumor cell metastasis.
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                                                                                                                                                                                              Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell adhesion molecule; CD44; antiinflammatory; rheumatoid; arthritis; tumor cell metastasis; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 25;
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Telen MJ;
                                                                                                                                                                                         100.0%; Score 164; DB 15; 100.0%; Pred. No. 1.4e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 69; DB 15;
Pred. No. 0.0015;
                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patton KL,
                                                                                                                                                                                                                                                                      1 LCLVPLSLAQIDLNITCRFAGVFHVEKNGRY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 47; 83pp; English
                                                                                                                                                                                                                                                                                                                                                                       AA.
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100.0%; Pre
0; '
Claim 4; Page 14; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human CD44H N-terminal sequence.
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                                                                                                                                                                                                                                                                                                                                                                    AAR53496 standard; peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LCLVPLSLAQIDLN 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hale LP, Haynes BF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1994-167121/20
                                                                                                                                                                                                        Similarity
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Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYDU-) UNIV DUKE.
                                                                                                                                            31 AA;
                                                                                                             protein sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-OCT-1992;
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WO9409811-A 11-MAY-1994

AAR53496;

AAR53496 RESULT

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metastasis

Sequence

Query Match

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Gaps

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Gaps
                          27..27
/label=leucine
/note="from Ile due to the BamHI adapter seguence."
                                                                                                                                                                                                                                                                                                                                                                                        The DNA sequence encoding hirudine is located downstream from the alpha-antitrypsin sequence ensuring the expression and release of hirudin in active form by cells into the culture medium. Between the two sequences is a BamHI site . See also AAN82293-95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Testis; brain; identification; genetic disorder; antibody; ds;
                                                                                                                                                                                                                                                                                                                   Hirudin expression vectors – contg. signal sequence allowing extracellular hirudin prodn. by eukaryotic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Racie LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McCoy JM, Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.9%; Score 42.5; Dilarity 66.7%; Pred. No. 17; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW47362 standard; Protein; 27 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immuno-modulator; anti-tumour
               label=BamHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0702081.
96US-0686878.
                                                                                                                                                                                 87FR-0002696.
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                                                                                                                                                 87FR-0002696.
                                                                                                                                                                                                                                                                                                                                                                  Disclosure; ; 10pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jacobs K, Lavallie ER, Spaulding V, Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 CLVPLSLAQIDLNIT 16
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17 clvpvslae-dltyt 30
24..25
                                                                                                                                                                                                                                            Courtney M;
                                                                                                                                                                                                               (TRAN-) TRANSGENE SA.
                                                                                                                                                                                                                                                                         WPI; 1988-301637/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 AA;
                                                                                                                                                                                                                                                                                        P-PSDB; AAP82917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone CC397_19
Cleavage-site
                            Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-AUG-1996;
26-JUL-1996;
                                                                                                                                                   27-FEB-1987;
                                                                                                                                                                               27-FEB-1987;
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                                                                                         FR2611723-A.
                                                                                                                     09-SEP-1988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                            Skern T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW47362;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Product from plasmid pTG1970 for extracellular hirudin expression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hirudin expression vectors; signal sequence cleavage site; thrombin inhibitor; anticoagulant; alpha-antitrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 9;
14;
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/note="alpha-antitrypsin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="alpha-antitrypsin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1..24
/label=signal_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAP82917 standard; protein; 31 AA.
              26..30
/label=hirudine
/note="native"
25..30
/label-huridine
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/label=hirudine
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28..31
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24..25
/label=StuI
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 26.2
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                      Courtney M;
                                                                                                                                                                                                                                                                         (TRAN-) TRANSGENE SA
                                                                                                                                                                                                                                                                                                                                   WPI; 1988-301637/43.
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|7 clvpvslaei 26
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                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAN82295
                                                                                                       Cleavage-site
                                                                                                                                                                                                                                            27-FEB-1987;
                                                                                                                                                                                                               27-FEB-1987;
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                                                                                                                                                                                                                                                                                                      Skern T,
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                 Peptide
                                                             Peptide
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                                                                                                                               Clone CC397-19 has been isolated from an adult human brain cDNA library, along with clones BV2325_17, CC25_17 and BV239_3. These clones and clone BL89_13 isolated from an adult human testis library, can be expressed in eukaryotic or prokaryotic host cells. The genes and protein sequences may be used for identification purposes for example for chromosome identification or to detect genetic disorders. They can also be used to
                                                                                                                                                                                                       identification or to detect genetic disorders. They can also be used to screen compounds for biological activity; to raise antibodies; as tissue markers; for isolation of related receptors and ligands and as nutritional sources. They may also have many biological activities such as cytokine and cell proliferation/differentiation activity;
                                                                                                                                                                                                                                                                            immunosuppressant/immunostimulant activity and regulation of haematopoiesis. Neutralising antibodies against the protein can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; human adult brain; cDNA library; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                       Nucleic acid encoding secreted protein from human testis or brain cells - and related vectors, transformed cells and proteins, potentially useful e.g. as immuno-modulators, antitumour agents, promoters of tissue growth, haemostatic and thrombolytic agents etc.
                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human testes derived cDNA and protein(s) - may be useful for laboratory use, or for stimulating cell proliferation and
                                                                                                                                                                                                                                                                                                                                                                           DB 19; Length 27;
68;
                                                                                                                                                                                                                                                                                                                                                                                                      7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                           Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Column 57-58; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V, Treacy M;
                                                                                                            Claim 21; Page 45; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LaVallie ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW42020 standard; Protein; 27
                                                                                                                                                                                                                                                                                                                                                                          23.28;
41.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LCLVPLSLAQIDLNITC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone CC397-11 protein.
                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity
'... 7; Conserva
WPI; 1998-130685/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC397-11 protein; hur cell differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spaulding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-109352/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jacobs K,
                                                                                                                                                                                                                                                                                                                                 27 AA;
              N-PSDB; AAV15714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JACOBS K.
                                                                                                                                                                                                                                                                                                         therapeutically.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     laboratory use, differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-1996;
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                                                                                                                                                                                                                                                                                                                                   Seguence
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AAW42020
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This sequence is the CC397_11 protein, which is 27 amino acids in length, and is isolated from adult human brain cDNA library. When the CC397_11 sequence was searched in the Genbank database, the clone demonstrated no homology with any of the known sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Secreted protein; testes; brain; blood; placenta; human; murine; thymus; bone marrow; treatment; prevention; nutrition; cytokine; immune; vaccine; cell prolliferation; cell differentiation; suppressor; tumour inhibition; haematopolesis regulator; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; receptor; ligand; anti-inflammatory; tumour; cadherin; tumour invasion suppressor; gene therapy; tissue growth.
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes novel human secreted proteins encoded by
                                                                                                                                                                                                 0;
                                                                                                                                                            Length 27;
                                                                                                                                                                                                 Indels
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                                                                                                                                                                                               7;
                                                                                                                                                          DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides encoding secreted proteins
                                                                                                                                                                            ed. No. 68;
Mismatches
                                                                                                                                                          Score 38;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 32a; Page 113; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                     AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein CC397_19.
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                                                                                                                                                                                                                                                                                                                                                            AAY08628 standard; Protein; 30
                                                                                                                                                        23.2%;
41.2%;
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98US-0080478,
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                        Best_Local Similarity 41.2
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-357813/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Collins-Racie LA,
                                                                                               AA;
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                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                       AAY08628;
                                                                                                                                                      Query Match
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us-08-753-851-12.rag

for gene therapy.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticorvulsant; antibacterial; antifungal; antiparasitic; and cardiant. The polynucleotides and polypeptides are useful for mice, rabbits, goats, horses, cats, dogs, chickens or sheep. The polypeptides can also be used as a food additive or preservative to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           particularly breast and/or ovary cancer. They are also useful in the gene therapy of breast and ovarian cancer. Nucleic acids, protein, antibodies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   increase or decrease storage capabilities. The polynucleotides are useful for chromosome identification. They are also useful as probes for diagnosing a disorder related to the female reproductive system,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fifty nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; secreted protein; diagnosis; cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; wound healing; neurological disease; infectious disease; chromosome identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The polynucleotide sequences given in AAC59966 to AAC60015 encode the
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein sequence encoded by gene 15 SEQ ID NO:75.
                                                                                                                            0;
                                                                                      Score 38; DB 20; Length 30; Pred. No. 77;
                                                                                                                          Indels
                                                                                                         Pred. No. 77;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Komatsoulis G;
                                                                                                                                                                                                                                                                                                AAB34787 standard; Protein; 30 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 381; 425pp; English
                                                                                          23.2%;
41.2%;
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99US-0172413.
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                                                                                                                                                                 1 LCLVPLSLAQIDLNITC 17
                                                                                                                                                                                      Conservative
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                                                                       Query Match
Best Local Similarity
7; Conserve
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                                    30 AA;
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                                      Seguence
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This is the human secreted protein CC397_19 amino acid sequence, the polynucleotide sequence encoding CC397_19 was obtained from a human ad adult brain cDNA library. The invention relates to secreted human and murine proteins. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Contection of the levels of the proteins can be used for the diagnosis of e.g. pre-eclampsia, placental pathology or cancer. Agents which modulate the expression or function of the proteins may be used for treating a compassit disease and inhibiting metastasis. Other suggested activities include nutritional activity (e.g. in feeds), cytokine and cell conditional activity, dead in feeds), cytokine and cell conditional activity, activity, immune stimulating (e.g. as vaccines) or suppressing activity, heamatopoissis regulating activity, tenemotactic/chemokinetic activity, heamatopoissis regulating activity, chemotactic/chemokinetic activity, haemacotatic and thrombolytic activity, cremotactic/chemokinetic activity, activi
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agonists and antagonists from the present invention are useful in the diagnosis, treatment and prevention of cancer, immune disorders, carditovascular disorders, wound healing, neurological diseases and infectious disease. AAC59955 and AAB34772 represents sequence used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides encoding secreted cDNA libraries, used to opposite for the diagnosis and treatment of neoplastic disease
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                                                                                                                                                                                                                                                                                         2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein CC397_19 amino acid sequence.
                                                                                                                                                                                                                           DB 77;
                                                                                                                                                                                                                                   Score 38; DB 2
Pred. No. 77;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 28; Page 120; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY67319 standard; Protein; 30 AA.
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                                                                                                                                                                                                                                      23.2%;
63.6%;
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Best Local Similarity 63.6
Matches 7; Conservative
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N-PSDB; AAZ59476.
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16 mclvplspahv 26
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                                                                                                                                                                AA;
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20-OCT-1998;
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                                                                                                                                                                Sequence
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DB 22; Length 23;

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1; Mismatches

Score 37; Pred. No. 8

22.6%; 87.5%;

Best Local Similarity 87.5 Matches 7; Conservative

Query Match

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The patent relates to a nucleic acid composition for introducing nucleic acid into a eukaryotic host cell to obtain expression of a recombinant protein which lacks all or a portion of the B domain of human Factor VII:: (hWVII::) and is capable of coagulation activity. The recombinant protein consists of a polypeptide substantially homologous to mature A domain of hWVII: as encoded by the polynucleotide present in plasmid pSVF8-200 (ATCC) number 40190); and a second polypeptide homologous to mature C domain of hWVII: as encoded by the polynucleotide present in plasmid pSVF8-200.

The composition is useful as an immunogen for the production of antibodies, for isolating vor-Wille-brand factor by affinity chromatography, in diagnostic assays for Factor VII:C and for treating Type A haemophilia and other bload clitting disorders.

The present sequence is human alphal-antitrypsin signal peptide used for secretion of recombinant protein of the invention.
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invasion suppressor activity, and tumour inhibition activity. The polynucleotide sequences are also stated to be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                           Human; Factor VIII:C; FVIII:C; coagulation; von-Wille-brand factor;
type A haemophilia; blood clotting disorder; haemostatic; gene therapy;
recombinant protein; immunogen; alphal-antitrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid complexes having factor VIII activity and coagulation activity, for treating hemophilia and other blood clotting disorders, or as immunogens for the production of antibodies
                                                                                                                                       Gaps
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                                                                                                     DB 21; Length 30; 77;
                                                                                                                                       Indels
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                                                                                                                                   7;
                                                                                                   Score 38; DB;
Pred. No. 77;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              Human alphal-antitrypsin signal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 6; Column 51-52; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rasmussen ME,
                                                                                                                                                                                                                                                                          AAE02383 standard; peptide; 23 AA.
                                                                                                Query Match 23.2%;
Best Local Similarity 41.2%;
Matches 7; Conservative
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86US-0822989.
87US-0051916.
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                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                              1 LCLVPLSLAQIDLNITC 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chapman B, Burke RL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-MAY-1995;
                                                                                                                                                                                                                                                                                                                                              10-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-DEC-1993;
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19-MAY-1987;
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                                                  Seguence
                                                                                                                                                                                                                                                                                                              AAE02383;
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 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                   Hirudin expression vectors; signal sequence cleavage site; pTG2902; thrombin inhibitor; anticoagulant; alpha-antitrypsin.
                                                                                                                                                                  plasmid pTG2902 for extracellular hirudin expression,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hirudin expression vectors - contg. signal sequence allowing extracellular hirudin prodn. by eukaryotic cells.
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                                                                                                                                                                                                                                                                         /note="alpha-antitrypsin"
                                                                                                                                                                                                                                                           /label-signal_sequence
                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                               AAP82918 standard; protein; 29 AA.
                                                                                                                                                                                                                                                                                  25..29
/label=hirudine
/note="native"
                                                                                                                                                                               signal sequence cleavage site.
                                                                                                                                                                                                                                                                                                                                                                                                   87FR-0002696.
                                                                                                                                                                                                                                                                                                                               /label=StuI
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                                                                                                                                              (first entry)
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Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Skern T, Courtney M;
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                                        16 clvpvsla 23
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                  2 CLVPLSLA
                                                                                                                                                                                                                                                                                                                   Cleavage-site
                                                                                                                                                                  Product from
                                                                                                                                                                                                                                                                                                                                                                                                  27-FEB-1987;
                                                                                                                                           23-NOV-1990
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                                                                                                                      AAP82918;
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98WO-US22376.
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| crfqgdshleqpdcy
                                                                                                                                                                                                                                    Williams LT;
                                                                                                                                                                                                         (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                WPI; 2001-425440/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lung disease; t)
infection; AIDS.
                                                                                      WO200144279-A2.
                                                                                                                                                                            17-DEC-1999;
                                                                                                                                                                                                                                                                                                                            colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9922243-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-1999
                                                                                                                 21-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY19691;
                                                                                                                                                                                                                                    Yan D,
                                                           Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method for treating systemic lupus erythematosus (SLE), which comprises administering an effective dose of at least one laminin peptide analogue or derivative. In one exemplairy embodiment, the laminin peptide is selected from the group consisting of R38 and claimed R38 analogues and derivatives including 5200, 5104, 5105, 5106, 5107, 5108, 5109 and 5110.

SLE is serologically characterised by the presence of autoantibodies in the serum, particularly anti-DNA autoantibodies, and the methods and products may be used to treat SLE using laminin derived peptides which cross react with those antibodies. At least one laminin, peptide may be used to prepare a therapeutic for administration to a mammal suffering in the immunosuppresive treatment is not associated with the side effects of prior art immunosuppresive treatment, and the monitoring assay is more specific and less invasive than prior art assays. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                aminin; systemic lupus erythematosus; SLE; R38; 5104; autoantibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Treatment of systemic lupus erythematosus - comprise administration of laminin peptides, particularly R38 and R38 derivatives and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 19; Length 21; 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       represents the laminin peptide analogue 5104
                                                                                                                                                                                                                                                                                                                                                        (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
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Pred. No. 1
                           AAW67044 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB84641 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 19; 28pp; English.
                                                                                                                 Laminin peptide analogue 5104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.0%;
70.0%;
                                                                                                                                                                                                                                                                                              98WO-IB00415
                                                                                      (first entry)
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Best Local Similarity 70.0
Matches 7; Conservative
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8 ldlnitlefa 17
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                                                                                                                                                                                                                                                                                             20-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                     Naparstek Y;
                                                                                      16-DEC-1998
                                                                                                                                                                                                                                                                01-0CT-1998
                                                                                                                                                                                          Synthetic.
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                                                      AAW67044;
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                                                                                                                                                               analogue
                                                                                                                                                                                                         Musc sp.
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               AAW67044
RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel mammalian dishevelled-associated proteins, nMkd and DAPlA, useful for inhibiting Wnt signalling in mammalian cells, and thus for treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Dishevelled-associated protein 1A; DAP1A; mNkd; dishevelled protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents an antigenic peptide of mNKD. The peptide was used to raise antibodies. The specification describes mNkd and dishevelled associated protein IA (DAPIA) proteins, that interact with mammalian dishevelled protein. mNkd is useful for inhibiting Wnt signalling in mammalian cells, and thus for treating colon cancer. mNkd is also useful for activating the JNK pathway. mNkd and DAPIA are also useful for screening drugs that are useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 22; Le
Pred. No. 1.3e+02;
2; Mismatches 6;
                                        Wnt signalling; colon cancer; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 34; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY19691 standard; Protein; 28 AA.
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The specification describes human secreted proteins. The polynucleotides and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Pathological conditions can also be diagnosed by determining the presence of mutations in the polypucleotides. Specific uses are described for each of the polynucleotides. Specific uses are described for each of the polynucleotides. Specific uses are described for each of the polynucleotides. Specific uses are described for each of the polynucleotides. Specific uses are described for each of the polynucleotides. Specific uses are described for each of the polynucleotides. Specific uses are described for each of the polynucleotides. Specific uses are described for each of the indian developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental diseases and fetal deficiencies, blood disorders, leukemias, dischamic sand renal disease, lymphomas, inflammation, allergies, ischemic shock, Alzheimer's and cognitive disorders, schizophrenia, prostate diseases, obesity, and inconvented alsoness and products for the indian set of the indi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          malignancies, diseases of testes, lung or thymus, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated human genes and the secreted polypeptides they encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brewer LA, Carter KC, Duan DR, Ebner R, Enuless ...
Feng P, Florence C, Florence KA, Greene JM, Janat F;
Kayw H, Laffeur DW, Moore PA, Ni J, Olsen HS, Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 499; 546pp; English.
                                                                                                  9705-0063089.
9705-0063090.
9705-0063091.
9705-0063092.
9705-0063097.
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97us-0063109.
97us-0063110.
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97US-0063088
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24-0CT-1997;
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24-0CT-1997
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Gaps ; 0 Length 28; Score 36; DB 20; Length 28 Pred. No. 1.4e+02; 6; Mismatches 8; Indels 22.0%; 26.3%; Conservative Query Match Best Local Similarity Matches 5; Conserva

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Search completed: February 21, 2002, 17:08:22 Job time: 188 sec

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us-08-753-851-12.rai

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SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                         PCT-US94-10257A-77
                                                                                                                                                                                                    US-08-440-103-28
US-08-440-542-28
US-08-231-368-28
US-08-440-210-28
                                                                    US-08-553-501A-76
US-08-553-501A-80
US-09-205-231-76
                                                                                                                                           US-08-023-764B-17
US-08-838-413A-5
                                                                                                              US-09-205-231-80
US-08-462-949-17
                                          US-09-399-494-14
US-09-399-494-21
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HAYNES, BARTON F.
APPLICANT: HALE, LAURA P.
APPLICANT: PATTON, KAREN L.
APPLICANT: TELEN, MARILYN J.
APPLICANT: TELEN, MARILYN J.
APPLICANT: AND TITLE OF INVENTION: AN ADHESION MOLECULE NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSE: ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                     -09-240-078-23
                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONTRACT A FELLICIAN DATA A PAPELICATION NUMBER: US/08/143,311B FILING DATE: 29-OCT-1993 CLASSIFICATION: 436 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/973,339 FILING DATE: 30-OCT-1992 CLASSIFICATION: 436 APPLICATION NUMBER: 07/669,730 FILING DATE: 15-MAR-1991 CLASSIFICATION: 436 ATTORNEY AGENT INFORMATION: NAME: WILSON, MARY J. REGISTRATION NUMBER: 32,955 REFERECAMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08143311B Patent No. 5863540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ZIP: 22201-4714
US-08-143-311B-10
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                                                                                             February 21, 2002, 17:06:49; Search time 12.47 Seconds (without alignments) 55:942 Million cell updates/sec
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.: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                     1 LCLVPLSLAQIDLNITCRFAGVFHVEKNGRY 31
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US-09-399-494-17
US-08-143-311B-1
US-08-687-702-5
US-09-494-13
US-09-399-494-13
US-09-399-494-13
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US-08-686-878A-17
US-08-620-151-105
US-08-441-943-35
US-07-679-052A-2
US-09-399-494-15
US-08-360-821B-39
US-08-360-821B-39
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-08-394-748A-6
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length
                                                                                                                                                                                                                                                                                                                   llength: 0
length: 31
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Maximum DB
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us-08-753-851-12.rai

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Score 58; DB 2; Length 25;
Pred. No. 0.012;
1; Mismatches 1; Indels
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COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/07679052A
Patent No. 5298400
GENERAL INFORMATION:
APPLICANT: MILTFELD, Peter L.
APPLICANT: BUNN, Clive L.
APPLICANT: BUNN, Clive L.
APPLICANT: BUNN, Clive L.
APPLICANT: APPLICANT:
CORRESPONDES: 17
CORRESPONDES: 17
CORRESPONDES: 17
CORRESPONDESSEE: FOLGY & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                APPLICANT: HALE, LAURA P.
APPLICANT: PATTON, KAREN L.
APPLICANT: TELEN, MARILYN J.
APPLICANT: LIAO, HOA-XIN.
TITLE OF INVENTION: AN ADHESION MOLECULE
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAPLICATION NUMBER: US/08/143,311B
FILING DATE: 29-OCT-1993
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,339
FILING DATE: 30-OCT-1992
CLASSIFICATION: 436
APPLICATION NUMBER: 07/669,730
                                                                                                                                                                                                                                   ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
Sequence 26, Application US/08143311B Patent No. 5863540 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                 HAYNES, BARTON F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
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Best Local Similarity 85.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                           ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-143-311B-26
                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                            CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A. ZIP: 22201-4714
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0
                                             Length 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                     Ouery Match
Best Local Similarity 100.0%; Score 164; DB 2;
Best Local Similarity 100.0%; Pred. No. 5.2e-19;
Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.1%; Score 69; DB 2; L. 100.0%; Pred. No. 0.00024; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: AN ADHESION MOLECULE NUMBER OF SEQUENCES: 28 CORRESPONDENCE ADDRESS:
                                                                                                                            · 1 LCLVPLSLAQIDLNITCRFAGVFHVEKNGRY 31
                                                                                                                                                  1 LCLVPLSLAQIDLNITCRFAGVFHVEKNGRY 31
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FILING DATE: 29-OCT-1993
CLASSIFICATION: 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                          Sequence 27, Application US/08143311B Patent No. 5863540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,339
FILING DATE: 30-OCT-1992
CLASSIFICATION: 436
APPLICATION NUMBER: 07/669,730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 15-MAR-1991
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/POCKET NUMBER: 1579-
TELECOMMUNICATION INFORMATION:
TELECHONE: 703-816-4000
TELEFAX: 703-816-4000
                                                                                                                                                                                                                                                                                                                                         BARTON F.
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: HALE, LAURA P.
APPLICANT: PATTON, KAREN L.
APPLICANT: TELEN, MARILYN J.
APPLICANT: LIAO, HUA-XIIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAR-1991
N: 436
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
FONCTH: 25 mmino acids
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Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: VIRGINIA
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US-08-143-311B-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DEPTIDYL FLUORESCENT CHEMOSENSOR FOR TITLE OF INVENTION: DIVALENT ZINC NUMBER OF SEQUENCES: 136 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                       Query Match 23.2%; Score 38; DB 1; Length 27; Best Local Similarity 41.2%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
STREET: Plaza Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                             3; Mismatches
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Pred. No. 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 105, Application US/08620151 Patent No. 5928955 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 PLSLAQIDLNITCRFAGVFH-VEKNG 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Imperiali, Barbara
APPLICANT: Walkup, Grant K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Shannon, Karen L.
REGIZETRATION NUMBER: 36,675
REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.9%;
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEO ID 00: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 422
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            312-321-4200
                                                                                                                                                                                                                                                                                                                                           7 LCLPFLEMLTLSLNVPC 23
                                                                                 27 amino acids
                                                                                                                                                                                                                                                                                                                    1 LCLVPLSLAQIDLNITC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Illinois
COUNTRY: USA
ZIP: G0611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                             7; Conservative
                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-686-878A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
US-08-620-151-105
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                                                                               LENGIH:
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CITY: C
                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                      δλ
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APPLICANT: Treacy, Maurice
APPLICANT: Evans, Cheryl
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 25;
11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                   COMPUTER: ILOPPY disk
COMPUTER: ILOPPY disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/679,052A
FILING DATE: 1991056
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 16786/147 CHAC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/686,878A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17, Application US/08686878A Patent No. 5708157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Brown, Scott A. REGISTRATION NUMBER: 32,724
                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.8%; 77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: LaVallie, Edward
APPLICANT: Racie, Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-07-679-052A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Massachusetts
                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 7. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 7; Conserv
                  22313-0299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-686-878A-17
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Gaps
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Pred. No. 21;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 4; Length 21;
Pred. No. 26;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Signal peptide from human
a-1-antitrypsin"
                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/679,052A
FILLNG DATE: 19910506
CLASSIFICATION: 514
ATTORNEY/AGINT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 16786/147 CHAC TELECOMMUNICATION INFORMATION:
1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/09399494 Patent No. 6228363 GENERAL INFORMATION:
                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.6%;
87.5%;
                                                                                                                                                                                                                                                                                                                (703)836-9300
(703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.0%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 87.55,
The Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     : 24 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                              TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: , ; OTHER INFORMATION: , ; US-07-679-052A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Peptide
                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
-Local 7; Conserve
                                  Virginia
                                                                22313-0299
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8 LDLNITLEFA 17
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                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                 CITY: AL
STATE: V
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                    APPLICANT: BURKE, RAE LYN
APPLICANT: RASMUSSEN, MIRELLA EZBAN
APPLICANT: MIKKELSON, JAN MOLLER
TITLE OF INVENTION: PROTEIN COMPLEXES HAVING FACTOR VIII:C
TITLE OF INVENTION: ACTIVITY AND PRODUCTION THEREOF
NUMBER OF SEQUENCES: 35
ADDRESSE: REED & ROBINS
STREET: 288 HAMILLON AVENUE, SUITE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 23;
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                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARES PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,943
FILING DATE: 16 MAY 1995
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: US 051,916
FILING DATE: 19 MAY -1987
PRIOR APPLICATION NUMBER: US 822,989
FILING DATE: 27-JAN-1986
ATTONEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BAROVSKY, KENNETH
REGISTRATION NUMBER: 36.442
REFERENCE/DOCKET NUMBER: 2300-0048.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: WHITFELD, Peter L.
APPLICANT: RICHARDSON, Michael A.
APPLICANT: BUNN, Clive L.
TITLE OF INVENTION: RECOMBINANT PRODUCT
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; Pred. No. 2
                                                                                                                                                                                                                                                                       STATE: CALIFORNIA COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                       Sequence 35, Application US/08441943 Patent No. 6228620
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87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                            CHAPMAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                           PALO ALTO
                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                         ZIP: 94301
                       US-08-441-943-35
                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
US-07-679-052A-2
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/871,355A

FILING DATE: 09-JUN 1997

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: PCT/GB95/02875

FILING DATE: 11-DEC-1995

CLASSIFICATION: 435

APPLICATION NUMBER: PCT/GB95/02875

ATORNEY/AGENT INFORMATION:

NAME: PABSE, PALYER L.

REGISTRATION NUMBER: 31,284

REGISTRATION NUMBER: 31,284
                                        SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPMS 101 CON
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Pred. No. 4
                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                             RPMS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 499, Application US/08871355A Patent No. 6015669
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Pabbet, Patrea L.
REGISTRATION NUMBER: 31,284
REPERENCE/DOCKET NUMBER: RPMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEPAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 499:
SEQUENCE CHARACTERISTICS:
                     COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.3%;
45.5%;
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                        23 amino acids
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Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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8 GLYHLRKDHRY 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 30309-3450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; HYPOTHETICAL:
US-08-637-759B-499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-871-355A-499
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                                                                                                                         APPLICANT: Clauss, ...
APPLICANT: Kao, Janet
APPLICANT: Kayton, Mark
APPLICANT: Libutti, Steven K
APPLICANT: Application Monocyte Activates Host Response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.30, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 499, Application US/08637759B
Fatent No. 5876931
GENERAL INFORMATION:
TITLE OF INVENTON: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
TRRET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEPHONE: 212-391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
                                                                                                                                                                                                                                                                                                       ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/360,821B
FILING DATE: 08-OCT-96
CLASSIFICATION: 435
                                                       Sequence 39, Application US/08360821B Patent No. 6228837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                    Stern, David M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 21.3
Best Local Similarity 38.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 30309-3450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1201 We
CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-637-759B-499
                                 US-08-360-821B-39
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56;
       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred. ...
       Mismatches
                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: AN ADHESION MOLECULE NUMBER OF SEQUENCES: 28 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: February 21, 2002, 17:08:41 Job time: 112 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.7%; Score 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/143,311B
FILING DATE: 29-OCT-1993
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                    Sequence 1, Application US/08143311B Patent No. 5863540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,339
FILING DATE: 30-OCT-1992
CLASSIFICATION: 436
                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: HAYRES, BARTON F.
APPLICANT: PALE, LAUGA P.
APPLICANT: PATTON, KAREN L.
APPLICANT: TELEN, MARRIXN J.
APPLICANT: LIAO, HUA XIN
TITLE OF INVENTION: AN ADHESIO
       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 07/6
FILING DATE: 15-MAR-1991
CLASSIFICATION: 436
       6; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
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7 ELDLNITLEF 16
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Best Local Similarity
Matches 6; Conserv
                                         10 QIDLNITCRF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                  VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                            CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 EKNGRY 31
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EKNGRY 7
                                                                                                                                                     US-08-143-311B-1
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     Matches
                                                                           q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Naparstek, Yaakov
TITLE OF INVENTION: PEPTIDES FOR THE TREATMENT OF SYSTEMIC LUPUS
TITLE OF INVENTION: ERYTHEMATOSUS
FILE REFERENCE: 56040-A-PCT-US/09/399,494
CURRENT APPLICATION NUMBER: US/09/399,494
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 16
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Naparstek, Yaakov
TITLE OF INVENTION: PEPTIDES FOR THE TREATMENT OF SYSTEMIC LUPUS
TITLE OF INVENTION: PEPTIDES FOR THE TREATMENT OF SYSTEMIC LUPUS
TITLE OF INVENTION: EXTYTHEMATOSUS
FILE REFERENCE: 56040-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/399,494
CURRENT APPLICATION NUMBER: 1999-09-20
NUMBER OF SEQ ID NOS: 2.2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                ..
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53;
                                                                                                                                                                                                                                           Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 21;
                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 4;
Pred. No. 53;
2; Mismatches 2
                                                                                                                                                                                                                                           Score 35; DB 3 Pred. No. 41; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16, Application US/09399494 Patent No. 6228363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/09399494 Patent No. 6228363
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 499
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.7%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.7%;
60.0%;
                                                                                                                                                                                                                                           21.3%;
45.5%;
                                                                                                                                                                                                                                           Query Match 21.3
Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 20.7
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                MOLECULE TYPE: protein; HYPOTHETICAL: NO US-08-871-355A-499
                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                       |::|: |: ||
| GLYHLRKDHRY 18
                                                                                                                                                                                                                                                                                                                   21 GVFHVEKNGRY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 QIDLNITCRF 19
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7 ELDLNITLEF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: mouse US-09-399-494-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: mouse
                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-399-494-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-09-399-494-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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Gaps

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## GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

February 21, 2002, 17:11:04; Search time 12.69 Seconds (without alignments) 168.076 Million cell updates/sec

US-08-753-851-13 147

1 LCKAFNSTLPTMAQMEKALSIGFETCRY 28 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

5648 Total number of hits satisfying chosen parameters:

219241 seqs, 76174552 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 28

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

PIR\_68:\* Database :

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
1	33.5		16	. 7	833590	beta-crystallin A3
7	30		19	7	867517	Na+/K+-exchanging
m	30	20.4	22	7	B60771	CDw40 antigen Hu54
4	29		24	Н	B32252	pyrrologuinoline q
2	29	19.7	24	Н	S58242.	
9	27.5	18.7	19	7	568394	~
7	27	18.4	18	~	A54651	insulin-like growt
89	27	18.4	20	7	A60802	-
6	27	18.4	28	7	A23691	apolipoprotein C-I
10	26	17.7	16	7	D32395	ribulose-bisphosph
11	26	17.7	21	7	A85712	unknown protein en
12	26	17.7	23	7	860567	homeodomain protei
13	26	17.7	23	7	A83397	pyrrologuinoline q
14	26	17.7	24	~	A53357	neurotoxin Bt-II -
15	26	17.7	25	7	A32203	dihydrofolate redu
16	26	17.7	27	7	144629	homeotic protein H
17	25.5	17.3	15	7	PA0020	protein QA100028 -
18	25.5	17.3	26	4	A01640	hypothetical prote
19	25.5	•	27	7	T17064	NADH dehydrogenase
20	25	17.0	17	7	D47274	calcium-binding pr
21	25	17.0	24	7	157644	
22	25	17.0	27	~	F38746	pro-B cell differe
23	24.5	16.7	20	7	A42865	Ca2+/calmodulin-de
24	24	16.3	13	7	S36668	hypothetical prote
25	24		13	7	A61288	spore proteinase g
56	24		13	7	B58533	모
27	24		13	7	B19434	probable sex-speci
28	24	16.3	22	~	0781	spike glycoprotein
29	24		22	7	T01859	

30 24 16.3 25 2 B69274 31 24 16.3 27 2 B446329 33 23.5 16.0 19 2 B39845 34 23.5 16.0 22 2 PT0316 35 23 15.6 17 2 A77636 36 23 15.6 18 2 A41877 37 23 15.6 19 2 B60822 39 23 15.6 19 2 B60822 40 23 15.6 21 2 A5359 41 23 15.6 23 2 H5506 42 23 15.6 23 2 B45087 44 23 15.6 23 2 B61318 45 23 15.6 27 2 B61318	hypothetical prote	homeotic protein H	homeotic protein H	pyrB leader peptid	Ig heavy chain CDR	cytotoxin B - Clos	LcrKc - Yersinia p	translation elonga	multicatalytic end	cytochrome P450 UT	translation elonga	epidermal keratin	cysteine proteinas	ribulose-bisphosph	momordin - balsam	probable pre-core
00000000000000000000000000000000000000	B69274	F44629	B44636	B39845	PT0316	A27636	A41877	S45373	PC2326	B60822	A20359	145916	H45087	807303	B61318	S20754
00000000000000000000000000000000000000	~	~	۰ ۵	~	~	~	~	~	~	~	7	7	N	7	7	4
	25	27	27	19	22	17	18	18	19	19	21	23	23	56	27	27
30 31 31 33 33 33 33 34 44 23 44 42 42 43 44 45 45 45 45 45 45 45 45 45 45 45 45	16.3	16.3	16.3	16.0	16.0	15.6	15.6	15.6	15.6	15.6	15.6	15.6	15.6	15.6	15.6	15.6
330 330 330 330 330 330 330 330 330 330	24	24	24	23.5	23.5	23	23	23	23	23	23	23	23	23	23	23

## ALIGNMENTS

RESULT

%33591 beta-crystallin A3 - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 17-Mar-1999 C;Accession: S33590 C;Accession: S33590 A;Title: beta-crystallins insolubilized by calpain II in vitro contain cleavage sites A;Reference number: S33586; MVID:94009594 A;Reference pype: protein A;Residues: 116 cDAV>

Gaps ij Length 16; Indels υ, ., DB 2; Score 33.5; DB Pred. No. 83; 3; Mismatches Conservative Query Match Best Local Similarity Matches 8; Conserva

1;

8 TLPTMAQMEKALSIGFE 24 Dp ŏ

RESULT

Na+/K+-exchanging ATPase (EC 3.6.1.37) alpha chain - pig (fragment)
Na+/K+-exchanging ATPase (EC 3.6.1.37) alpha chain - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 17-Mar-1999
C;Accession: S67517
Ex. i.inder, D.; Hahnen, J.; Schoner, W.
Eur. J. Biochem. 227, 61-67, 1995
A;Attle: Affinity labeling of a sulfhydryl group in the cardiacglycoside receptor sit
A;Reference number: S67517; MUID:95154347
A;Accession: S67517
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-19 <AMT>
C;Keywords: hydrolase

Query Match 20.4%; Score 30; DB 2; Length 19; Best Local Similarity 31.2%; Pred. No. 3.5e+02; Matches 5; Conservative 6; Mismatches 5; Indels

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Gaps

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|: | |:::|:|: 4 NALTPDMDELKKXVSM 19 6 NSTLPTMAQMEKALSI 21 δλ

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RESULT B60771

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Gaps

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Length 24;

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A;Accession: S5842
A;Molecule type: DNA
A;Residues: 'MYRQHPSHPPQRSNF',1-24 <SCH>
A;Cross-references: EMBL:X87299; NID:9929799; PIDN:CAA60731.1; PID:9929803; PIDN:CAA6
A;Note: in GenBank entry PFPQQABCF, release 116.0, the indicated alternative sequence
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S68394
H+-transporting ATP synthase (EC 3.6.1.34) chain G - Chlamydomonas reinhardtii (fragm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Chlamydomonas reinhardiii
C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 17-Mar-1999
C;Accession: 588394
R;Fiedler, H.R.; Schmid, R.; Leu, S.; Shavit, N.; Strotmann, H.
FEBS Lett. 377, 163-166, 1995
A;Title: Isolation of CF(0)CF(1) from Chlamydomonas reinhardtii cw15 and the N-termin A;Reference number: 568388; MUID:96128220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 13-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995
C;Date: 13-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995
C;Accession: A54651
R;Roghani, M.; Segovia, B.; Whitechurch, O.; Binoux, M.
Growth Regul. 1, 125-130, 1991
A;Title: Purification from human cerebrospinal fluid of insulin-like growth factor bi
A;Reference number: A54651; MUID:93091816
                                                                                                                                                                                                                                              C;Superfamily: pyrroloquinoline quinone precursor pqqA
C;Keywords: quinoprotein
F:16,20/Product: pyrroloquinoline quinone #status predicted <MAT>
F:16-20/Cross-link: pyrroloquinoline quinone (Glu, Tyr) #status predicted
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A;Experimental source: cerebrospinal fluid
A;Note: sequence extracted from NCBI backbone (NCBIP:121074)
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Pred. No. 9.4e+02;
2; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 29; DB 1; I
Pred. No. 6.3e+02;
0; Mismatches 4;
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Pred. No. 8.4e+02;
2; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N; Alternate names: ATP synthase chain G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.4%; Scor
46.7%; Pred
ative 2;
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C;Keywords: chloroplast; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Experimental source: strain CW15 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                      19.7%;
60.0%;
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53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 19.7
Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 53.3
Matches 8; Conservative
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Best Local Similarity 46.7'
Matches 7; Conservative
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4 KIFDFNTLPVMAGEE 18
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                    A; Reference number: S58239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 1-19 <FIE>
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A;Molecule type: protein
A;Residues: 1-18 <ROG>
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11 LRIGFEVTMY 20
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                                                                                                                                                                                                                    A; Gene: pqqA
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                                                                                                                                                J. Immunol. 142, 562-567, 1989
A; Title: Biochemical characteristics and partial amino acid sequence of the receptor-lik
A; Reference number: A60771; MUID:89093941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Goosen, N.; Horsman, H.P.A.; Huinen, R.G.M.; van de Putte, P.
J. Bacteriol. 171, 447-455, 1989
A;Title: Acinetobacter calcoaceticus genes involved in biosynthesis of the coenzyme pyrr
A;Reference number: A32252; MUID:89123056
A;Accession: B32252
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N;Alternate names: pyrroloquinoline quinone biosynthesis A
C;Species: Pseudomonas fluorescens
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C;Accession: S56242
R;Schiider, U.; Keel, C.; Defago, G.; Haas, D.
submitted to the EMBL Data Library, May 1995
A;Description: Tn5-directed cloning of pqq genes from Pseudomonas fluorescens CHAO: thei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:X06452; NID:g38740; PID:g130796
A)Note: Litis ORF 1s not annotated in GenBank entry ACPQQSYN, release 116.0
R;Goosen, N.; Huinen, R.G.; van de Putte, P.
J. Bacteriol. 174, 1426-1427, 1992
A;Title: A 24-amino-acid polypeptide is essential for the biosynthesis of the coenzyme A;Reference number: A59183; MUID:92138642
A;Contents: annotation
                                                                                                                                 Ф.
                                                                                        C;Accession: B60771
R;Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann,
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CDw40 antigen Hu549 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-May-2000
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A:Gene: pqqA
C:Superfamily: pyrrologuinoline quinone precursor pqqA
C:Superfamily: quinoprotein
C:Keywords: quinoprotein
C:Keywords: quinoprotein
C:16,20/Product: pyrrologuinoline quinone #status predicted
F:16-20/Cross-link: pyrrologuinoline quinone (Glu, Tyr) #status predicted
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    Acinetobacter calcoaceticus

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                                                                                                                                                                                                                                  A Accession: B6071
A;Status: preliminary
A;Moldcule type: protein
A;Residous: 1-22 <BRA>
C;Superfamily: CD27 antigen; NGF receptor repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30; DB 2;
Pred. No. 4e+02;
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N;Alternate names: pqq gene IV protein
C;Species: Acinetobacter calcoaceticus
                                                                                                                                                                                                                                                                                                                                                                                                                                              20.48;
41.28;
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'-hag 7; Conservat
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Best Local Similarity
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Length 18; Indels - Escherichia coli (strain 015

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Gaps

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Length 16 4; Indels

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"CSpecies: Hallotis rufescens (California red abalone (fragment)
CSpecies: Hallotis rufescens (California red abalone)
CSpecies: Hallotis rufescens (California red abalone)
CSpecies: 19-Mar. 1997 #sequence_revision 09-May-1997 #text_change 15-Oct-1999
CSAccession: S60567
RSDegnan, B.M.; Morse, D.E.
Mol. Marine Biol. Biotechnol. 2, 1-9, 1993
ASTILLE: Identification of eight homeobox-containing transcripts expressed during lar A; Reference number: S60564; MUID:93372986
Asterior S60567
Asterior S60567
                                               A.Description: catalyzes the reaction of carbon dioxide with D-ribulose 1,5-bisphosph C;Superfamily: ribulose-bisphosphate carboxylase large chain C;Keywords: acctylated amino end; carbon dioxide fixation; carbon-carbon lyase; carbo F;1/Modified site: acetylated amino end (Frc) #status experimental F;12/Modified site: N6,N6,N6.trimethyllysine (Lys) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: GB:AE005174; NID:q12515036; PIDN:AAG56157.1; GSPDB:GN00145; UWGP:
A,Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown protein encoded by prophage CP-9330 [imported] - Escherichia coli (; C;)Species: Escherichia coli (c;)Bete: 16.Feb-2001 #sequence_revision 16.Feb-2001 #text_change 31-Mar-2001 C;Accession: A85712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: A85712 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 26; DB 2; Lengtn 21, Pred. No. 1.6e+03;
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                                                                                                                                                                                                                                          Score 26; DB 2;
Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                          17.78;
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Best Local Similarity 45.5
المالية 5; Conservative
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Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-23 <DEG>
A; Residues: 1-16 <HOU>
C; Function:
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A;Gene: Z2087
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                                                                                                                                                                          A60802.
25K acrosomal autoantigen - guinea pig (fragment)
25K acrosomal autoantigen - guinea pig)
C:Species: Cavia porcellus (guinea pig)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: A60802.
B:Aurdy, D.M.: Huang Jr., T.T.F.; Driscoll, W.J.; Tung, K.S.K.; Wild, G.C.
B:A.Title: Purification and characterization of the primary acrosomal autoantigen of guine A:Reference number: A60802; MUID:88193219
A:Reference number: A60802; MUID:88193219
A:Residues: 1-20 cHAR>
C:Comment: This protein comprises 6.4% of acrosomal protein. It appears not to be glycos C:Reywords: sperm
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apolioprotein C-I - rabbit (fragment)
apolioprotein C-I - rabbit (fragment)
c; species: Oryctolagus cuniculus (domestic rabbit)
C; pecies: Oryctolagus cuniculus (domestic rabbit)
C; Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 31-Dec-1993
C; Accession: A23691
B; Weisgraber, K.H.; Mahley, R.W.; Kowal, R.C.; Herz, J.; Goldstein, J.L.; Brown, M.S.
J. Biol. Chem. 265, 22453-22459, 1990
A; Title: Apolipoprotein C-I modulates the interaction of apolipoprotein E with beta-migr ceptor-related protein.
A; Reference number: A23691; MUID:91093092
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Pred. No. 1.1e+03;
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A;Status: preliminary
A;Molecule type: protein
A;Resions: 1-28 <WEI>
C;Superfamily: apolipoprotein A-I
C;Keywords: lipid binding; lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.4%;
25.0%;
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15 KEFGNTLEEKARM 27
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Score 26; DB 2; Length 25; Pred. No. 1.9e+03; 6; Mismatches 3; Indels

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Search completed: February 21, 2002, 17:12:55 Job time: 111 sec
                                                                                                                  17.78;
30.88;
          A; Residues: 1-25 <BAC>
C; Keywords: NADP; oxidoreductase
                                                                                                               Query Match 17.7
Best Local Similarity 30.8
Matches 4; Conservative
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10 VAALKPALGLGYK 22
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                                                                                                                               pyrrologuinoline quinone biosynthesis protein A PA1985 [imported] - Pseudomonas aerugind
Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: A83397
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Toxicon 32, 325-338, 1994
A:Title: Purification, N-terminal sequence and structural characterization of a toxic pr
A:Reference number: A53357; MUID:94287436
A:Reference number: A53357
A:Reference number: preliminary
A:Molecule type: protein
A:Residues: 1-24 < IAL>
C:Keywords: neurotoxin
                                                                                                                                                                                                                                 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                              A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
A;Reference number: A82950; MUID:20437337
A;Accession: A83397
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA'
*Residues: 1-23 SSTO>
A;Cross-references: GB:AE004625; GB:AE004091; NID:g9947983; PIDN:AAG05373.1; GSPDB:GN001
A;Experimental source: strain PAO1
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C; Date: 20-Jul-1989 #sequence_revision 20-Jul-1989 #text_change 20-Mar-1996
C; Date: 20-Jul-1989 #sequence_revision 20-Jul-1989 #text_change 20-Mar-1996
C; Accession: A32203
R; Baccanari, D.P.; Tansik, R.L.; Joyner, S.S.; Fling, M.E.; Smith, P.L.; Freisheim, J.H.
J. Biol. Chem. 264, 1100-1107, 1989
A; Title: Characterization of Candida albicans dihydrofolate reductase.
A; Reference number: A32203; MUID:89093095
A; Status: preliminary
A; Molecule*type: protein
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C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Feb-1997
C;Accession: A53357
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Pred. No. 1.7e+03;
1; Mismatches 4; Indels
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50.08;
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Best Local Similarity 50.0°
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A;Gene: pqqA; PA1985
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Leucophaea

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us-08-753-851-13.rsp

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation-the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                     01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
COENZYME PQQ SYNTHESIS PROTEIN A (COENZYME PQQ SYNTHESIS PROTEIN IV).
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P31718
P21843
P27503
P12800
P12358
P80447
P86633
P80280
                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Acinetobacter.
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Pred. No. 2.9e+02;
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ACHB_ELEEL
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G3P2_JACOR
CXK7_CONPU
DMS4_PHYSA
                  CRBL_VESLE
CPXX_RHORH
MCT3_MOUSE
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MEDLINE=89123056; PubMed=2536663;
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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length: 28
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Score 27; DB 1; Length 25;
Pred. No. 7.1e+02;

18.4%;

2; Mismatches

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28 AA; 3165 MW; 2903C027F676541C CRC64;
  -!- TISSUE SPECIFICITY: SECRETED IN PLASMA...
-!- SIMILARITY: BELONGS TO THE APOCI FAMILY.
PIR; A23691.
HSSP; P03654; 10PP.
Plasma; Lipid transport; VLDL.
                                                                                                                                                               6; Conservative
                                                                                                                                  Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                        MEDLINE-96064397; PubMed-8526497;
Schnider U., Keel C., Defago G., Haas D.;
Schnider U., Keel C., Defago G., Haas D.;
Schnider d. Cloing of pag genes from Pseudomonas fluorescens CHAO:
"Tn5-directed cloing of pag genes from Pseudomonas fluorescens CHAO:
mutational inactivation of the genes results in overproduction of the
antibiotic pyoluteorin.",
Appl. Environ. Microbiol. 61:3856-3864(1995).
-: FOWCTION: REQUIRED FOR COENTYME PYRROLO-QUINOLINE-QUINONE (PQQ)
BIOSYNTHESIS AND PROVIDE THE GLUTAMATE AND TYROSINE RESIDUES WHICH
ARE NECESSARY FOR THE SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Apolipoprotein C-I modulates the interaction of apolipoprotein E with beta-majorating very low density lipoproteins (beta-VLDL) and inhibits binding of beta-VLDL to low density lipoprotein receptor-related protein.";

J. Blol. (Shem. 265:22453-22459(1990).

J. BLOL. CHEM. 265:22453-22459(1990).

MICRATION: APPEARS TO MODULATE THE INTERACTION OF APOE WITH BETA-MICRATING VLDL AND INHIBIT BINDING OF BETA-VLDL TO THE LDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus (Rabbit).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
NCBI_TaxID-9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weisgraber K.H., Mahley R.W., Kowal R.C., Herz J., Goldstein J.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                        Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.7%; Score 29; DB 1; Length 24; 60.0%; Pred. No. 2.9e+02; Live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 AA; 2871 MW; ED13A879B2EA3E8E CRC64;
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
COENZYME PQQ SYNTHESIS PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 AA.
                                                                                                                                                                                                                                                                                                         SIMILARITY: TO OTHER BACTERIAL POQA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APOLIPOPROTEIN C-I (APO-CI) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAA60731.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-91093092; PubMed-2266137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RECEPTOR-RELATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X87299; CAA60732.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                            Pseudomonas fluorescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 LSIGFETCRY 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X87299;
                                                                                                                                                 STRAIN-CHAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APC1_RABIT
P33047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APC1_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APOC1
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"Posttranslational modifications in the amino-terminal region of the large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase from several plant species.";
Plant Physiol. 98:1170-1174(1992).
-!- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSXNTHEFTIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGENTATION OF THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
                                                                                                                                                                                                                                                                                                      01-AUG-1992 (Rel. 23, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXXLASE LARGE CHAIN (EC 4.1.1.39) (RUBISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 3-PHOSEPHO-D-GLYCERATE.
-!- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) = 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOCLYCOLATE.
-!- SUBUNIT: B LARGE CHAINS + 8 MAALL CHAINS.
-!- SUBUNIT: B LARGE CHAINS + 8 MAALL CHAINS.
-!- SUBCELLOLAR LOCATION: CHLOROPLAST.
-!- SUBLICARITY: BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.
-!- SIMILARITY: BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.
--- PROSITE: PSO0157; RUBISCO_LARGE: PARTIAL.
--- Photosynthesis: Carbon dioxide fixation; Photorespiration;
--- Lyase: Oxidoreductase; Monooxygenase; Chloroplast; Acetylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 26; DB 1; Length 16; Pred. No. 5.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOAD959A82688872 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METHYLATION (TRI-).
                                                                                                                                                                                                       AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE, METHYLATION, AND ACETYLATION.
                                                                                                                                                                                                                                                                   01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last seq
15-DEC-1998 (Rel. 37, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Capsicum annuum (Bell pepper).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.78;
45.58;
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                                                                                                                                                                                                                                                                                                                                                                                                               LARGE SUBUNIT) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 17.7
Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                       STANDARD;
| | :|| |:|
15 KEFGNTLEEKARM 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | | |:||:
| 2 QTETKASVGFK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 QMEKALSIGFE 24
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12
16
16 AA;
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Methylation.
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P45668;
           SEQUENCE,
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SEQUENCE
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MOD_RES
NON_TER
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                                                                                                                                                                                                                             Houtz R.L., Poneleit L., Jones S.B., Royer M., Stults J.T.;
"Posttranslational modifications in the amino-terminal region of the large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase from several plant species.";
Plant Physiol. 98:1170-1174(1992).
-!- FUNCTION: RUBISCO CARALYZES TWO REACTIONS: THE CARBOXYLATION OF D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGENTATION OF THE PENTOSE SUBSTRATE IN THE PHOTORESPLATION PROCESS. BOTH REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
NCBI_TaxID=3920;
                                                                    01-AUG-1992 (Rel. 23, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.1.1.39) (RUBISCO LARGE SUBUNIT) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RIBULOSE BISPHOSPHATE CARROXYLASE LARGE CHAIN (EC 4.1.1.39) (RUBISCO LARGE SUBUNIT) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00157; RUBISCO_LARGE; PARTIAL.
Photosynthesis; Carbon dioxide fixation; Photorespiration;
Lyase; Oxidoreductase; Monooxygenase; Chloroplast; Acetylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) =
                                                                                                                                                                                                                                                                                                                                                                             2 3-PHOSPHO-D-GLYCERATE.
-!- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2)
3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
-!- SUBUNIT: 8 LARGE CHAIN & SMALL CHAINS.
-!- SUBCELLULAR LOCATION: CHLOROPLAST.
-!- SUBCELLULAR : BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 26; DB 1; Length 16;
Pred. No. 5.7e+02;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOAD959A82688872 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METHYLATION (TRI-).
                                  16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 AA.
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                                                                                                                                                                                                                   SEQUENCE, METHYLATION, AND ACETYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000685; RuBisCO_large.
                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.7%;
45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 AA; 1648 MW;
                                                                                                                                Cucumis sativus (Cucumber).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Conservative
                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vigna sinensis (Cowpea).
Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 QMEKALSIGFE 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 OTETKASVGFK 12
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Best Local Similarity
                                                       01-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methylation.
                                                                                                                                             Chloroplast
                               RBL_CUCSA
P27064:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RBL_VIGSI
P27067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEOUENCE
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                     RBL_CUCSA
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        RESULT
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several plant species.";
Plant Physiol. 98:1170-1174(1992).
Plant Physiol. 98:1170-1174(1992).
PRINCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF THE PRATOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS: BEACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
                      Houtz R.L., Poneleit L., Jones S.B., Royer M., Stults J.T.; "Posttranslational modifications in the amino-terminal region of the large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Purification, N-terminal sequence and structural characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEUROTOXIN II (Br-II) (FRAGMENT).
Mesobuthus tamulus (Eastern Indian scorpion) (Buthus tamulus).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Mesobuthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lyase; Oxidoreductase; Monooxygenase; Chloroplast; Acetylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                        -1 - CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) -3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
-1 - SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
-1 - SUBCELIUTAR LOCATION: CHLOROPLAST.
-1 - SUBLITY: BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.
InterPro; PRO001651; RUBISCO_LARGE; PARTIAL.
Photosynthesis; Carbon dioxide fixation; Photorespiration;
                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 26; DB 1; Length 16;
Pred. No. 5.7e+02;
Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.7%; Score 26; DB 1; Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOAD959A82688872 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2686 MW; DA1990C8FF8E2769 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METHYLATION (TRI-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACETYLATION.
METHYLATION, AND ACETYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neurotoxin; Sodium channel inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94287436; PubMed=8016854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.7%;
45.5%;
                                                                                                                                                                                                                                                                                                                                                          2 3-PHOSPHO-D-GLYCERATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1648 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 17.7
Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lala K., Narayanan P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 QTETKASVGFK 12
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12
16
16 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=34647;
                                                                                                                                                                                                                                                                                                       ACTIVE SITE.
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.19 LSIGFETC 26
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                                                                                                                                                                                                                                                                         10 LLLGFSLC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaeoglobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Venter J.C.;
                                                                                                                                                                                                                                                                                                                               Y194_ARCFU
030045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reducing
                                                                                                                                                                                                                                                                                                                                                                                                 AF0194.
                                                                                                                                                                                                                                                                                                           RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-89150295; PubMed-3147698; Poch O., Tordo N., Keith G.; "Sequence of the 3386 3' nucleotides of the genome of the AVOI strain trables virus: structural similarities in the protein regions involved
              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                         of
                                                                                                                                                                                           Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                                                                                                                                                                                                                           Engler J.A., Hoppe M.S., van Bree M.P.;
"The nucleotide sequence of the genes encoded in early region 2b
             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.0%; Score 25; DB 1; Length 27; 50.0%; Pred. No. 1.4e+03; Live 2; Mismatches 3; Indels
             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rabies virus (strain AVO1).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Rhabdoviridae; Lyssavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                              Late protein.

27 27

SEQUENCE 27 AA; 3108 MW; E5A8288B117BB533 CRC64;
 100.0%; Pred. No. 8.6e+02;
tive 0; Mismatches 0;
                                                                                                                                01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
LATE LI 52 KDA PROTEIN (FRAGMENT).
Human adenovirus type 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1990 (Rel. 14, Last annotation update)
SPIKE GLYCOPROTEIN PRECURSOR (FRAGMENT).
                                                                                                                27 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 AA.
                                                                                                                                                                                                                                                                                                       -! - FUNCTION: INVOLVED IN VIRION ASSEMBLY.
                                                                                                                                                                                                                                               MEDLINE-83183660; PubMed-6301944;
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X03000; CAA26776.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in transcription.";
Biochimie 70:1019-1029(1988)
                                                                                                                                                                                                                                                                                 human adenovirus type 7.";
Gene 21:145-159(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 50.0
Matches 5; Conservative
            Conservative
                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 PTMAQMEKAL 19
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 PSQQQPQKAL 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                     NCBI_TaxID=10519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=11293;
                                                                                                                                                                                                                                      STRAIN-GOMEN;
                                 25 TCRY 28
                                                     18 TCRY 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VGLG_RABVA
P15199;
                                                                                                             L52_ADE07
P05663;
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                                                                                                L52_ADE07
            Matches
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STRAIN-VC-16 / DSM 4304 / ATCC 49558;

MEDLINE-98049343; PubMed=9389475;

MIDALINE-98049343; PubMed=9389475;

MIDALINE-98049343; PubMed=9389475;

MICHARDAN R.J., Godwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Kerlavage A.R., McKenney K., Adams M.D., Loftus B.,

Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 24; DB 1; Length 22;
Pred. No. 1.6e+03;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane; Envelope protein; Glycoprotein; Signal. SIGNAL 1 19 SPIKE GLYCOPROTEIN. CHAIN 20 > 22 2 22 22 22 24 SEQUENCE 22 AA; 2469 MW; BBA59CE12F3EFEB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGR; AF0194; -.
Hypothetical protein; Complete proteome.
SEQUENCE 25 AA; 2828 MW; 5F480F03C367419F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE001093; AAB91054.1; -.
                                                                                                                                                                                                                                                                                                                                        EMBL; X13357; CAA31737.1; -. PIR; S07817; S07817.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL PROTEIN AF0194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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RBL_VICFA
P05699;
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NON_TER
SEQUENCE
                                                           SEQUENCE
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                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -:- CATALYTIC ACTIVITY: 4-MALEYLACETOACETATE = 4-FUMARYLACETOACETATE.
-:- CATALYTIC ACTIVITY: RX + EUTATHIONE = HX + R-5-G.
-:- COFACTOR: THE MAAI ACTIVITY REQUIRES GLUTATHIONE (BY SIMILARITY).
-:- PATHWAY: CATABOLLISM OF TYROSINE; FOURTH STEP, CATABOLLISM OF
                                                                                                                                                                                                                                                                                                                                                                                             GLUTATHIONE-CONJUGATING ACTIVITY WITH ETHACRYNIC ACID AND 7-CHLORO-4-NITROBERZ-2-OXA-1, 3-DIAZOLE AND MALEYLACETOACETATE ISOMERAES ACTIVITY. HAS ALSO LOW GLUTATHIONE PEROXIDASE ACTIVITY WITH T-BUTYL AND CUMENE HYDROPEROXIDES (BY SIMILARITY). IS ABLE TCATALYZE THE GLUTATHIONE DEPENDENT OXYGENATION OF DICHLOROACETIC
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                      S
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01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ALPHA-LYTIC PROFEASE (EC 3.4.21.12) (ALPHA-LYTIC ENDOPEPTIDASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                   rong Z., Board P.G., Anders M.W.;
"Glutathione transferase zeta catalyses the oxygenation of the
carcinogen dichloroacetic acid to glyoxylic acid.";
Blochem. J. 331:371-374(1998).
-!- FUNCTION: PROBABLE BIFUNCTIONAL ENZYME SHOWING MINIMAL
                                   5
                                                                                                                                                              20-AGG-2001 (Rel. 40, Created)
20-AGG-2001 (Rel. 40, Last sequence update)
20-AGG-2001 (Rel. 40, Last sequence update)
AGG-AGG-2001 (Rel. 40, Last sequence update)
MALEYLACETOACETATE ISOMERASE (EC 5.2.1.2) (MAAI) (GLUTATHIONE STANSFERASE ZETA 1) (EC 2.5.1.18) (GSTZ1-1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- PTM: THE N-TERMINUS IS BLOCKED (PROBABLE).
-i- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. ZETA FAMILY ISOMERASE; Transferase; Multifunctional enzyme; Phenylalanine catabolism; Tyrosine catabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 24; DB 1; Length 28; Pred. No. 2.1e+03;
            Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2943 MW; 1070608C44491C25 CRC64;
Score 24; DB 1; Len
Pred. No. 1.8e+03;
                                                                                                                                           28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 AA.
                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYTOSOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                             STRAIN=FISCHER 344; TISSUE=Liver; MEDLINE=98198370; PubMed=9531472;
                                                                                                                                                                                                                                                                                                  CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHENYLALANINE; FIFTH STEP
           16.3%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACID TO GLYOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 16.3
Best Local Similarity 50.0
Matches 4; Conservative
                                   Conservative
                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Achromobacter lyticus.
                                                        15 MEKALSI -- GFE 24
                                                                        :||| | |||
11 LEKAYRIEAGFE 22
            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 AA;
                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 EKALSIGF 23
                                                                                                                                                                                                                                                                                       [1]
SEQUENCE, AND
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P27459;
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                                                                                                                                           MAAI_RAT
                                                                                                                   11
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                                  Matches
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                                                                                                                                                                                                                                                                            "Molecular cloning and nucleotide sequence of the beta-lytic protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR (EC 4.1.1.39)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Vicia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                         gene from Achromobacter lyticus.";
J. Bacteriol. 172:6506-6511(1990).
-:- CATALYTIC ACTIVITY: HYDROLYSIS OF PROTEINS, ESPECIALLY BONDS
ADJACENTS TO L-ALANINE RESIDUES.
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2A; ALSO KNOWN AS THE
ALPHA-LYTIC PROTEASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shinozaki K., Sun C.-R., Sugiura M.; "Gene organization of chloroplast DNA from the broad bean Vicia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) 2 3-PHOSPHO-D-GLYCERATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE. -: SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS. -: SUBCELLULAR LOCATION: CHLOROPLAST. -: SUBCELLULAR LOCATION: CHLOROPLAST. -: SIMILARITY: BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 23; DB 1; Length 25; Pred. No. 2.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33F56B45BF81573E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001254; Trypsin.
PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
PROSITE; PS00135; TRYPSIN_SER; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase; Serine protease; Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (RUBISCO LARGE SUBUNIT) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Gen. Genet. 197:363-367(1984).
                                                                                                                                                                    STRAIN=M497-1;
MEDLINE=91035265; PubMed=2228973;
                                                                                                                                                                                                                                            S.L., Norioka S., Sakiyama F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.6%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 AA; 2572 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vicia faba (Broad bean).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P00778; 1P04
MEROPS; S01.268; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVGFSVTR 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 SIGFETCR 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTIVE SITE.
                                                                    NCBI_TaxID=224;
                                       Achromobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chloroplast.
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the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                               R PIR; S07303; Sov. L
R HSSP; P00805; IBUR.
DR Mendel: 5434; VICfa;rbcL;1.
DR InterPro; IPR000685; RuBisCO_Large.
DR PROSITE; P8010157; RUBISCO_Large.
DR PROSITE; P8010157; RUBISCO_Large.
DR PROSYTE; P8010157; RUBISCO_Large.
DR PROSYTE; P8010157; Carbon dioxide fixation; Photorespiration;
KW Photosynthesis; Carbon dioxide fixation; Photorespiration.
Lyase; Oxidoreductase; Monooxygenase; Chloroplast; Acetylation.
BY SIMILARITY.
The property of the prospective fixation and the property of th
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00027; HOMECBOX_1; PARTIAL.
PROSITE; PS50071; HOMECBOX_2; PARTIAL.
Homecbox; DNA-binding; Nuclear protein; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HOMEOBOX PROTEIN GBX-1 (GASTRULATION AND BRAIN-SPECIFIC HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murtha M.T., Leckman J.F., Ruddle F.H.;
"Detection of homeobox genes in development and evolution.";
Proc. Natl. Acad. Sci. U.S.A. 88:10711-10715(1991).
-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 23; DB 1; Length 26; Pred. No. 2.7e+03; 2; Mismatches 5; Indels
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STRAIN-C57BL/6; TISSUE-Spleen;
MEDLINE-92073357; PubMed-1720547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:95667; Gbx1.
InterPro; IPR001356; Homeobox.
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25
2873 MW;
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Best Local Similarity 36.4
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN 1) (FRAGMENT).
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P82976;
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SEQUENCE
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                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pteryyota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea; Blaberidae; Leucophaea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 22; DB 1; Length 10;
Pred. No. 1.5e+03;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMIDATION.
9E469D66D9C87685 CRC64;
15.3%; Score 22.5; DB 1; 35.0%; Pred. No. 3.1e+03;
                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
TACHYKININ-RELATED PEPTIDE 9 (LEMTRP 9).
                                                                                                                                       10 AA
                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: February 21, 2002, 17:15:40 Job time: 180 sec
                                                                                                                                                                                                               Leucophaea maderae (Madeira cockroach)
                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
MEDLINE=97269266; Pubmed=9114447;
                                                                                                                                                                                                                                                                            [1]
SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.0%;
50.0%;
                                                                        1 CKKYLS-LTERSQIAHALKL 19
                                                2 CKAFNSTLPTMAQMEKALSI 21
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Best Local Similarity 50.0
Matches 5; Conservative
                        7; Conservative
                                                                                                                                       STANDARD;
Query Match
Best Local Similarity
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                                                                                                                                      TRP9_LEUMA P81741;
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Q9wrll hepatitis b

human immun

homo sapien

Q9qex3 Q9uce6 h 09tr36

bos taurus

Q9k5a9 enterobacte

099x07 rattus norv 046193 holopneuste 094450 chaetopteru 026389 tenodrilus 023740 ctenodrilus 06872 branchlosto P83741 rana catesb 079901 oplurus cuv

Q9ps00 micropogoni

Ogtwc4 dirofilaria Q16397 homo sapien

052411 thermophili 09uc92 homo sapien Q9uc92 homo sapien Q9uc84 homo sapien

Q9zaaO pseudomonas Q9ucg9 homo sapien Q25136 hallotis ru Q25873 polycelis f Q9njr8 euprymna sc Q9njr5 euprymna sc

us-08-753-851-13.rspt

OM protein

Run on:

Sequence:

Title:

Searched:

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Okada H., Yoshida J., Seo H., Wakabayashi T., Sugita K., Hagiwara M.;
"Anti-(glioma surface antigen) monoclonal antibody G-22 recognizes
overexpressed CD44 in glioma cells.";
Cancer Immunol. Immunother. 39:313-317(1994).
InterPro: IPR000538; Link.
ProDom; PD000918; Link.; 1.
SEQUENCE 25 AA; 2810 MW; C65A2E285F780F4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2000 (TrEMBLrel. 14, Last annotation update)
LYMPHOCYTE HOMING RECEPTOR CD4444 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
85 KDA GLIOMA MEMBRANE PROTEIN/CD44 HOMOLOG.
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Pred. No. 1.2e-13;
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100.0%; Pred. No.....
0; Mismatches
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                         098549
090CE6
090CE6
091R36
091CG9
090CG9
025136
090CR9
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094450
026389
023740
006872
P82741
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09UC92
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MEDLINE=95079448; PubMed=7527301;
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                                                                                                                                                                                        2813
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Best Local Similarity 100.
Matches 25; Conservative
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Q9UCB0
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 RESULT
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Q9nfk8 brugia paha
Q79455 human immun
Q79461 human immun
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09f9ul pseudomonas
026207 phagocata w
027442 stylaria la
09nj93 steatoda tr
09nj93 steatoda tr
                                                                                                                  (without alignments)
186.080 Million cell updates/sec
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Q86380 rubella vir
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Q9bm01 hydra litto
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Q50436 methylobaci
Q9bm19 lissomyema
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                                                                                                    February 21, 2002, 17:12:20; Search time 22.01 Seconds
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                                                                                                                                                                                                                                                                                              11317
               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                 473505 segs, 146272329 residues
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Maximum Match 100%
Listing first 45 summaries
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Q86380
Q96705
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Q79461
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09F9U1
026207
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Q9NJG3
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Q50436
Q9BM19
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sp_human:*
sp_invertebrate:*
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sp_bacteria:*
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sp_virus:*
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Match Length DB
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   HSSP; P02833;
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                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-8908564; PubMed-2909990;
MEDLINE-8908564; PubMed-2909990;
Frey T.K., Marr L.D., Sanchez A., Simmons R.B.;
"Identification of the 5' end of the rubella virus subgenomic RNA.";
Virology 168:191-194(1989).
BEMBL: M23030; AAA72714.1; -.
NON_TER 18 18 18
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                                                               Shepley M.P., Racaniello V.R.;
"A monoclonal antibody that blocks poliovirus attachment recognizes the lymphocyte homing receptor CD44.";
J. Virol. 68:1301-1308(1994).
SEQUENCE 23 AA; 2573 MW; 2D6C726199AD402D CRC64;
                                                                                                                                                                                                                                                                                                                                              Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ilyanassa obsoleta.
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Muricoidea; Nassariidae; Ilyanassa.
                                                                                                                                             Score 58; DB 4; Length 23;
Pred. No. 0.025;
0; Mismatches 1; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-NOV-1998 (TrEMBLrel. 08, Last ann
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                                                       MEDLINE-94149816; PubMed-7508992;
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57.1%;
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Best Local Similarity 92.3%;
Matches 12; Conservative
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nes 8; Conservative
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MEDLINE=99318125; PubMed=10391241;
de Rosa R., Grenier J. G., Andreeva T., Cook C.E., Adoutte A., Akam M.,
de Rosa R., Grenier J. G., Andreeva T., Cook C.E., Adoutte A., Akam M.,
Carroll S.B., Balavoine G.,
"Hox genes in brachiopods and priapulids and protostome evolution.";
Nature 399:772-776(1999).
Nature 399:772-776(1999).
EMBL: AF144884; AAA40640.1; -
HSSP: PO2833; 9AWT.
InterPro; IPR001356; Homeobox.
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Hydridae; Hydra.
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"Transposable elements in sexual and ancient asexual taxa.";
Proc. Natl. Acad. Sci. U.S.A. 97:14477(2000).
EMBL; AY014005; AAG59977.1; -.
                                                                                                                                                           Length 23;
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                                                                                         D0556DA25DA41458 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MARINER-LIKE TRANSPOSASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
LABIAL HOMSODOMAIN PROPEIN (FRAGMENT).
                                                                                                                                    Score 29; DB 5; Le
Pred. No. 1.1e+03;
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Pred. No. 1.2e+03;
5; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                            25 AA
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InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
NON_TER 1 1
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2665 MW;
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38.9%;
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38.9%;
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25 AA; 2777 MW;
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| FNKYLTRARRIEIAASLG 18
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Best Local Similarity 30...
7; Conservative
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Best Local Similarity
Matches 7; Conserv
                                                                                       23 AA;
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NCBI_TaxID=27900;
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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Chang C.-H., Herrick J.B., Okinaka R.T., Brainard J.B.,
Terwilliger T.C.;
Tidentification and characterization of genes activated by :
Toloroethanol in Pseudomonas stutzeri BC-2.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AT176640; AA609250.1;
SEQUENCE 23 AA; 2809 MW; 8081599997EBCC47 CRC64;
                                                                                    Score 29; DB 5; Length 27;
Pred. No. 1.3e+03;
3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.0%; Score 28; DB 2; Length 23; 60.0%; Pred. No. 1.6e+03; tive 0; Mismatches 4; Indels
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MEDLINE-94297796, PubMed-7912986;
BATCLIS J.L., Murtha M.T., Ruddle F.H.;
"Multiple Hox/HOM-class homeoboxes in Platyhelminthes.";
Mol. Phylogenet. Evol. 2:143-151(1993).

EMBE: L19217AAB39344.1; -.
InterPro; IP77001356; Homeobox.
                                                     888ED4749D6DA25D CRC64;
                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                            23 AA.
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      PRINTS; PRO0024; HOMEOBOX.
HOMEOBOX; DNA-binding; Nuclear protein.
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NON_TER 27 27
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                                                    27 AA; 3143 MW;
                                                                                    Query Match
Best Local Similarity 38.9%;
Matches 7; Conservative
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Pfam; PF00046; homeobox; 1.
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                                                                                                                                5 FNSTLPTMAQMEKALSIG 22
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2 FNKYLTRARRIEIAASLG 19
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Best Local Similarity
Matches 6; Conserv
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10 LRIGFEVTLY 19
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NCBI_TaxID=316;
                                                     SEQUENCE
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Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
Tubificina; Naididae; Stylaria.
NCBI_TaxID=41694;
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Abzhanov A., Popadic A., Kaufman T.C.;
Chelicerate Hox genes and the homology of arthropod segments.";
Evol. Dev. 0:0-0(2000).
Ewol. AF151987; AAF73203.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metázoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Araneomorphae; Entelegynae; Araneoidea; Theridiidae; Steatoda.
NCBL_TaxID=114396;
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MEDLINE=95211276; PubMed=7697193;
MNOW P., Buss L.W.;
"HOM/Hox-type homeoboxes from Stylaria lacustris (Annelida: Oligochaeta).";
                                                                                                                          Score 28; DB 5; Length 27;
Pred. No. 1.9e+03;
3; Mismatches 8; Indels
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Pred. No. 1.9e+03;
3; Mismatches 8; Indels
                                                              293591649C6DB3BD CRC64;
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SEQUENCE 27 AA; 3171 MW; 7907D4749D6DA24F CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                                                                                      3; Mismatches
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EMBL, S76354; AAB33895.1; --
EMBL, S76352; AAA73975.1; --
HSSP; P02833; 9ANT.
Homeobox; DNA-binding; Nuclear protein. NON_TER 1 27 27 NON_TER 27 27 SEQUENCE 27 AA; 3164 MW; 293591649C
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                                                                                                                              19.0%;
38.9%;
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38.9%;
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                                                                                                                                                                                                                   5 FNSTLPTMAQMEKALSIG 22
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Best Local Similarity 38.99
                                                                                                      Ouery Match
Best Local Similarity 38.5.
7; Conservative
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01-JUN-2001 (TrEMBI
LABIAL (FRAGMENT)
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Indels

Length 19;

Score 27.5; DB 10; Pred. No. 1.6e+03;

2; Mismatches

us-08-753-851-13.rspt

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18.7%;
53.3%;
   Query Match
Best Local Similarity 53.3.
Rest Conservative
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                                                           3 KAFN-STLPTMAQME 16
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| AFSATSLMMKQMKQ 14
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                                                                                                                                                                                                                                                                                                                       Brugia.";
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Q9NFK8;
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Fiedler H.R., Schmid R., Leu S., Shavit N., Strotmann H.;
"Isolation of CFOCF1 from Chlamydomonas reinhardtii cw15 and the N-
"Isolation of GFOCF1 from Chlamydomonas reinhardtii cw15 and the N-
Figs Lett. 377:163-166(1955).
SEQUENCE 19 AA: 2081 MW; AOAC64A247D406A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 Hedderich R., Albracht S.P., Linder D., Koch J., Thauer R.K.;
"Isolation and characterization of polyferredoxin from
Methanobacterium thermoautotrophicum. The mvhB gene product of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
NCBI_TaxID=3055;
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Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
Methanothermobacter.
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Pred. No. 1.9e+03;
3; Mismatches 8; Indels
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Pred. No. 2e+03;
0; Mismatches 6; Indels
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Pfam; PF00037; fer4; 1.
PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
SEQUENCE 28 AA; 2923 MW; D222573BF296D235 CRC64;
                                               888ED462476DA25D CRC64;
                                                                                                                                                                                                                                    (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                    methylviologen-reducing hydrogenase operon.";
FEBS Lett. 298:65-68(1992).
HSSP; P55907; 1XER.
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01-JUN-2001 (TrEMBLrel. 17, Last
POLYFERREDOXIN-MVHB GENE PRODUCT
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.0%;
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38.9%;
                                              27 AA; 3159 MW;
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FNKYLTRARRIEIASSLG 19
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Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                       Conservative
                                                                                                                                                                                                               PRELIMINARY;
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                                                                                            Best_Local Similarity
Matches 7; Conserv
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01-JUN-2000
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A large array of human monoclonal antibodies to type 1 human immunodeficiency virus from combinatorial libraries of asymptomatic seropositive individuals.";
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Brugia.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
LIGHT-CHAIN COMPLEMERARITY-DETERMINING REGION 3 MRNA (CLONE 14),
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Pred. No. 1.4e+03;
4; Mismatches 4; Indels
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EMBL; AJ277990; CAB9315.1; -.
NON_TER 14 14
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EMBL, M80720; AAA4780.1; --
HSSP; P01607; 1REI.
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NCBL_TaxID=11676;
     14 AA.
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     PRT;
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Emes R.D., Thompson F., Devaney E.
                                                                                             01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 AA; 1602 MW;
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18.4%;
Best Local Similarity 42.9%;
Matches 6; Conservative
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16 AA; 1883 MW;
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PRELIMINARY;
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MEDLINE-92052225; Pubmed=1719545;
Burton D.R., Barbas C.F. III, Persson M.A., Koenig S., Chanock R.M.,
Lerner R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A large array of human monoclonal antibodies to type 1 human immunodeficiency virus from combinatorial libraries of asymptomatic seropositive individuals.";
Proc. Natl. Acad. Sci. U.S.A. 88:10134-10137(1991).
EMBL; M80726; AAA44786.1;
                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 15, Last annotation update)
10-CT-2000 (TrEMBLREL. 15, Last annotation update)
LIGHT-CHAIN COMPLEMETARITY-DETERMINING REGION 3 MRNA (CLONE 31),
PARTIAL CLOS (FRAGMENT).
Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Best Local Similarity 38.5%; Pred. No. 1.6e+03;
Matches 5; Conservative 2; Mismatches 6; Indels
Best Local Similarity 38.5%; Pred. No. 1.6e+03;
Matches 5; Conservative 2; Mismatches 6; Indels
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SEQUENCE 16 AA; 1883 MW; 9015605C32B3D65E CRC64;
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3 CQKYNSAPRTFGQ 15
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079461;
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M. tuberculosis an Grb2 N-terminal SH Plasmodium sp mala Malaria CS T3 T-ce Malaria circumspor Malaria circumspor HLA class II bindi Human secreted pro CD4+ T cell epitop

C-terminal substd.
Amphiphilic peptid
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Use of CD44 protein and new peptide derivs - for developing prods for inflammation, immune-mediated tissue damage and tumour cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell adhesion molecule; CD44; antiinflammatory; rheumatoid; arthritis; tumor cell metastasis; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Telen MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patton KL,
                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                 AAY18902
AAY18639
AAY45348
                                                                                         AAR11136
AAY85439
AAR03455
                                                                                                                                           AAB45441
AAB46168
AAB49067
                              AAY19410
AAY19156
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AAY99032
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AAR36312
AAE03101
AAB13659
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                                                                                AAY29363
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                                                                                                                                                                                                                                       AAY99033
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                                                                                                                                                                                                                                                                                                                                                                                                                           58
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 AAR53483 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93WO-US10412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD44 peptide CD44-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hale LP, Haynes BF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1994-167121/20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunosuppressive.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-OCT-1992;
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                                                                               metastasis
31.5
31.5
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 RESULT
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Peptide #4 having
Peptide region of
M. tuberculosis an
M. tuberculosis an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fragment of human
Domain 1 from inte
C. pneumoniae Swib
Chlamydia Swib pep
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                                                                               (without alignments)
87.329 Million cell updates/sec
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                                                                     February 21, 2002, 17:09:04; Search time 23.75 Seconds
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                                                                                                                                                                                                                                                                                                                           /SIDSB/gcgdata/geneseq/geneseqp/AA1981.1A71:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                1 LCKAFNSTLPTMAQMEKALSIGFETCRY 28
                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                   522463 seqs, 74073290 residues
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Maximum Match 100%
Listing first 45 summaries
                                                 OM protein - protein search, using sw model
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AAR06539
AAR72687
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Gapop 10.0 , Gapext 0.5
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Result Š. 

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The M.pirum adhesin gene was isolated using a probe based on the 3'-end of the known M.genitalium adhesin gene. M.pirum is found in AIDS patients and the adhesin may have a role in infection of cells by HIV. If so, the M.pirum adhesin protein will be useful in vaccines to protect against the cytopathic effect of the Mycoplasma and against that of HIV. Specifically, antibodies raised against the peptides K77856 and R77857 (amino acids 201-219 and 1055-1072 of the adhesin, respectively) can inhibit infection of human cells by M.pirum and infection of human T lymphocytes by HIV.
                                                                                                                                                                                          Adhesin; cytoadherence; Mycoplasma; human immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding Mycoplasma pirum adhesin - and related proteins and antibodies, useful in diagnosis, treatment and prevention of M.pirum and HIV infection
                                                                                                                                                Mycoplasma pirum adhesin immunogenic peptide (1055-1072).
                                                                                                                                                                                                                 HIV; vaccine; immunogen; antigen; infection.
           AAR77857 standard; Protein; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 23; 55pp; French.
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| makhkkaikvgfe 17
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                                                                                                                                                                                                                                                              Mycoplasma pirum.
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                                                                                                 08-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                              04-JUN-1993;
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                                                                                                                                                                                                                                                                                                     FR2705970-A.
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                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       deficiencies eg. myeloma, chronic articular rheumatism and endotoxin shock. Antagonist comprises BSF2 peptide (pref. AAs 20-40) with sustitutions of two or more C- and/or N-terminal AAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                         The peptide can be used for treating inflammation and immune-mediated tissue damage such as occurs in the course of autoimmune diseases, e.g. rheumatoid arthritis. It can also be used for determining metastatic potential or to treat or prevent tumor cell metastasis. This peptide corresponds to AA 52-79 of the CD44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BSF2 antagonists are useful in diagnosis and treatment of immuno-
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Pred. No. 7.9;
2; Mismatches 9; Indels
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endotoxin shock;
                                                                                                                                                                                                                                                                       ch 100.0%; Score 147; DB 15; 1 Similarity 100.0%; Pred. No. 1.9e-16; 28; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human B-cell simulator 2 (BSF2) antagonist.
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Claim 4; Page 14; 83pp; English.
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Matches 10; Conservative
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                                                                                                                                                              protein sequence.
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Montagnier L;

Ferris S,

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                                   Indels
                                   2;
Score 40; DB 16;
Pred. No. 11;
                                                                                                                                                                                                                                                                                Peptide #4 having inflammation site affinity.
                  Pred. No. 11;
4; Mismatches
                                                                                                                                                                             AAR72687 standard; peptide; 22 AA.
27.2%;
53.8%;
                                                                                                                                                                                                                                               19-DEC-1995 (first entry)
                Best Local Similarity 53.8
Matches 7; Conservative
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AAR77857

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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The synthetic peptide correspond to regions of immunologically important
                                                                                                                                                                                                               The sequences given in AAR72684-89 are peptides which have an affinity to sites of inflammation. These peptides may be radioactively labelled and used for imaging inflammation sites as diagnostic agents. Tests on rats showed that these peptides would be safe at levels upto 1000 times the recommended clinical dose, The peptides were found to accumulate at sites of inflammation and remain there long enough to allow effective imaging.
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                      DB 16; Length 22;
                                                                                                                                              New peptide(s) with affinity for inflammation sites - and radio:labelled derivs. useful as diagnostic agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide region of human immunodeficiency virus-1 GAG 3.
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Pred. No. 2
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                                                                                         Hanaoka K, Itaya Y, Shirakami Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP80569 standard; protein; 23 AA.
                                                                (NIMD ) NIHON MEDIPHYSICS CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rymo
                                                                                                                                                                                      Claim 1; Page 11; 21pp; English.
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                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.9%;
Best Local Similarity 47.4%;
Matches 9; Conservative
                                     93JP-0287752.
           94EP-0116583
                                                                                                                                                                                                                                                                                                                                                                                                                          2 CKAFNSTLPTMAQMEKALS 20
                                                                                                                                                                                                                                                                                                                                                                                                                                          88EP-0850105
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87US-0051726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Svennerholm B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (VIRO-) VIROVAHL SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1988-272997/39.
                                                                                                                    WPI; 1995-156718/21
                                                                                                                                                                                                                                                                                                                            22 AA;
           20-0CT-1994;
                                     22-0CT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-MAR-1987;
18-MAY-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-SEP-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP284587-A.
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                                                                                                                                                                                                                                                                                                                               Sequence
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This sequence represents an immunogenic portion of a Mycobacterium
tuberculosis antigen of the invention. The polypeptides are useful for
tuberculosis antigen of the invention. The polypeptides are useful for
immunotherapy to treat or prevent tuberculosis (especially in humans),
e.g. they can be included with an acceptable carrier in pharmaceutical
compositions or included in vaccines, and administered to induce
protective immunity in a patient against M. tuberculosis. Tuberculosis is
a chronic, infectious disease generally caused by M. tuberculosis is
infection, and if left untreated typically results in serious
complications and death. Fusion proteins containing the antigen, or DNA
molecules can similarly be included with an acceptable carrier in
pharmaceutical compositions or in vaccines and administered as above. The
polypeptides are also useful for diagnosis of tuberculosis, by contacting
dermal cells with at least one polypeptide and detecting an immune
response (especially induration) on the patient's skin. Inhibiting the
spread of tuberculosis requires vaccination and accurate diagnosis, since
antibiotic therapy may not be effective due to the existence of an
symptomatic but contagious stage and to patient non-compliance. The
polypeptides overcome concerns of safety and efficacy of current
vaccination with live bacteria (usually Bacillus Calmette-Guerin) and
lack of sensitivity and specificity of existing diagnostic techniques.
                                                                                                                                                                                                                                                                             ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antigen; M.tuberculosis protein; immunotherapy; tuberculosis; diagnosis;
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated Mycobacterium tuberculosis antigens - used to develop products for the prevention, treatment and diagnosis of tuberculosis
selected to facilitate coupling of the peptide to a carrier protein. Y is absent or Cys, and Z is OH or NH2.
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                                                                                                                                                                                                          DB 9; Length 23;
                                                                                                                                                                                                                                                                          6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Skeiky YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M. tuberculosis antigen clone ORF-1 peptide 1-10.
                                                                                                                                                                                                                                             1.6e+02;
                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                      Score 33.5;
Pred. No. 1.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 53; 104pp; English.
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                                                                                                                                                                                                                                                                                                                                             3 KAFNSTLPTMAQMEKALSIGFE 24
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5 kafs---pevipmfsalsegyz 23
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                                                                                                                                                                                                      22.8%;
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97US-0858998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                   Query Match
Best Local Similarity 40.5.
Local Similarity 40.5.
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                                                                                                   23 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 AA;
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Gaps

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Indels

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Mismatches

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AAY36359 standard; Protein; 24 AA.
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 Conservative
                               8 TLPTMAQMEKA 18
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sldtmaqmnqa
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Florence K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-DEC-1997;
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18-DEC-19
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18-DEC-1
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19-DEC-1
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Yu G;
Matches
                                                                                                                           AAY36359
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                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents an ammunogente political of a myconoctation to the formation of the invention. The polypeptides are useful for immunotherapy to treat or prevent tuberculosis (especially in humans), and they can be included with an acceptable carrier in pharmaceutical compositions or included in vaccines, and administered to induce protective immunity in a patient against M. tuberculosis. Tuberculosis a chronic, infections disease generally caused by M. tuberculosis is infection, and if left untreated typically results in serious complications and death. Fusion proteins containing the antigen, or DNA molecules can similarly be included with an acceptable carrier in pharmaceutical compositions or in vaccines and administered as above. The polypeptides are also useful for diagnosis of tuberculosis, by contacting dermal cells with at least one polypeptide and detecting an immune response (especially induration) on the patient's skin. Inhibiting the spread of tuberculosis requires vaccination and accurate diagnosis, since antibiotic therapy may not be effective due to the existence of an
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                                                                                                                                                                                                                                                                                                                                     Antigen; M.tuberculosis protein; immunotherapy; tuberculosis; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      asymptomatic but contagious stage and to patient non-compliance. The polypeptides overcome concerns of safety and efficacy of current vaccination with live bacteria (usually Bacillus Calmette-Guerin) and lack of sensitivity and specificity of existing diagnostic techniques
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptide comprising immunogenic Mycobacterium tuberculosis antigen - useful for immunisation against M. tuberculosis infection to treat or prevent tuberculosis, and in diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents an immunogenic portion of a Mycobacterium
                                                             .
0
                             Length 15;
                        Score 33; DB 20; Length 15
Pred. No. 1.2e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Skeiky YAW;
                                                                                                                                                                                                                                                                                                      M. tuberculosis antigen clone ORF-1 peptide 1-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 52; 100pp; English
                                                                                                                                                                                                      AAW73796 standard; Peptide; 15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campos-Neto A,
                            22.4%;
63.6%;
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97US-0859381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-US10407
                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis,
                                                                                                                                                                                                                                                                        (first entry)
                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-045314/04.
                                     Similarity
7; Conserva
                                                                                          TLPTMAQMEKA 18
                                                                                                        :| |||||| :|
| sldtmaqmnqa 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 AA;
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                                                                                                                                                                                                                                                                      24-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                   WO9853075-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAY-1998;
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                                                                                                                                                                                                                                       AAW73796;
                            Query Match
Best Local
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                                                         Matches
                                                                                                                                                                                         AAW73796
                                                                                                                                                                        RESULT
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%XCCCCCCCCCCCCCCCCX8XBABAAXAXBXBXBXAXAXAXAXAXAX

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AAX97916 to AAX98029 represent 110 isolated human secreted protein genes. AAY3624 to AAX36727 represent the secreted proteins encoded by the 110 human genes. The genes and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 110 genes, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders, atherosclerosis, diabetes, cardiovascular
                                                               Human; secreted protein; cancer; tumour; developmental abnormality; foetal deficiency; blood disorder; immune system disorder; inflammation; autoimmune disease; allergy; Alzheimer's disease; cognitive disorder; schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder; digestive disorder; endocrine disorder; infection; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated human genes encoding secreted polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ferrie AM, Florence C;
Fragment of human secreted protein encoded by gene 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moore PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soppet DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Janat F, Kyaw H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feng P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 970S-0068008.
970S-0068053.
970S-0068054.
970S-0068057.
970S-0068064.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US27059
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97us-0068007
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97US-0068367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-418749/35.
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Length 15;

Score 33; DB 20; Pred. No. 1.2e+02;

22.4%; 63.6%;

Query Match Best Local Similarity

AA.

(first entry)

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Isolated polypeptide for diagnosis and treatment of Chlamydia infection comprises immunogenic portion of Chlamydia antigen, which comprises amino acid sequence encoded by polynucleotide sequence
                                                                                                                                                        Chlamydial infection; sexually transmitted disease; belvic inflammatory disease; PID; tubal obstruction; infertility; trachoma; blindness; acute respiratory tract infection; atherosclerosis; coronary heart disease; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 229; 256pp; English.
                                                                                                                        pneumoniae Swib peptide 61-80.
                       AAB13658 standard; Peptide; 20
                                                                                                                                                                                                                                             Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-431303/37.
                                                                                                                                                                                                                                                                               WO200034483-A2.
                                                                                                                                                                                                                                                                                                                                                08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1999;
22-0CT-1999;
                                                                                     02-FEB-2001
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                                                                                                                                                                                                                                                                                                                 .5-JUN-2000
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                                                     AAB13658;
   AAB13658
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disorders, kidney disorders, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners. The sequences given in AAX97907 to AAX97915 and AAX36223 are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is domain I from the integrase like protein cre. The whole coding sequence of the enzyme could be included in an expression vector in order to aid its integration into its host. The expression vector also includes at least the secretion signal of a lipoprotein and a second sequence encoding a heterologous protein and a mycobacterial promoter to control expression of the
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expression vector for expressing protein or polypeptide in mycobacterium - contg DNA sequences encoding lipoprotein secretion signal and peptide heterologous to bacteria expressing fusion protein of lipoprotein heterologous to bacteria
                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium smegmātis; vaccine; cell mediated immunity; HIV; pertussis; malaria; influenza virus; CTL; herpes virus.
                                                                                                                                      Score 33; DB 20; Length 24;
Pred. No. 2e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytotoxic T-lymphocyte response; transformed Mycobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                Domain 1 from integrase like protein cre.
                                                                                                                                                                                                                                                                                                                               AAR34568 standard; Protein; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIsclosure; Fig 29; 86pp; English.
                                                                                                                                        22.4%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91US-0780261.
                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                        Query Match 22.4
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MEDI-) MEDIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neterologous protein.
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                                                                                      24 AA;
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15 psraqmekcm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sednence
                                                                                      Seguence
                                                                                                                                                                                                                                                                                                                                                                AAR34568;
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                                                                                                                                                                                                                                                                                                           AAR34568
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Stromberg

s, Jen

Fling SP,

Skeiky YAW,

Bhatia A,

99US-0288594. 99US-0410568. 99US-0426571.

98US-0208277

99WO-US29012

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1;
The present invention relates to new nucleic acid sequences and the proteins encoded by the nucleic acid sequences. The encoded proteins comprise an immunogenic portion of a Chlamydia antigen. The encoded proteins are useful for the serodiagnosis and treatment of Chlamydia infection. Chlamdiae are intracellular bacterial pathogens that are responsible for a wide variety of human infections. C. trachomatis infection is one of the most common sexually transmitted diseases and can lead to pelvic inflammatory disease (PID), resulting in tubal obstruction and infertility. Trachoma due to ocular infection with C. trachomatis is the leading cause of preventable blindness worldwide. C. pneumonia is a major cause of acute respiratory tract infections in humans and is also
                                                                                                                                                                                                                                                                                                               thought to play a role in the pathogenesis of atherosclerosis and coronary heart disease. The present sequence is a protein isolated in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32.5; DB 21;
Pred. No. 2e+02;
; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
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52.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LCKAFNSTLP-TMAQMEKA 18
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                         coronary heart dia
present invention
                                                                                                                                                                                                                                                                                                                                                                                                                       20 AA;
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Gaps

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22.4%; Score 33; DB 14; Length 28; 70.0%; Pred. No. 2.4e+02; ive 2; Mismatches 1; Indels

Best Local Similarity 70.0 Matches 7; Conservative

Query Match

| :|||||:| agvekals1g 11

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RESULT

13 AQMEKALSIG 22

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                                                                                                                                                                                                                                                                                                 Chlamydia polypeptides and fusion proteins useful for preventing pelvic inflammatory disease, trachoma, acute respiratory tract infections, atherosclerosis and heart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; finmune system disorder; ALDS; autoimmune disease; rheumation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; skin disorder; psoriasis; passis; diabetes; atherosclerosis; addiovascular disorder; pregnancy-related disorder; endocrine disorder; pregnancy-related disorder; gene therapy; cell culture; chemotaxis; food additive; chromosome 15;
                                            pelvic inflammatory disease; trachoma; atheroscierosis; heart disease; acute respiratory tract infection; Capl; CT529; OMCB; polymorphic membrane protein; pmp; thiol specific antioxidant; TSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                  The present peptide is provided in a specification relating to compounds and methods for the treatment and diagnosis of chlamydial infection. The compounds provided include polypeptides and fusion proteins comprising immunogenic portions of Chlamydia antigens and DNA sequences encoding such polypeptides. They are useful for vaccinating against chlamydial infection, which causes pelvic inflammatory disease, trachoma, acute respiratory tract infections, atherosclerosis and heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human gene 13 encoded secreted protein HOEDE28, SEQ ID NO:135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 20;
                                                                                                                                                                                                                                                       Scholler J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                  Chlamydia; vaccine; infection; fusion protein; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.1%; Score 32.5; DB 252.6%; Pred. No. 2e+02; tive 1; Mismatches
                                                                                                                                                                                                                                                       Skeiky YAW, Fling SP,
                                                                                                                                                                                                                                                                                                                                              Claim 66; Page 235; 295pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE03101 standard; Protein; 20 AA.
          Chlamydia Swib peptide 61-80.
                                                                                                                                                            04-DEC-2000; 2000WO-US32919.
                                                                                                                                                                                   99US-0454684
                                                                                                                                                                                             19-APR-2000; 2000US-0556877.
20-JUN-2000; 2000US-0598419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LCKAFNSTLP-TMAQMEKA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                      Probst P, Bhatia A,
                                                                                                                                                                                                                                 CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                            WPI; 2001-374831/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                               WO200140474-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
                                                                                                                                                                                   03-DEC-1999;
                                                                                                                                      07-JUN-2001
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Matches
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Komatsoulis GA, Shi Y, Olsen HS, Soppet DR;

(HUMA-) HUMAN GENOME SCI INC

Ruben SM,

25-OCT-2000; 2000WO-US29365. 29-OCT-1999; 99US-0162237. 21-JUL-2000; 2000US-0219666.

40200132676-A1

10-MAY-2001.

17..20 /note= "Mature secreted protein"

cocation/Qualifiers 1..16 /label= Signal\_peptide

binding partner identification.

Homo sapiens.

Peptide Protein

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Ab007571-AAD07645 represent CDNAs corresponding to 25 human secreted protein genes, and AAE03052-AAE03126 represent the proteins they encode. AAE03127-AAE03150 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions are useful for preventing, the therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, allergies, neurological disorders, diseases of the immune system, allergies, neurological disorders (e.g., Alzheimer's disease, cardiovascular disorders (e.g., Alzheimer's disease, eardiovascular disorders, pregnancy-related disorders, endicorders, eardiovascular disorders, pregnancy-related disorders, endicorders, endicorders, and infections. The proteins can also be used to aid wound subnum, to maintain organs before transplantation, for supporting cell contained and infections before transplantation, for supporting cell contained by and in the company transplantation, to prevent skin a be used contained and addition or procents, and in the company transplantation, to maintain organs before transplantation, for supporting cell contained by addition or and in the company transplantation, to maintain organs before transplantation, to resent be used to and used to a bused and addition or and and addition to maintain organs and in the company transplantation because by and in the company transplantation and and the company transplantation because by the company transplantation because the contained by and the company transplantation because the contained by and the company transplantation because the contained by and the contained by and the contained by a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                         Nucleic acids encoding 25 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. Gaucher's disease, Alzheimer's disease, Scinitar syndrome, Creutzfeldt-Jacob disease, diabetes mellitus and multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as a food additive or preservative to modify storage properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 32; DB 22; L
Pred. No. 2.4e+02;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 482; 546pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunosorbent assay (ELISA). The p
secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.8%;
66.7%;
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WPI; 2001-328773/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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3 alsisfytc 11
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                                               N-PSDB; AAD07620.
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(first entry)

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Chlamydia polypeptides and fusion proteins useful for preventing pelvic inflammatory disease, trachoma, acute respiratory tract infections,
                                                                                Chlamydia; vaccine; infection; fusion protein; antigen; pelvic inflammatory disease; trachoma; atheroscierosis; heart disease; acute respiratory tract infection; Capl; CT529; OMCB; polymorphic membrane protein; pmp; thiol specific antioxidant; TSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 66; Page 235; 295pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                    atherosclerosis and heart disease
                                                       Chlamydia Swib peptide 66-87.
                                                                                                                                                                                                                                                                       03-DEC-1999; 99US-0454684.
19-APR-2000; 2000US-0556877.
20-JUN-2000; 2000US-0598419.
                                                                                                                                                                                                                                              04-DEC-2000; 2000WO-US32919
                                                                                                                                                                                                                                                                                                                                                              Probst P, Bhatia A,
                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-374831/39.
                                                                                                                                                                                     WO200140474-A2
                                                                                                                                                       Chlamydia sp.
                            05-SEP-2001
                                                                                                                                                                                                                 07-JUN-2001
AAG83227;
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δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to new nucleic acid sequences and the proteins encoded by the nucleic acid sequences. The encoded proteins comprise an immunogenic portion of chlamydia antigen. The encoded proteins are useful for the serodiagnosis and treatment of Chlamydia infection. Chlamdiae are intracellular bacterial pathogens that are responsible for a wide variety of human infections. C. trachomatis infection is one of the most common sexually transmitted diseases and can lead to pelvic inflammatory disease (PID), resulting in tubal obstruction and infertility. Trachoma due to ocular infection with C. trachomatis is the leading cause of preventable blindness worldwide. C. pneumonia is a major cause of acute respiratory tract infections in humans and is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thought to play a role in the pathogenesis of atherosclerosis and coronary heart disease. The present sequence is a protein isolated in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated polypeptide for diagnosis and treatment of Chlamydia infection comprises immunogenic portion of Chlamydia antigen, which comprises amino acid sequence encoded by polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stromberg EJ;
                                                                                                                                                                    Chlamydial infection; sexually transmitted disease; pelvic infilammetrory disease; PID; tubal obstruction; infertility; trachoma; blindness; acute respiratory tract infection; atherosclerosis; coronary heart disease; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 22;
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Pred. No. 3.2e+02;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fling SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 229; 256pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Skeiky YAW,
                                                    AAB13659 standard; Peptide; 22 AA.
                                                                                                                                        C. pneumoniae Swib peptide 66-87.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.4%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                           98US-0208277.
99US-0288594.
99US-0410568.
99US-0426571.
                                                                                                                                                                                                                                                                                                                                  99WO-US29012
                                                                                                             (first entry)
                                                                                                                                                                   Chlamydial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probst P, Bhatia A,
                                                                                                                                                                                                                                           Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-431303/37.
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Best Local Similarity
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                                                                                                                                                                                                                                                                       WO200034483-A2
                                                                                                                                                                                                                                                                                                                                  08-DEC-1999;
                                                                                                             02-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                          08-APR-1999;
01-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                       22-OCT-1999;
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                                                                                                                                                                                                                                                                                                    15-JUN-2000
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                                                                                AAB13659;
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                         13
                                        AAB13659
                         RESULT
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Scholler J;

Skeiky YAW, Fling SP,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lecithin: cholesterol acyltransferase activation exhibiting peptide #223.
                                                                                                                                                                                                                                                                                      Gaps
The present peptide is provided in a specification relating to compounds and methods for the treatment and diagnosis of chlamydial infection. The compounds provided include polypeptides and fusion proteins comprising immunogenic portions of chlamydia antigens and DNA sequences encoding such polypeptides. They are useful for vaccinating against chlamydial infection, which causes pelvic inflammatory disease, trachoma, acute respiratory tract infections, atherosclerosis and heart disease.
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                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                           Score 31.5; DB 22;
Pred. No. 3.2e+02;
l; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY19410 standard; Peptide; 18 AA.
                                                                                                                                                                                                                                               21.48;
58.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                 Query Match
Best Local Similarity 58.8
                                                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                                                                 FNSTLP-TMAQMEKALS
                                                                                                                                                                                    22 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             septic shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
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                                                                                                                                                                                        Sequence
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Gaps

1;

Indels

1; Mismatches

5 FNSTLP-TMAQMEKALS 20 

ò a

10; Conservative

Matches

AAG83227 standard; Peptide; 22 AA.

RESULT 14

AAG83227 ID AAG8 XX

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The present invention describes an agonist (A) of apolipoprotein A-I (apoA-I) which is a 15-29 residue peptide, or analog, that forms an amphipathic alpha-helix in presence of lipids. (A), and their lipid complexes, are used to treat or prevent diseases associated with dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or apoA-I deficiency; hypertholesterolamia and metabolic syndrome, also for treating septic shock. When labeled, (A) can also be used diagnostically to measure serum levels of HDL, in particular the HDL subpopulation that is involved in retrograde cholesterol transport, also to image HDL at e.g. atherosclerotic streaks, and to raise antibodies. AAY1941 represent lecithin.cholesterol acyltransferase (LCAT) activity exhibiting core peptides, which are apoA-I agonists.
                                                                                                                                                                                                                                                                                     Metz G;
                                                                                                                                                                                                                                                                                  Buttner K, Cornut I, Dasseux J, Dufourcq J,
                                                                                                                                                                                                                                                                                                                                                                Peptide agonists of apolipoprotein A-I
                                                                                                                                                                                                                                                                                                                                                                                                  Example; Page 128; 280pp; English.
                                                                                                  98WO-US20327.
                                                                                                                                 97US-0940095.
                                                                                                                                                              (BUTT/) BUTTNER K.
(CORN/) CORNUT I.
(DASS/) DASSEUX J.
(DUFO/) DUFOURCO J.
(METZ/) METZ G.
(SEKU/) SEKUL R.
                                                                                                                                                                                                                                                                                                                                  WPI; 1999-277035/23
Homo sapiens.
                                WO9916459-A1.
                                                                                                 28-SEP-1998;
                                                                                                                                 29-SEP-1997;
                                                                08-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                   Sekul R;
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Search completed: February 21, 2002, 17:12:17 Job time: 193 sec

; 0

0; Gaps

21.1%; Score 31; DB 20; Length 18; 42.9%; Pred. No. 3e+02; Live 3; Mismatches 5; Indels

Query Match 21.1 Best Local Similarity 42.9 Matches 6; Conservative

4 AFNSTLPTMAQMEK 17 | | | | :||::| | 5 afrellealagikk 18

QŽ Dp 8, Appli 8, Appli 7, Appli

Sequence 8, Al Sequence 8, Al Sequence 7, Al Sequence 33,

Appl

Sequence

Sequence

PCT-US95-02885-7

Appl Appl Appl Appl

Sequence

Appli

Seguence 9 Sequence

Sequence

Sequence 478, Sequence 478, Sequence 355, Sequence 355,

US-08-637-759B-478

Sequence 26, Appl

ALIGNMENTS

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PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                             US-08-871-355A-478
US-09-258-754-355
US-09-042-107-355
US-08-268-251-26
                                                     PCT-US95-07542-17
US-09-057-762-8
US-08-325-119A-8
US-07-908-455A-7
US-08-465-325-33
US-08-465-325-33
US-08-609-187D-9
PCT-US95-12502-23
PCT-US93-09704A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HAYNES, BARTON F.
APPLICANT: HALE, LAURA P.
APPLICANT: PATTON, KAREN L.
APPLICANT: TELEN, MARILYN J.
APPLICANT: LIAO, HUA-XIN
TITLE OF INVENTION: AN ADHESION MOLECULE
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/143,311B
FILING DATE: 29-OCT-1993
CLASSIFICATION: 436
PRIOR APPLICATION NUMBER: 07/973,339
FILING DATE: 30-OCT-1992
CLASSIFICATION: 436
APPLICATION NUMBER: 07/669,730
FILING DATE: 15-MAR-1991
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11. Application US/08143311B Patent No. 5863540 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Rele
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 28 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: peptide US-08-143-311B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1100 NORT
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
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US-08-143-311B-11
Patent No. 5164481
Patent No. 5169933
Sequence 7, Appli
Sequence 226, App
                                                                                                                               February 21, 2002, 17:10:44; Search time 12.47 Seconds (without alignments) 50.529 Million cell updates/sec
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Appli
Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 223,
Sequence 223,
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Sequence 32,
Sequence 48,
Sequence 54,
Sequence 54,
Sequence 97,
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Sequence 45,
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Seguence 14,
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Sequence 223
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep:*
                                  Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-602-999A-226
PCT-US95-02121-96
US-09-024-198-15
US-09-186-409-15
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US-08-940-095-223
US-08-940-093-223
US-08-940-096-223
US-09-465-719-223
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US-09-100-409A-54
PCT-US95-02121-97
PCT-US95-13841-20
US-08-143-311B-1
US-08-385-375-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-024-198-1
US-09-186-409-1
US-07-908-455A-6
US-08-434-120-32
US-08-186-266-6
US-08-465-325-32
US-08-46-692-48
                                                                                                                                                                                                                                                        1 LCKAFNSTLPTMAQMEKALSIGFETCRY 28
                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-143-311B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-817-933A-7
                                                                                                                                                                                                                                                                                                                                                         212252 segs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                  GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                              OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued_Patents_AA:*
                                                                                                                                                                                                         US-08-753-851-13
147
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0 Maximum DB seq length: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database :
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                                                                                                                                     Run on:
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В
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ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
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APPLICATION NUMBER:
                                  Roseland
New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 AQMEKALSIG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AGVEKALSLG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 29
CLASSIFICATION:
                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-940-095-223
                                  CITY: ROS
STATE: NE
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                                                      Gaps
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Sequence 45, Application US/07977630

Sequence 45, Application US/07977630

Patent No. 5583038

GENERAL INFORMATION:
APPLICANT: Stover, Charles K.
TITLE OF INVENTION: BACTERIAL EXPRESSION VECTORS CONTAINING
TITLE OF INVENTION: DNA ENCODING SECRETION SIGNALS OF LIPOPROTEINS
NUMBER OF SEQUENCES: 84

CORRESPONDENCE ADDRESS:
ADDRESSE: Carella, Byrne, Bain, Gilfillan, Cecchi,
                                                                      .;
0
                                Length 28;
                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 26; 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,767A
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: ANDERSON, ROBERT J.
APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
                            100.0%; Score 147; DB 2;
100.0%; Pred. No. 7.1e-18;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34;
Pred. No.
                                                                                                                         1 LCKAFNSTLPTMAQMEKALSIGFETCRY 28
                                                                                                                                                                                                                                                                                                                                                                                                   SSEE: NIXON & VANDERHYE P.C. F: 1100 NORTH GLEBE ROAD ARLINGTON
                                                                                                                                                                                                                                 ; Sequence 67, Application US/08751767A
; Patent No. 5994104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFREENCE/DOCKET NUMBER: 117-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164091
TELEFAX: 7038164100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 703B164100
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
FRUGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 23.1%;
Best Local Similarity 47.1%;
Matches 8; Conservative
                          Ouery Match
Best Local Similarity 100.C
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 STLPTMAQMEKALSIGF 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-751-767A-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                             RESULT 2
US-08-751-767A-67
                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
CITY: AF
STATE: V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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Gaps
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APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.4%; Score 33; DB 1; Length 28; 70.0%; Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                        OPERATING CONTRACT SOUTHWARE ASCII
SOUTHWARE ASCII
SOUTHWARE APPLICATION DATA:
APPLICATION NUMBER: US/07/977,630
FILING DATE: No. 5583038ember 17, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEE: Pennie & Edmonds LLP
: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,095
FILING DATE: 29-58P-1997
CLASSIFFCATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 223, Application US/08940095
Patent No. 6004925
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM
                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Herron, Charles J.
REGIGSTRATION NUMBER: 28,019
REFERENCE/CDCKET NUMBER: 4695
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
                                                                                                                                                                                                                                                                28,019
                                                                                      OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                      : 28 amino acids
amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 70.0.
است 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: ADD THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                             Score 31; DB 3; Length 18; Pred. No. 77;
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Pred. No. 77;
3; Mismatches 5; Indels
                                                                                                                                              5; Indels
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30,742
30,742
                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FRASESQ Version 2.0
SOFTWARE: PASTSEQ VERSION 2.0
APPLICATION NUMBER: US/08/940,096
                                                                                                                                                                                                                                                                                                                                                        Sequence 223, Application US/08940096 Patent No. 6046166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: COTUZZI, LGUTA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 0091
TELECOMMUNICATION INFORMATION:
TELEPRONE: 650-493-4935
TELEFAX: 650-493-556
TELER: 66141 PRINIE
INFORMATION FOR SEQ ID NO: 223:
                                                                                                                                                                                                                                                                                                                                                                                                                              Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No. 6046166e
    No. 6037323e
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                                                                                                21.1%;
42.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/C
FILING DATE: 29-SEP-1997
                                                                        Query Match
Best Local Similarity 42.97
                                                                                                                                                                                                                                                                                                                                                                                                                              Dasseux, Jean
Sekul, Renate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 18 amino acids
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Best Local Similarity 42.9
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                         4 AFNSTLPTMAQMEK 17
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5 AFRELLEALAQLKK 18
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5 AFRELLEALAQLKK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM CON OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE:
US-08-940-096-223
    ; MOLECULE TYPE:
US-08-940-093-223
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                                                                                                                                                                                                                                                                                                          RESULT 6
US-08-940-096-223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY:
STATE:
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APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31; DB 3; Length 18; Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                NAME: Coruzzi, Laura A

RESISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 009196-0004-999

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935

TELEEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 223:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 223:
STRANDEDNESS: single
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/940,093
FILING DATE: 29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 223, Application US/08940093 Patent No. 6037323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.1%;
42.9%;
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 21.1
Best Local Similarity 42.9
Matches 6; Conservative
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 AFRELLEALAQLKK 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 29 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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US-08-940-093-223
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Gaps

Length 21;

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APPLICANT: ANDERSON, DAVID C.; MORGAN, CHARLES JR.; FRITZBERG, ALAN R.; NICHOLS, EVERETT J.
TITLE OF INVENTION: CAVALENTLY-LINKED COMPLEXES AND METHODS FOR ENHANCED CYTOTOTALCITY AND IMAGING
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: STANWORTH, DENIS R.
APPLICANT: LEWIN, IAN V.
TITLE OF INVENTION: PEPTIDES FOR ANTI-ALLERGY TREATMENT
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Nixon & Vanderhye
1100 No. 5945104th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FPLICATION NUMBER: US/08/817,933A
FILING DATE: 27-JUN-1997
CLASSIFICATION: 424
    Score 30.5; DB 6;
Pred. No. 1.1e+02;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 30;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/390,241
FILING DATE: 07-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 232,337
FILING DATE: 15-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9422294.0
FILING DATE: 04-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08817933A Patent No. 5945104 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Mitchard, Leonard C. REGISTRATION NUMBER: 29,009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.4%;
60.0%;
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(703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 20.4
Best Local Similarity 60.0
Matches 6; Conservative
                                               Conservative
                                                                                     7 STLP-TMAQMEKAL 19
                                                                                                              3 STIPITMEDLOKAL 16
        Query Match
Best Local Similarity
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3 IAKMEKASSV 12
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                                                                                                                                                                                     RESULT 9
5169933-30
;Patent No. 5169933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-817-933A-7
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                                             Matches
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                                                                        APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
CORRESPONDENCE ADDRESS:
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;Patent No. 5164481
; Patent No. 5164481
; TITLE OF INVENTION: PETIDES AND ANALOGUES AND MIXTURES
;FOR DETECTING AND ELICITING ANTIBODIES TO RUBELLA VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 660-493-556
TELEFAX: 661-493-556
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Pred. No. 77;
3; Mismatches
                                                                                                                                                                                                                                                                  E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATION SYSTEM: DOSCING SOFTWARE: FASTSEQ VERSION 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/465,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/397,767
FILING DATE: 23-AUG-1989
                    Sequence 223, Application US/09465719 Patent No. 6265377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,093
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
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US-09-465-719-223
                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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42.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 3
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 21.1
Best Local Similarity 42.9
Matches 6; Conservative
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5 AFRELLEALAQLKK 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                            GENERAL INFORMATION:
APPLICANT: Dasseux
                                                                                                                                                                                                                                                                                                            New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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                                                                                                                                                                                                                                                                    ADDRESSEE:
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; LENGTH: 21
516448149
US-09-465-719-223
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COMPOSITIONS AND METHODS FOR ELLCITING CTL IMMUNITY 153
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382-398"
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APPLICANT: FASANO, ALESSIO
TITLE OF INVENTION: ZONULA OCCLUDENS TOXIN RECEPTOR
                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT 108 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR DATE: 20.00152.

PRIOR DATE: 20.0152.

APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992

PRIOR APPLICATION NUMBER: US 07/749,568
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US95/02121
FILING DATE: 16-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,484
FILING DATE: 16-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
                                                                                           Sequence 96, Application PC/TUS9502121 GENERAL INFORMATION:
                                                                                                                                                                                                                             3: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15, Application US/09024198 Patent No. 5912323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INPORMATION FOR SEQ ID NO: 96: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                  TITLE OF INVENTION: COMP
TITLE OF INVENTION: CTL
NUMBER OF SEQUENCES: 153
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CT-US95-02121-96
2 FDFPLPTHPNLQKA 15
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                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid STRANDEDNESS: un}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 MAQMEKALSI 21
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2 IAKMEKASSV 11
                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1 CLASSIFICATION:
                                                       RESULT 12
PCT-US95-02121-96
                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-024-198-15
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                                                                                                                                                                                                                                                                                                                                                JUGANT: SPARKS, Andrew B.

APPLICANT: KAY, Brian K.

APPLICANT: THORN, Judith M.

APPLICANT: TFOWLKES, Dana M.

APPLICANT: FOWLKES, Dana M.

APPLICANT: ROBER, Channing J.

APPLICANT: RIDER, James E.

TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: ISOLATING AND USING SAME

NUMBER OF SEQUENCES: 467

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the CITY: New York

STATE: New V.

COUNTER: New V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30; DB 4; Length 16;
Pred. No. 98;
3; Mismatches 5; Indels
                                                                                                                                                                                       Length 16;
                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A FILING DATE: 16-FEB-1996 CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION: NAME: Misrock, S. Leslie
                                                                                                                                                                                      DB 2;
98;
                                                                                                                                                                                                         Pred. No. 98;
3; Mismatches
                                                                                                                                                                                       Score 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENUE
INFORMATION FOR SEQ ID NO: 226:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                      20.4%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.48;
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Best Local Similarity 42.95
             SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 amino acids
                                                                                                                                                                                                         Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
INFORMATION FOR SEQ ID NO:
                                                                       single
                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-817-933A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide US-08-602-999A-226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 FNSTLPTMAQMEKA 18
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                                                   TYPE: amino acid
STRANDEDNESS: si
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4 IAKMEKASSV 13
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Gaps

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Sequence 1, Application US/09024198
| Patent No. 591223
| GENERAL INFORMATION:
| APPLICANT: FASANO, Alessio | TILE OF INVENTION: ZONULA OCCLUDENS TOXIN RECEPTOR NUMBER OF SEQUENCES: 18 | CORRESPONDENCE ADDRESS: ADDRESSE: SUGHRUE, MION, ZINN, MACPEAK & SEAS | STREET: 2100 Pennsylvania Avenue, N.W., Suite 800 | CITY: Washington, D.C. | STATE: D.C. |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.4%; Score 30; DB 2; 145.5%; Pred. No. 1.1e+02; iive 4; Mismatches 2
                                                                                                                                                           REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: A-7306
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER: US/09/024,198
17 FEB 1998
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REFERENCE/DOCKET NUMBER: A-6988
TELECOMMUNICATION INFORMATION:
TELEPRAK: (202) 293-7060
TELEFAX: (202) 293-7060
INFORMATION FOR SEQ ID NO: 1:
    FILING DATE: 17 FEB 1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,364
FILING DATE: 20 FEB 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,364
FILING DATE: 20 FEB 1997
CLASSIFICATION:
                                                                                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KIT, Gordon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: KIT, Gordon
                                                                                                                                                                                                                                                                                                        LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 19 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 20.4
Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                 peptide
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                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
HYPOTHETICAL: 1
                                                                                                                                                                                                                                                                                                                                                                                                     US-09-186-409-15
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Pred. No. 1.1e+02;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/09186409
Fatent No. 5948629
GENERAL INFORMATION:
APPLICANT: FASANO, Alessio
TITLE OF INVENTION: ZONULA OCCLUDENS TOXIN RECEPTOR
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
CITY: Washington, D.C.
STAFF: D.C.
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHNUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Penisylvania Avenue, N.W., Suite 800
CITY: Mashington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURREWT APPLICATION DATA:
APPLICATION NUMBER: US/09/186,409
FILING DATE: 5 NOV 1998
                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                        UMBER: US/09/024,198
17 FEB 1998
                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A-6988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 5 NOV 1998
ALASSIETGATION D:
PRIÓR APPLICATION NUMBER: 09/024,198
                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,364
FILING DATE: 20 FEB 1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: A-69:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: KIT, Gordon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 5; Conserva
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                                                                                                                         U.S.A.
                                                                                                                                                                                                                                                                                                FILING DATE: 1 CLASSIFICATION:
                                                                                                                                     20037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-186-409-15
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                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
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Length 18;

; HYPOTHETICAL: NO US-09-024-198-1

Query Match
20.4%; Score 30; DB 2; Length 19;
Best Local Similarity 45.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 4; Mismatches 2; Indels

0;

0; Gaps

12 MAQMEKALSIG 22 : ::||||: | 2 LTELEKALNXG 12 ολ

оp

Search completed: February 21, 2002, 17:12:36 Job time: 112 sec

us-08-753-851-14.rpr

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

February 21, 2002, 16:44:16; search time 33.6 Seconds (without alignments) 47.609 Million cell updates/sec Run on:

US-08-753-851-14 122 1 CRYGFIEGHVVIPRIHPNSIC 21

score: Title: Perfect sc Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues

Searched:

4046 hits satisfying chosen parameters: Total number of

Minimum DB seq length: 0 Maximum DB seq length: 21

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\* Database

pir1:\* pir2:\* pir3:\* pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# STIMMARTES

		æ			SUMMARIES	
Result No.	Score	Query Match	Length	DB	QI	Description
-	30	24.6	1	2	140065	shikimate 5-dehydr
2	29	23.8	3 21	7	140066	shikimate 5-dehydr
m	28	23.0	1	7	B49254	TCR C gamma 1 chai
4	28	23.0	19	7	C56049	superoxide dismuta
S	27	22.1	-	7	B41868	hypothetical prote
9	27	22.1	1	7	F57789	gallbladder stone
7	26	21.3	1	7	H35141	T-cell receptor de
8	25	0	Π.	7	S12904	protein kinase (EC
6	25	20.5		7	A36133	hypothetical prote
10	24.5	20.1	1 21	7	S02643	RNA-directed RNA p
11	24	19.7	, 13	7	A26999	carboxylesterase (
12	24	19.7	, 16	7	A47393	neuropeptide calla
13	24	19.7	17	~	B86323	protein F14D16.5 [
14	24	19.7	, 18	Н	DRDPPP	distal-retinal-pig
15	24	19.7	, 18	4	139461	anti-angiotensin,
16	24	٠	7	7	809720	
17	23	18.9	) 12	7	C30503	Ig gamma-2b chain
18	23	•	9 ' 14	7	D35141	
19	23	18.9	9 14	7	C35141	T-cell receptor de
20	23		~	~	E35141	T-cell receptor de
21	23	18.9	,Τ	~	B35141	T-cell receptor de
22	23		_	~	A35141	T-cell receptor de
23	23	18.9		7	PN0149	beta-Gliadine 13 -
24	23		1	7	140062	shikimate 5-dehydr
25	23	٠	7	7	S69371	duodenase - bovine
56	23	٠	7	7	D49048	T-cell receptor be
27	22.5	18.4	~	7	B36079	hypothetical prote
28	22	18.0	10	7	B61218	alpha-gliadin 6Ha
29	22	18.0	12	7	PA0037	plastocyanin 2 - A

Ig heavy chain CRD fibrinopeptide A -	L-ascorbate peroxi	histidine-rich pro	chymotrypsin (EC 3	prolamin - gama gr	calmodulin - elect	phosphoenolpyruvat	angiotensin I - Ja	gonadoliberin - ch	bradykinin-potenti	angiotensin precur	kassinin-like pept	ribosomal protein	T-cell receptor al	outer membrane por
PT0304 A32654	532587	B32473	A61414	S09516	I50535	S55696	A60624	A21114	н37196	A90917	D60409	S78765	PT0209	B58503
~ ~	a	7	~	~	7	7	7	a	~	~	N	7	7	7
13	17	18	20	. 21	21	σ	10	10	10	10	11	11	11	12
18.0 18.0	18.0	18.0	18.0	18.0	18.0	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2
22 18.0 22 18.0			22 18.0											

# ALIGNMENTS

```
Sinkimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)
C;Species: Buchnera aphidicola
C;Accession: 140065
R;Rouhbakhsh, D.; Baumann, P.
Gene 155, 107-112, 1995
A;Title: Characterization of a putative 23S-5S rRNA operon of Buchnera aphidicola (en A;Reference number: 140061; MUID:95212914
A;Reference number: 140061; MUID:95212914
A;Recession: 140065
A;Genetics: preliminary; translated from GB/EMBL/DDBJ
A;Getule type: DNA
A;Residues: 1-16 <RES>
C;Genetics: 1-16 <RES>
C;Genetics: A;Genetics: A;Genetics: A;Genes: aroE
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 30; DB 2; Length 16;
Pred. No. 1.5e+02;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 24.6%;
Best Local Similarity 38.5%;
Matches 5; Conservative 3
```

5 FIEGHVVIPRIHP 17 qq δ

7

shik/mate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)
C; Species: Buchnera aphidicola
C; Species: Buchnera aphidicola
C; Species: Buchnera aphidicola
C; Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 11-Jun-1999
C; Accession: 140066
R; Roubbakhsh, D.; Baumann, P.
Gene 155, 107-112, 1995
A; Title: Characterization of a putative 23S-5S rRNA operon of Buchnera aphidicola (en A; Reference number: 140061; MUID:95212914
A; Accession: 140066
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-21 <RES>
A; Cross-references: EMBL:U10500; NID:9854719; PIDN:AAA79129.1; PID:9854720
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: shikimate dehydrogenase; shikimate dehydrogenase homology
C; Keywords: oxidoreductase

Length 21; Score 29; DB 2; Pred. No. 2.9e+02; 23.8%; 55.6%; Query Match Best Local Similarity

```
A:Title: Conjugative transfer of Enterococcus faecalis plasmid pAD1: nucleotide seque
A:Reference number: A41868; MUID:92250408
A:Contents: plasmid pAD1
                                                                                                                                                                    A; Note: sequence extracted from NCBI backbone (NCBIN:99901, NCBIP:99906)
R;Clewell, D.B.; Pontius, L.T.; An, F.Y.; Ike, Y.; Suzuki, A.; Nakayama, J.
Plasmid 24, 156-161, 1990
A;Title: Nucleotide sequence of the sex pheromone inhibitor (iAD1) determinant of Ent
A;Reference number: A37391; MUID:91261999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Sim, G.K.; Augustin, A.
Cell 61, 397-405, 1990
A;Title: Dominantly inherited expression of BID, an invariant undiversified T cell re
A;Reference number: A35141; MUID:90242386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 23-Feb_1996 #sequence_revision 23-Feb-1996 #text_change 03-May-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T-cell receptor delta chain V region (105.23) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 30-May-1997
C;Accession: H35141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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A;Status: preliminary; not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: F57789
R; Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, February 1996
A; Description: The proteins of gallbladder stones.
A; Reference number: A57789
A; Accession: F57789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Le
4.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 27; DB 2; 1
Pred. No. 4.3e+02;
0; Mismatches 1
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100.0%; Pred. No. 4...
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83.3%;
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C; Keywords: T-cell receptor
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A;Molecule type: protein
A;Residues: 1-15 <BIN>
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-15 <CLE>
                                                                                                                             A; Molecule type: DNA
A; Residues: 1-15 <PON>
                                                                                                       A; Status: preliminary
                                                                              A; Accession: B41868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 HVVIPR 14
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R;Ezquerra, A.; Wilde, D.B.; McConnell, T.J.; Sturmhofel, K.; Valas, R.B.; Shevach, E.M. Eur. J. Immunol. 22, 491-498, 1992
A;Title: Mouse autoreactive gamma/delta T cells. II. Molecular characterization of the TA;Reference number: A49037; MUID:92164730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     superoxide dismutase (EC 1.15.1.1) (Fe/Mn) [similarity] - unidentified organism (fragmer
C;Species: unidentified organism
C;Date: 12-Apr_1995 #sequence_revision 12-Apr-1995 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Experimental source: urate-calcium oxalate kidney stones

Note: the source is designated as Homo sapiens, however the true source probably origit
C;Superfamily: superoxide dismutase (Mn)
C;Reywords: metalloprotein; oxidoreductase
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                                                                                                                                                                                                                 TCR C gamma 1 chain V-J region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
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C.Date: 04 Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999
C.Acceston: B41868; B37391
R;Pontlus, L.T.; Clewell, D.B.
J. Bacteridl. 174, 3152-3160, 1992
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         Gaps
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A;Experimental source: Y93A cells
A;Note: sequence extracted from NCBI backbone (NCBIN:90688, NCBIP:90690)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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Pred. No. 3.8e+02;
2; Mismatches 2; Indels
       Indels
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    3;
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R'Binette, J.P.; Binette, M.B.
Scanning Microsc 8, 233-239, 1994
A;Title: Sequencing of proteins extracted from stones.
A;Reference number: A56049; MUID:95215817
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 28; DB 2; I
Pred. No. 3.6e+02;
1; Mismatches 3;
    Mismatches
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50.0%;
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Best Local Similarity 50.0%;
Matches 4; Conservative
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Best Local Similarity 50.0
Matches 4; Conservative
    Conservative
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                                                   HVVIPRIHP 17
                                                                                             HNVLPNIEP 14
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A; Residues: 1-18 <EZQ>
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YGALEXHI 19
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carboxylesterase (EC 3.1.1.1), intestinal - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 07-Feb-1997
C;Accession: A26999
R;McGhee, J.D.
Biochemistry 26, 4101-4107, 1987
A;Title: Purification and characterization of a carboxylesterase from the intestine of A;Reference number: A26999; MUID:88000636
A;Accession: A26999
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Cispecies: Calliphora vomitoria (Cispecies: Calliphora vomitoria)
Cispecies: Calliphora vomitoria (Cispecies: Calliphora vomitoria)
Cispecies: Calliphora vomitoria (Cispecies: Cispecies: Calliphora vomitoria)
Cispecies: Calliphora vomitoria (Cispecies)
Cispecies: Calliphora (Cispecies)
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A; Accession: Ad1393
A; Molecule type: protein
A; Residues: 1-16 cDUv>
A; Residues: 1-16 cDUv>
A; Residues: 1-16 cDUv>
A; Rocession: B47393
A; Molecule type: protein
A; Rocession: B47393
A; Molecule type: protein
A; Residues: 3-16 cDU2>
A; Rocession: C47393
A; Molecule type: protein
A; Residues: 1-8 cDU3>
A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                Length 21;
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C;Keywords: amidated carboxyl end; neuropeptide
F;1-16/Product: callatostatin 1 #status experimental <MAI>
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Pred. No. 1.1e+03;
1; Mismatches 1;
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Pred. No. 1.6e+03;
1; Mismatches 0;
                                    A;Status: not compared with conceptual translation A;Status: not compared with conceptual translation A;Molacule type: mRNA A;Residues: 1-21 <MES> C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Superfamily: cucumber mosaic virus RNA 1 protein C;Keywords: nucleotidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 1-13 <MCG>
C;Keywords: carboxylic ester hydrolase; intestine
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60.0%;
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Best Local Similarity 60.09
Matches 6; Conservative
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Best Local Similarity 66.73
Matches 4; Conservative
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8 YGKVEG 13
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C; Date: 30-Nov-1990 #sequence_revision 30-Nov-1990 #text_change 30-Sep-1993
C; Accession. 43613;
C; Accession. 43613;
Madhusudhan, K.T.; Huang, G.; Burns, G.; Sokatch, J.R.
J. Bacteriol. 172, 5655-5663, 1990
A; Title: Transcriptional analysis of the promoter region of the Pseudomonas putida branch. A; Reference number: A36133; MUID:91008935
A; Accession: A36133
A; Accession: A36133
A; Molecule type: DNA
A; Residues: 1-18 <AMD>
A; Cross-references: GB:M33715
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N.Alternate names: RNA replicase
S.Species: tobacco mosaic virus, TMV
C.Species: tobacco mosaic virus, TMV
C.Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 30-Sep-1993
C.Accession: S02643
R.Meshi, T.: Motoyoshi, F.; Adachi, A.; Watanabe, Y.; Takamatsu, N.; Okada, Y.
B.Meshi, T.; Motoyoshi, F.; Adachi, A.; Watanabe, Y.; Takamatsu, N.; Okada, Y.
A.Title: Two concomitant base substitutions in the putative replicase genes of tobacco na. A.Reference number: S02643
A.Accession: S02643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: S12904
R;Banghera, J.S.; Aebersold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L.
FEBS Lett. 273, 223-226, 1990
A;Title: Identification of the sites in myelin basic protein that are phosphorylated l A;Reference number: S12904; MUID:91032186
A;Accession: S12904
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                                                                                                                                                                                                                                                                                                                                                                                                                                  protein kinase (EC 2.7.1.37) - starfish (Pisaster ochraceus)
C;Species: Pisaster ochraceus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
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C;Species: Pseudomonas putida
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Pred. No. 1.1e+03;
                                        Length 16;
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Pred. No. 8.5e+02;
. ____hes 4; Indels
                                    Score 26; DB 2; Length 16;
Pred. No. 6.7e+02;
2; Mismatches 6; Indels
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                                    21.3%;
38.5%;
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80.0%;
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A;Molecule type: protein
A;Residues: 1-14 <SAN>
C;Keywords: phosphotransferase
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity
5; Conserve
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5 GFLEG 9
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Indels

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anti-angiotensin, hypothetical - human (fragment)
N:Alternate names: hypothetical angiotensin receptor antagonist, angiotensin mRNA com
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R, Moore, G.J.; Ganter, R.C.; Franklin, K.J.
Biochem. Biophys. Res. Commun. 160, 1387-1391, 1989
Biochem. Biophys. Res. Commun. 160, 1387-1391, 1989
A; Title: Angiotensin 'antipeptides': (') messenger RNA complementary to human angioten A; Reference number: 139461; MuID:89273605
A; Recession: 139461
A; Moil A; Residues: 1-18 < AMOO>
A; Cross-references: GB:MZ6228; NID:g178641; PIDN:AAA35530.1; PID:g178642
A; Note: this sequence is the conceptual translation of an nucleotide sequence complem
                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 15-Feb-1996 #sequence_revision 15-Feb-1996 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 24; DB 4; Length 18;
Pred. No. 1.6e+03;
2; Mismatches 2; Indels
               Mismatches
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42.98;
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12 VHPVTCC 18
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N;Alternate names: light-adapting hormone
C;Species: Pandalus borealis (northern shrimp)
C;Date: 13-U1-1981 #sequence_revision 13-Ju1-1981 #text_change 23-Aug-1996
C;Accession: A01473
R;Fernlund, P.
Biochim. Blophys. Acta 439, 17-25, 1976
A;Title: Structure of a light-adapting hormone from the shrimp, Pandalus borealis.
A;Reference number: A01473; MUID:76253762
A;Residues: 1-18 <FER>
C;Comment: This peptide causes migration of the distal retinal pigment into the proximal the amount of light entering the retinulas.
C;Comment: This peptide causes migration of the distal structure of light entering hormone
C;Reywords: amidated carboxyl end; hormone
F;18/Modified site: amidated carboxyl end (Ala) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein F14D16.5 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: D2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Accession: B86323
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hudjes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sacano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon, A; Telenence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719
A; Accession: B86323
A; Stelenence and Arither Arabidopsis.
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F;3-16/Product: callatostatin 2 #status experimental <MA2>
F;9-16/Product: callatostatin 3 #status experimental <MA3>
F;16/Modified site: amidated carboxyl end (Leu) #status experimental
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25.0%;
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Best Local Similarity
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A; Residues: 1-17 <STO>
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OM protein - protein search, using sw model

Run on:

February 21, 2002, 16:52:21 ; Search time 20.15 Seconds
(without alignments)
38.211 Million cell updates/sec

US-08-753-851-14 122 1 CRYGFIEGHVVIPRIHPNSIC 21 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

1160 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 21

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

SUMMAKIES	no troinged and the social section of RG	CALVO P41	P0120	PSECA P19921	HUMAN P31940	P81555	PSEPU P41147	STRRM P80575	TEAST P36522	CHICK	OTIN P30426	NCKE P20367	SEGU P42988	LOCMI P41490	P36503	P80489	IUMAN P04277	P01370	ALZE P80614 zea	P14477	JA	P11382		P01016	ASHE	P28879	1 LPRM_STAAU P03063 staphylococ		. P3772	P2593	STRTR P81622	_PERAM P82691 peripla	1 TAL3 PICIA
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ANG1_BOTJA ANGT_BOVIN	ANGT_CRIGE BPPB_AGKHA MLG THETS	TINI_HOPTI AH4_PRUSE	TP13_PHYRO COCO_LIMPO	DCMM_PSECF HY14_PIG	DCMM_PSECH
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### ALIGNMENTS

RESULT ALL1_C ID A	RESULT 1 ALL1_CALVO ID ALL1_CALVO	STANDARD;	PRT;	16 AA.				
A F	P41839; 01-NOV-1995 / Pal	33	, roa+					
Z		32,	sequence update)	pdate)				
DT	20-AUG-2001 (Re	(Rel. 40, Last	c annotation update)	update)				
E C	CALLATOSTATIN 1 (LEU-CALLATOSTATIN 1) [CONTAINS: CALL	CLEU-CALL	ATOSTATIN 1)	CONTAI	NS: CALLATOSTATIN		2 (LEU-	
OS	Calliphora vomi	vomitoria (Blue	(Blue blowfly)	O-CALLAI	JSIMITIN S)).			
8		zoa; Arthro	poda; Trach	eata; He	Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta	ta:		
8		tera; Endo	terygota; D	iptera; I	Brachycera; M	uscome	orpha;	
8	Oestroidea; Cal	liphoridae	: Calliphora					
Š	NCBI_TaxID=27454;	.4;						
z o	[T] CEOITENCE							
ת ה	SEQUENCE. TISSHE=Thoracio	noi [puep ,	Drain and	and Hoad.				
XX	MEDLINE=93211980; PubMed=8460157;	0; PubMed=8	3460157;	nead,				
RA	Duve H., Johnse	Johnsen A.H., Sco		Yu C.G., Ya	Yagi K.J., Tobe	e S.S.		
RA	Thorpe A.;							
RT	"Callatostatins: neuropeptides from the blowfly Calliphora vomitoria	: neuropept	ides from t	he blowf	Ly Calliphora	vomit	coria	
K.T.	with sequence homology		to cockroach allatostatins	allatostatins.	ins.";			
2 2	[2]	SCI.	5.A. 90:2430		. ( c ,			
ND	CHAPACTERIZATIC	N						
RX XX	MEDLINE=94291167: PubMed=8020069	7: PubMed=8	3020069:					
RA	Duve H., Thorpe	Α.:						
RT	"Distribution and functional significance of Leu-callatostatins	ind function	nal signific	ance of I	eu-callatost	atins	in	
RT	the blowfly Calliphora vomitoria.";	liphora von	nitoria.";					
RL	Cell Tissue Res	. 276:367-3	276:367-379(1994).					
ပ္ပ	-!- FUNCTION: N	IAY ACT AS A	A NEUROTRANS	MITTER OF	FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND	TOR A	ш.	
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ე წ	INVOLVED IN	THE CONTRO	INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE	AL MUSCLE	S DUE TO ITS ABILITY	ABILI	TY TO	
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9	SYSTEM AND INTESTINE	INTESTINE.						
ပ္ပ	-!- SIMILARITY:	BELONGS TO	SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY	STATIN FA	MILY.			
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ı E	PEPTIDE 3	1 1 2	CALLATOSTATIN	TATIN 2.				
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o d			01		Length 16;			
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1 HIGLVRLIPTEV 12
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                                                                                                                                  Pandalus borealis (Northern red shrimp).

Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea; Pandaloidea;
Pandalidae; Pandalus.

NCBI_TaxID=6703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1991 (Rel. 17, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
CARBON MONOXIDE OXYGENASE [CYTOCHROME B-561] SMALL CHAIN (EC 1.2.2.4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- COFACTOR: MOLYBDENUM.
-1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                        Blochim. Biophys, Acta 439:17-25(1976).

-!- FUNCTION: CAUSES THE MIGRATION OF THE DISTAL RETINAL PIGMENT INTO THE PROXIMAL END OF THE PIGMENT CHROMATOPHORE CELLS AND THUS DECREASES THE AMOUNT OF LIGHT ENTERING THE RETINULAS.

-!- SIMILARITY: TO THE PDH OF OTHER ARTHROPODS.

PIR; A01473; DRDPPP.
                                                                                                                                                                                                                            Fernlund P.; "Structure of a light-adapting hormone from the shrimp, Pandalus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group; Oligotropha.
NCBI_TaxID=40137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kraut M., Hugendieck I., Herwig S., Meyer O.;
"Homology and distribution of CO dehydrogenase structural genes
carboxydotrophic bacteria.";
Arch. Microbiol. 152:335-341(1989).
-!- CATALYTIC ACTULYT: CO + H(2)O + FERROCYTOCHROME B-561 = CO(
2 H(+) + FERRICYTOCHROME B-561.
                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
PIGMENT-DISPERSING HORMONE (PDH) (LIGHT ADAPTING DISTAL RETINAL
                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                     Score 24; DB 1; Length 18;
Pred. No. 1e+03;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                           AMIDATION.
B2346B6D0178650E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68D4380629401B9C CRC64;
                                                         18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                  MEDLINE=76253762; PubMed=952951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 19.7%;
Best Local Similarity 41.7%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas carboxydovorans.
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Oxidoreductase; Molybdenum.
NON TER 21 21
SEQUENCE 21 AA; 2270 MW;
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                                                                                                                       PIGMENT HORMONE) (DRPH)
                                                                                                                                                                                                                                                                                                                                           18
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                                                                                                                                                                                                                                                                                                                                Hormone; Amidation.
11 RYGF 14
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01-JUN-1994
                                                      DRPH_PANBO
P01209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1991
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P19921;
                                                                                                                                                                                                                                                    borealis."
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                                DRPH_PANBO
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01-JUL-1993 (Rel. 26, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF EPIDERMAL KERATINOCYTES (SPOT 1118)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Predel R., Rapus J., Eckert M., Holman G.M., Nachman R.J., Wang Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein database of normal human epidermal keratinocytes.";
Electrophoresis 13:960-969(1992).
-!- MISCELLANBOUS: ON THE 2D-CEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 7.24, ITS MW IS: 23.5 KDA.
Aarhus/Ghent-2DPAGE; 1118; IEF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Microsequences of 145 proteins recorded in the two-dimensional
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blattcidea; Blattidae; Periplaneta.
NCBI_TaxID=6978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Keratinocytes;
MEDINE=93162043; PubMed=1286667;
Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.
Vandekerckhove J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EF7515F79D50DE12 CRC64;
Score 24; DB 1; Ler
Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23; DB 1; Ler
Pred. No. 1.5e+03;
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PERIVISCEROKININ-2 (PEA-PVK-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 AA.
                                                                                                                                                                                                                                                                                                                  AA.
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TISSUE-Abdominal perisympathetic organs;
MEDLINE-98326577; PubMed-9663444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.9%;
25.0%;
                     19.7%;
ilarity 41.7%;
Conservative
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Saccharomyces cerevisiae (Baker's yeast).
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Aromatic amino acid biosynthesis; Lyase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91285106; PubMed=2060626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ribosomal protein; Mitochondrion.
                                                                                                                                                                                       SEQUENCE, AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4932
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13 GFFEVH 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GFIEGH 9
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P36522;
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SEQUENCE
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SEQUENCE
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ID RM12_Y
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"Isolation of periviscerokinin-2 from the abdominal perisympathetic organs of the American cockroach, Periplaneta americana."; Peptides 19:801-809(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wilson S.D., Wang M., Filpula D.;
Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CATALYZES AN ELECTRONEUTRAL EXCHANGE BETWEEN ARGININE AND ORNITHINE TO ALLOW HIGH-EFFICIENCY ENERGY CONVERSION IN THE ARGININE DEIMINASE PATHWAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1 - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                            -!- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITATORY ACTIONS ON THE HYPERNEURAL MUSCLE.
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Transport; Amino-acid transport; Transmembrane; Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas putida.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
-1- SIMILARITY: BELONGS TO THE ARCD/CADB/GERAB/LYSI FAMILY OF
                                                                                                                                                                     Score 22; DB 1; Length 12;
Pred. No. 1.4e+03;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 22; DB 1; Length 16;
Pred. No. 1.9e+03;
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                                                                                                          AMIDATION.
2F4D8EE1EB05728 CRC64;
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                                                                         -!- MASS SPECTROMETRY: WW=1189.3; METHOD=MALDI.
Neuropeptide; Amidation.
Neuropeptide: Amidation.
MOD_RES
SEQUENCE 12 AA: 1190 MW; ZP4DBEEELEB05728 C
                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ARGININE/ORNITHINE ANTIPORTER (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                             16 AA.
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                                                                                                                                                                     18.0%;
33.3%;
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30.0%;
                                                                                                                                                                                    Best Local Similarity 33.3
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                  4 GFIEGHVVIPRI 15
                                                                                                                                                                                                                                                                  1 GSSSGLISMPRV 12
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas
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P80575;
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15) (PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE) (PAHP SYNTHETASE) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN THE BIOSYNTHESIS OF AROMATIC 'AMINO ACIDS (THE SHIKIMATE PATHWAY).
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- PTM: THE N-TEMBENIUS IS BLOCKED.
-!- SIMILARITY: BELONGS TO CLASS-II DAHP SYNTHETASE FAMILY.
-!- DIACEPPIO; IPR002480; DAHP—SYNTH—2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ISOLATE 4018;
MEDLINE=96349103; PubMed=8760910;
Walker G.E., Dunbar B., Hunter I.S., Nimmo H.G., Coggins J.R.;
Walker G.E., Dunbar B., Hunter I.S., Nimmo H.G., Coggins J.R.;
"Evidence for a novel class of microbial
3-deoxy-D-arabino-heptulosonate-7-phosphate synthase in Streptomyces coelicolor A3(2), Streptomyces rimosus and Neurospora crassa.";
Microbiology 142:1973-1982(1996).
-!- CATALYTIC ACTIVITY: 7-PHOSPHO-2-DEHYDRO-3-DEOXY-D-ARABINO-
HEPTONATE + ORTHOPHOSPHATE = PHOSPHOENOLIPYRUVATE + D-ERYTHROSE
4-PHOSPHATE + H(2)0.
                                                                                                                                                                                                                                              Streptomyces rimosus.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L12 (YML12) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2209 MW; 7FE627E713C871BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 AA; 1851 MW; 74BCD9FEDDDB3900 CRC64;
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PIR; H37196; H37196
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Best Local Similarity
Matches 3; Conserv
                                           ENZYME INHIBITOR)
                                                                                                                                                                                                                                                                                     16 HPN 18
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SEQUENCE
                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ANGIOTENSINOGEN (CONTAINS: ANGIOTENSIN I; ANGIOTENSIN II] (FRAGMENT).
                                                                                                                                                                      Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                               BALANCE OF BODY FLUIDS.

-1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
-1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
PIR; A01250, A01250.
PIR; A90917; A90917.
PIR; A60624; A60624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
        Score 21.5; DB 1; Length 15; Pred. No. 2.1e+03; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                            Structure of fowl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CEFBEDD761F2DB42 CRC64;
                                                                                                                                                                                                                                                 Nakayama T., Nakajima T., Sokabe H.; "Comparative studies on angiotensins. 3. Structure angiotensin and its identification by DNS-method."; Chem. Pharm. Bull. 21:2085-2087(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 21; DB 1; I
Pred. No. 1.7e+03;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 AA.
                                                                                                    10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PSUGGO, CERTICAL Plasma; Serpin.

Vasoconstrictor; Plasma; Serpin.

10 ANGIOTENSIN I.
                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000215; Serpin.
PROSITE; PS00284; SERPIN; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                    SPECIES-C.c.japonica;
MEDLINE-90284684; PubMed-2191893;
                                                                                                                                                                                                                                 SPECIES=Chicken;
MEDLINE=74127845; PubMed=4361802;
        17.6%;
46.2%;
                                                                                                                                                               Gallus gallus (Chicken), and
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50.0%;
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Σ
                          Conservative
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                                                                                                    STANDARD;
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                                                                                                                                                                                                         NCBI_TaxID=9031, 93934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10
                                                                                                                                                                                                                                                                                                                      Takei Y., Hasegawa Y.;
                                                   |:| || |:|
FVE---VIVRENP 15
                                         FIEGHVVIPRIHP 17
Query Match
Best Local Similarity
Local 6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                       SERPINAS OR AGT
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5 VHPFSL 10
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BPP8_BETIN
ID BPP8_BOTIN
AC P30426;
                                                                                                   ANGT_CHICK
P01018;
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SEQUENCE
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                                                                                           ANGT_CHICK
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01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GONADOLIBERIN III (GONADOTROPIN-RELEASING HORMONE III) (GNRH-III) (LH-GNRH).
                                                                                                                                                                                                                                                                                                                                                                             Cintra A.C.O., Vieira C.A., Giglio J.R.;

"Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";
J. Protein Chem. 9:221-227(1990).
-!- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE ANGIOTENSITY-CONVERTING ENZYME AND ENHANCES THE ACTION OF BRADXKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.

IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3
                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clupea pallasii (Pacific herring).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostel; Euteleostel;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8018, 30724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES-O.keta;
BADLINE-81195140; PubMed-6341999;
Sherwood N., Eiden L., Brownstein M., Spiess J., Rivier J., Vale
"Characterization of a teleost gonadotropin-releasing hormone.";
Proc. Natl. Acad. Sci. U.S.A. 80:2794-2798(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
01-APR-1993 (Rel. 25, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
BRADYKININ-POTENTIATING PEPTIDE S5,1 (ANGIOTENSIN-CONVERTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.2%; Score 21; DB 1; Length 10; 100.0%; Pred. No. 1.7e+03; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYRROLIDONE CARBOXYLIC 2FF835545761F6D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE GNRH FAMILY.
PIR; A21114; A21114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oncorhynchus keta (Chum salmon), and
                                                                                                                                                                                                                                                                                                                                IISSUE=Venom;
MEDLINE=90351557; PubMed=2386615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 AA; 1173 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypotensive agent; Venom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Conservative
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LOCUSTAMYOTROPIN 4 (LOM-MT-4).
Locusta migratoria (Migratory locust).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Peterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
Acridomorpha; Acridoidea; Acrididae; Locusta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
LANTIBIOTIC DURANCIN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 AA.
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MEDLINE-91107436; PubMed-2125590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRUCTURE BY NMR.
MEDLINE=93387292; PubMed=8375380;

    Antibiot. 43:1403-1412(1990).

                                                                                                                                                                                                                                                                                                                                                                                                      17.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces griseoluteus.
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 17.2
Best Local Similarity 42.9
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                          SEQUENCE, AND SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRUCTURE BY NMR
                                                                            NCBI_TaxID=7004;
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1 RLHQNGM 7
                                                                                                                        TISSUE-Brain,
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P36503;
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DURC_STRGP
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0
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Roberts J.D., Malchiorri P., Erspamer V.;
"Six novel tachykinin- and bombesin-related peptides from the skin of
the Australian frog Pseudophryne guntheri.";
Peptides 11:299-304(1990).
-!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
                                                                                                                                                                                                                                                                                                                                                                                                    Pseudophryne guentheri (Frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                      Score 21; DB 1; Length 10;
Pred. No. 1.7e+03;
2; Mismatches 1; Indels
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                                    HORDIDI FOURTH HORDING HORDING AMIDATION HORDING AMIDATION HORDING CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYRROLIDONE CARBOXYLIC ACID. AMIDATION.
                                                                            AMIDATION.
284B3233786B45A3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY. PIR; D60409; D60409.
                                                                                                                                                                                                                                                                                                     PRT; 11 AA. P4298; 10 NOV-1995 (Rel. 32, Created) 1.NOV-1995 (Rel. 32, Last sequence update) 30-NAY-2000 (Rel. 39, Last annotation update) RASSININ-LIKE PEFFIDE FILE (FG-KIII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LATAT LOCMI STANDARD; PRT; 13 AA. P41490; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 01-NOV-1995 (Rel. 32, Last annotation update)
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InterPro; IPR002040; Tachykinin.
Pfam; PF02202; Tachykinin; 1.
SMART; SM00203; TK; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00267; TACHYKININ; 1
                                                                                                                                      17.2%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 AA; 1268 MW;
                                                                                          10 AA; 1230 MW;
               Pfam; PF00446; GnRH; 1.
PROSITE; PS00473; GNRH; 1.
InterPro; IPR002012; GnRH.
                                                                                                                                      Query Match 17.2
Best Local Similarity 50.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Conservative
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Best Local Similarity
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NCBI_TaxID=30349;
                                                                            10
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5 YGWLPG 10
                                                                                                                                                                                                   3 YGFIEG 8
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3 HPN 5
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MOD_RES
SEQUENCE
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                                                    Zimmermann N., Freud. S., Fredenhagen A., Jung G.;
Zimmermann N., Freud. S., Fredenhagen A., Jung G.;
"Solution structures of the lantibiotics duramycin B and C.";
Eur. J. Biochem. 216:419-428(1993).
-!- FUNCTION: ACTS AS INHIBITOR OF PHOSPHOLIPASE A2.
-!- PTM: MATURATION OF LANTIBIOTICS INVOLVES THE ENZYMIC CONVERSION OF THR, SER, AND CYS INTO DEHYDRATED AA AND THE FORMATION OF SULFIDE BRIDGES. THIS IS FOLLOWED BY THE MEMBRANE TRANSLOCATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fredenhagen A., Fendrich G., Marki F., Marki W., Gruner J., Raschdorf F., Peter H.H.;
"Duramycins B and C, two new lanthionine containing antibiotics as inhibitors of phospholipase A2. Structural revision of duramycin and cinnamycin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinomycetales; Streptomycineae, Streptomycetaceae; Streptomyces. NCBI_TaxID=29306;
Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P., de Loof A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 21; DB 1; Length 13;
Pred. No. 2.2e+03;
2; Mismatches 2; Indels
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"Biochemical characterization of the 8 hydroxy'5-deazaflavin-reactive hydrogenase from Wethanosarcina barkeri Fusaro.";
Eur. J. Biochem. 233:727-735(1995).
-! FUNCTION: REDUCES THE PHYSIOLOGICAL LOW-POTENTIAL TWO-ELECTRON ACCEPTOR COENZYME F420, AND THE ARTIFICIAL ONE-ELECTRON ACCEPTOR METHYLVIOLOGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- CATALYTIC ACTIVITY: H(2) + COENZYME F420 = REDUCED COENZYME F420.
-!- COFACTOR: FRH CONTAINS NICKEL, IRON-SULFUR, AND FAD COFACTORS.
-!- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS AND A GAMMA CHAIN.
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                P80489;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
COENZYME F420 HYDROGENASE ALPHA SUBUNIT (EC 1.12.99.1) (8-HYDROXY-5-
DEAZAFLAVIN-REDUCING HYDROGENASE ALPHA SUBUNIT) (FRH) (FRRGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
   OF THE MODIFIED PRECURSOR.

IY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE [NIFE]/[NIFESE] HYDROGENASE LARGE SUBUNIT FAMILY.
InterPro; IPR001501; NiFeSe_Hases.
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                                                                                                                             ABU-S-CYS (METHYLLANTHIONINE).
ALA-S-CYS (LANTHIONINE).
ABU-S-CYS (METHYLLANTHIONINE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 21; DB 1; Length 20;
Pred. No. 3.3e+03;
1; Mismatches 0; Indels
                                                                                                                                                                                                                        Score 21; DB 1; Length 19;
Pred. No. 3.2e+03;
); Mismatches 1; Indels
                                                                                                                 LYSINOALANINE (BONDED TO 6)
                                                              D-ALANINE (BONDED TO 19).
D-ABU (AMINOBUTYRIC ACID).
D-ABU (AMINOBUTYRIC ACID).
                                                                                                                                                                              E2404ECE3F95286A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                   20 AA
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PROSITE; PS00508; NI_HGENASE_L_2; PARTIAL.
                                                   D-ALANINE.
CLEAVAGE OF THE MODIFIED PRECURSC
-!- SIMILARITY: STRUCTURAL SIMILARITY
Antibiotic; Bacteriocin; Lantibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-FUSARO / DSM 804;
MEDLINE-96085134; Pubmed-8521835;
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75.08;
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75.08;
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Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methanosarcina barkeri.
                                                                                                                                                                                                                                          Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methanosarcina.
NCBI_TaxID=2208;
                                                                                                                                                                                                                                                                                                          RESULT 15
FRHA_METBA
ID FRHA_METBA
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12 LEGH 15

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O9pry8 triakis scy

Perfect score:

Title:

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OM protein -

Run on:

Scoring table:

Searched:

Database :

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013767 homo sapien
041541 human immun
0405061 bos taurus
090cb9 homo sapien
090cb8 homo sapien
09177 xenopus lae
0910cq4 homo sapien
075595 human immun
08559 pridates s
08550 hiller's e
088579 theiler's e
                  095795 homo sapien
Q91md7 arabidopsis
P82396 litoria ran
                                                                                                                                                                                                                                                                                                                                                                                                                                          Okada H., Yoshida J., Seo H., Wakabayashi T., Sugita K., Hagiwara M.; "Anti-(glioma surface antigen) monoclonal antibody G-22 recognizes overexpressed CD44 in glioma cells.", EQUENCE Immunol. Immunother. 39:313-317(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9UC28;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
01-MAY-2000 (TrEMBLREL. 13, Last annotation update)
85 KDA GLIOMA MEMBRANE PROTEIN/CD44 HOMOLOG.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
85 KDA GLIOMA MEMBRANE PROTEIN/CD44 HOMOLOG.
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090CB9
090CB8
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MEDLINE=95079448; PubMed=7527301;
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Mammalia; Eutheria; Primates;
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 Q9UC29;
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Q44610 buchnera ap
Q93iw8 oryza sativ
Q44611 buchnera ap
Q8273 cucumber mo
Q9ucf4 homo sapien
Q9uc62 homo sapien
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O9pxb3 duck hepati
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                                                                February 21, 2002, 16:51:55; Search time 60.03 Seconds
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                       473505 seqs, 146272329 residues
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1 CRYGFIEGHVVIPRIHPNSIC 21
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Q9PXB3
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P82600
Q9R5V7
Q9UCN0
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Q9XIW8
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Score 30; DB 2; Length 16; Pred. No. 4.6e+02; 3; Mismatches 5; Indels

24.6%; 38.5%;

72A8175598D30DF1 CRC64;

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Query Match 24.6
Best Local Similarity 38.5
Matches 5; Conservative
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                             MEDLINE-95079448; pubmed=7527301; Okada H., Yoshida J., Seo H., Wakabayashi T., Sugita K., Hagiwara M.; "Anti-(glioma surface antigen) monoclonal antibody G-22 recognizes overexpressed CD44 in glioma cells."; Cancer Immunol. Immunother. 39:313-317(1994).

SEQUENCE 17 AA; 1788 MW; 7806F51C97A3E217 CRC64;
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MEDLINE-95212914; PubMed=7535281;
MEDLINE-95212914; PubMed=7535281;
MeDLINE-95212914; PubMed=7535281;
MeDLINE-95212914; PubMed=7535281;
Rouhbakhsh D., Baumann P.;
"Characterization of a putative 23S-5S rRNA operon of Buchnera aphidicola (endosymbiont of aphids) unlinked to the 16S rRNA-encoding tene.";
"Gene 155:107-112(1995).
EMBL; U10499; AAA79128.1; -.
                                                                                                                                                                                                                                                                                                        Aplysia californica (California sea hare).
Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
Aplysiidae; Aplysia.
NCBL_TAXID=6500;
                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95083478; PubMed=7991459;
Vilim F.S., Cropper E.C., Rosen S.C., Tenenbaum R., Kupfermann I.,
Weiss K.R.;
                                                                                                                                                                                                                                                                                                                                                                                                       "Structure, localization, and action of buccalin B: a bioactive
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                                                                                                                                                                                                                                                                                                                                                                                                                 peptide from Aplysia.";
Peptides 15:959-969(1994).
SEQUENCE 11 AA; 1153 MW; 692253F9C9C86B44 CRC64;
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Last annotation update)
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Pred. No. 2.2e+02;
1; Mismatches. 1;
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28;
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                                                                                                                    31.1%; Score 38; DB 100.0%; Pred. No. 28; ive 0; Mismatches
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(TrEMBLrel. 13, Last seq
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71.4%;
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hes 6; Conservative
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01-MAY-2000 (TrEMB
01-MAY-2000 (TrEMB
01-MAY-2000 (TrEMB
BUCCALIN B, BUCB.
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MEDLINE=95212914; PubMed=7535281;
Rouhbakhsh D., Baumann P.;
"Characterization of a putative 23S-5S rRNA operon of Buchnera
aphidicola (endosymbiont of aphids) unlinked to the 16S rRNA-encoding
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                                    01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
HYPOTHETICAL PROTEIN.
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HYPOTHETICAL PROTEIN.
Cryza sativa (Rice).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta: Magnoliophyta; Liliopsida; Poales; Poaceae; Enhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki T., Nagamura Y., Yamamoto K.;
Coryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC clone:P0681F10...
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AB026295; BAA81863.1; -
SEQUENCE 20 AA; 2312 MW; A5EE9C9093D159F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.8%; Score 29; DB 10; Length 20; llarity 71.4%; Pred. No. 8.2e+02; Conservative 1; Mismatches 1; Indels
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Last annotation update)
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Pred. No. 8.6e+02;
20 AA
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PRT;
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PRELIMINARY;
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01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
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Gene 155:107-112(1995)
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
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RIHDNSV 12
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us-08-753-851-14.rspt

6 Matches

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083273

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Binette J.P., Binette M.B.;

"Sequencing of proteins extracted from stones.";

"Sequencing Microsc. 8:233-239(1994).

-!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = 0(2) + H(2)0(2).

-!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-91261999; PubMed-2128961; MEDLINE-91261999; PubMed-2128961; Clewell D.B., Nortius L.T., An F.Y., Ike Y., Suzuki A., Nakayama J.; Nucleotide sequence of the sex pheromone inhibitor (iAD1) determinant of Enterococcus faecalis conjugative plasmid pAD1."; Plasmid 24:156-161(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid PADI.
Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.0%; Score 28; DB 4; Length 19; 50.0%; Pred. No. 1.1e+03; ive 2; Mismatches 2; Indels
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Pred. No. 1.2e+03;
0; Mismatches 1; Indels
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01-NAY-1999 (TrEMBLrel. 10, Last annotation update)
PLASMID PADI SEX PHEROMONE INHIBITOR (IADI) DETERMINANT.
Enterococcus faecalis (Streptococcus faecalis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 AA; 2162 MW; AD703A074F3C9655 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OD9D07E3079E3559 CRC64;
                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 AA
                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequen
01-JUN-2001 (TrEMBLrel. 17, Last annote
22 KDA STONE MATRIX PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                  MEDLINE-95215817; PubMed-7701298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M62888; AAA98040.1; -. Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.1%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P17670; 1IDS.
InterPro; IPR001189; SOD_MI.
Pfam; PF00081; sodfe; 1.
Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 AA; 1874 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 YGFIEGHV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             || :| |:
12 YGALEXHI 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterococcus.
NCBI_TaxID=1351;
                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               || |||
|HVYIPR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 HVVIPR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid pAD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q52135
Q52135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P79480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
P79480
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     SO DER RELEGIE DE LA COCCO COC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Masuta C., Hayashi Y., Wang W.Q., Takanami Y.;
"Comparison of four satellite RNA isolates of cucumber mosaic virus.";
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kim Y.J., Zhou Z., Hurtado J., Wood D.L., Choi A.S., Pescovitz M.D.,
Warfel K.A., Vandagriff J., Davis J.K., Kwon B.S.;
"IDDM patients' sera recognize a novel 30-kD pancreatic autoantigen
                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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     ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 19;
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Pred. No. 1e+03;
1; Mismatches 1; Indels
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                        cucumber mosaic virus (cucumber mosaic cucumovirus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ann. Phytopathol. Soc. Jpn. 56:207-212(1990).
EMBL; D10039; BAA00929.1; -.
SEQUENCE 19 AA; 2467 MW; 51A5A51EDDD2F38B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38105D1037CA6837 CRC64;
                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 28.5; DB 12;
Pred. No. 9.3e+02;
  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 AA
                                                                                                                                                                                                                                          19 AA
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     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O9UCF4;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHYMOTRYPSINGEN HOMOLOG (FRAGMENT)
                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Invest, 22:219-227(1993).
18 AA; 1826 MW; 38105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE.
MEDLINE=93285747; Pubmed=8509158;
     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.4%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      related to chymotrypsinogen.
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66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 23.4
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 23.0
Best Local Similarity 66.7
Matches 4; Conservative
     Conservative
                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CRYHGFRKKHSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRY-GFIEGHWV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                | |:| | |
6 HNVLPNIEP 14
                                                    HVVIPRIHP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=12305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 IPRIHP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  æ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-T43;
5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cucumovirus
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                                                                                                                                                                                                                                                                   083273;
                                                                                                                                                                                                                                        083273
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RESULT Q9UC82

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Query Match 22.1
Best Local Similarity 50.0
Matches 5; Conservative
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Best Local Similarity 33.3
Matches 3; Conservative
                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                  1 | 1 | 1 | 4 GHEVXPHSRP 13
                                                                                                                                                     8 GHVVIPRIHP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |::|:
| VIVPSLNPD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 VVIPRIHPN 18
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     [1]
SEQUENCE.
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                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thogersen I.B., Salvesen G., Brucato F.H., Pizzo S.V., Enghild J.J., Purification and characterization of an alpha-macroglobulin proteinase inhibitor from the mollusc Octopus vulgaris."; Blacchem. J. 285:521-527(1992).

SEQUENCE. 20 AA, 2370 MM; 4A90386BBF226BD9 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                 Cervus elaphus (Red deer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
Cervidae; Cervinae; Cervus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mahmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10095;
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
Incirrata; Octopodidae; Octopus.
                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5,
                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
ALPHAN, ALPHA-MAROGLOBULIN PROTEINASE INHIBITOR (FRAGMENT).
Octopus vulgaris (Octopus)
                                                                                                                                                                                                                           Length 17;
                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                            Swarbrick P.A., Crawford A.M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                          2B7EEBCF17F004FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4A903B6BBF226BD9 CRC64
                  01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
MHC CLASS II DRB (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                          Score 27; DB 7; Pred. No. 1 4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 27; DB 5; 1 Pred. No. 1.7e+03;
                                                                                                                                                                                                                                                                                                                                             20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 AA.
                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
          01-MAY-1997 (TrEMBLrel. 03, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92344633; PubMed-1379044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                               17
2022 MW;
                                                                                                                                                                                                                          22.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.1%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9QVB2;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SERINE PROTEASE (FRAGMENT).
                                                                                                                                                 EMBL; U63083; AAB37783.1;
                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                               CR--YGFIEGHVV 11
                                                                                                                                                                                                            Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                      1
17
17 AA;
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5 EGHYMILVPR 14
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                                                                                                                  SEQUENCE FROM N.A
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SEQUENCE
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               Damianov A., Damianov I.:
Damianov A., Damianov I.:
"Isolation of serine protease from granulated metrial gland cells of mice and rats with lectin from Dolichos biflorus.";
J. Reprod. Fertil. 95:679-684(1992).
SEQUENCE 20 AA; 2290 WW; 0A304F61A22C500D CRC64;
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Helicacea; Bradybaenidae; Euhadra.
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Tong S., Li J., Mands J.R.;
Tong S., Li J., Mands J.R.;
Interaction between duck hepatitis B virus and a 170-kilodalton
cellular protein is mediated through a neutralizing epitope of the
pre-S region and occurs during viral infection.";
J. Virol. 69:7106-7112(1995).
SEQUENCE 21 AA; 2329 MW; A464BC8EBFR230E CRC64;
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Yamazaki N., Ueshima R., Terrett J.A., Yokobori S., Kaifu M.,
Segawa R., Kobayashi T., Numachi K., Ueda T., Nishikawa K.,
Watanabe K., Thomas R.H.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
Bibni 271697; CAA96373.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
170 KDA DHBV PRE-S REGION BINDING PROTEIN (FRAGMENT).
Duck hepatitis B virus (DHBV).
Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.
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01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
ATPASE SUBUNIT 8 (FRAGMENT).
                                                                                                                                                                                                                                 22.1%; Score 27; DB 11;
50.0%; Pred. No. 1.7e+03;
iive 0; Mismatches 5;
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MEDLINE=93020730; PubMed=1404084;
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SO SEQUENCE 9 AA; 977 MW; 25BBBIF775B736C7 CRC64;

0; Gaps Query Match 21.3%; Score 26; DB 8; Length 9; Best Local Similarity 33.3%; Pred. No. 4.7e+05; Matches 3; Conservative 5; Mismatches 1; Indels

12 IPRIHPNSI 20 :|::|:|: 1 VPQLSPHSL 9 Qy

qq

Search completed: February 21, 2002, 16:51:55 Job time: 534 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                               OM protein - protein search, using sw model
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February 21, 2002, 16:42:58 ; Search time 64.88 Seconds
(without alignments)
23.976 Million cell updates/sec Run on:

US-08-753-851-14 Perfect score:

122 1 CRYGFIEGHVVIPRIHPNSIC 21 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

206698 Total number of hits satisfying chosen parameters: 522463 seqs, 74073290 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_1101:\* Database :

(SIDSB/)Ggdata/geneseq/p/Atts., JATI:
(SIDSB/)Ggdata/geneseq/p/Atts., JATI:
(SIDSB/)Ggdata/geneseq/peneseqp/Att) BB DAT:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	CD44 peptide CD44-	CD44 peptide CD44-	Synthetic human nN	Cyclic peptide inh	Cyclic peptide inh	HTLV-I protease cl	Chick muscle-speci	Tumour necrosis fa	Tumour necrosis fa	Tumour necrosis fa	Tumour necrosis fa
	ID	AAR53484	AAR53485	AAW81195	AAU03735	AAU03751	AAW36883	AAW26612	AAW83548	AAW83549	AAW83550	AAW83551
	DB	15	15	19	22	22	18	18	20	20	20	20
	Query Match Length DB ID	21	19	16	6	σ	12	18	σ	10	11	12
æ	Query	100.0	85.2	26.6	26.2	26.2	26.2	26.2	25.4	25.4	25.4	25.4
	Score	122	104	32.5	32	32	32	32	31	31	31	31
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Tumour necrosis fa Tumour necrosis fa Tumour necrosis fa Diastercomer pepti Antipathogenic pep	hogenic p necrosis necrosis	nepattis vitas Immunogenic peptid Angiogenic vascula Human complementar Human complementar	Membrane dipeptida Membrane dipeptida Japanese cedar pol Japan cedar pollen Japan cedar pollen	leptin le #571 le #604 le #604	Human protease-act Reactive peptide w Antigenic peptide Human MHC Class II Human MHC Class II	Human MHC Class II Cysteine noose lib Peptide which bind Leptin receptor an Human MHC Class II Peptide #4398 enco
AAW83552 AAW83553 AAW83554 AAW82923	AAB17458 AAW83556 AAW83557 AAY38164	2 m m w w	AAY48698 AAR53696 AAR97942 AAR97943	AAY57842 AAM19282 AAM32006 AAR54374	87 87 25 57	AAY25575 AAY08385 AAB76504 AAW22108 AAY25560 AAM17964
20 20 10 10 10 10	20 20 20 20 20 20 20 20 20 20 20 20 20 2	22222	20 20 17	25 17 17 17	70 70 70 70 70	20 20 20 20 20 20
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### ALIGNMENTS

Cell adhesion molecule; CD44; antiinflammatory; rheumatoid; arthritis; tumor cell metastasis; autoimmune disease; immunosuppressive. AAR53484 standard; peptide; 21 AA. 93WO-US10412 92US-0973339 (first entry) CD44 peptide CD44-11. (UYDU-) UNIV DUKE. Homo sapiens. 29-OCT-1993; 30-OCT-1992; WO9409811-A. 01-DEC-1994 11-MAY-1994. AAR53484; AAR53484 RESULT 

Hale LP, Haynes BF, Liao H, Patton KL, Telen MJ;

WPI; 1994-167121/20

Use of CD44 protein and new peptide derivs - for developing prods for inflammation, immune-mediated tissue damage and tumour cell metastasis

Claim 4; Page 14; 83pp; English.

Sequence

Query Match Best Local

Matches

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1 rygfieghvviprihpnsi 19

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This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (1NOS) or mimics of this protein is used to detect the presence of human 1NOS protein in the sample. The method can be used for the detection and quantitation of human 1NOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a synthetic peptide analogue of human neuronal nitric oxide synthase (nNOS) which is used in the method of the invention.
                                                                                                                                                                                                                    Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection; monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus; myocardial infarction; tissue rejection; transplantation; psoriasis; autofimmune disease; multiple sclerosis; neuronal; nNOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human INOS or mimics.
                                                                                                                                                                                Synthetic human nNOS amino-terminal peptide analogue.
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                                                            AAW81195 standard; peptide; 16 AA.
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The peptide can be used for treating inflammation and immunemediated tissue damage such as occurs in the course of autoimmune diseases, e.g. rheumatoid arthritis. It can also be used for determining metastatic potential or to treat or prevent tumor cell metastasis. This peptide corresponds to AA 77-97 of the CD44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The peptide can be used for treating inflammation and immune-mediated tissue damage such as occurs in the course of autoimmune diseases, e.g. rheumatoid arthritis. It can also be used for determining metastatic potential or to treat or prevent tumor cell metastasis. This peptide corresponds to AA 76-96 of the CD44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of CD44 protein and new peptide derivs - for developing prods for inflammation, immune-mediated tissue damage and tumour cell
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Pred. No. 4.5e-13;
Mismatches 0;
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100.0%; Pred. No. 3.3e-10;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                              AAR53485 standard; peptide; 19 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1994-167121/20
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                Similarity
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                                                                                                                                          21 AA;
                                                                                                  orotein sequence.
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Homo sapiens

WO9409811-A

01-DEC-1994

AAR53485;

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AAR53485 RESULT

30-OCT-1992; 29-OCT-1993;

netastasis

;

Gaps

ä

Indels

Cyclic peptide inhibitor of LFA-1/ICAM-1 interaction #12.

Sequence

Length 16;

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The sequence represents the amino acid sequence of cyclic peptide inhibitor #28 of lymphocyte function associated antigen-1 and intracellular adhesion molecule (LFA-1/TCAM-1) interaction. A composition comprising a cyclic peptide inhibitor of LFA-1/TCAM-1 interaction is useful for treating haematopoietic neoplastic disease, myocardial infarction, radiation injury, asthma, rheumatoid arthritis or lymphoma metastasis. The composition is also useful for inhibiting in a subject the interaction between LFA-1 expressed on a leukocyte and ICAM-1 expressed on another cell, preventing retinoic acid syndrome in a subject receiving all-trans retinoic acid, inhibiting growth of leukaemia cells, inhibiting emigration of leukocytes from blood into tissue and screening a candidate compound for binding to ICAM-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition comprising a cyclic peptide inhibitor of lymphocyte function associated antigen-1 and intracellular adhesion molecule 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ricin; toxin; antiviral; virucide; retrovirus; protease; HTLV-I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interaction, for treating e.g. asthma and myocardial infarction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32; DB 22; Length 9;
Pred. No. 4.3e+05;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTLV-I protease cleavage recognition site.
                                                                                                                                                                                                                                                                                                  (SCTE-) SCI & TECHNOLOGY CORP @UNM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ¥
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 22; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW36883 standard; Peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.2%;
71.4%;
                                                                                                                                 16-JAN-2001; 2001WO-US01382
                                                                                                                                                                                                2000US-0483550.
2001US-0760599.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CANG-) CANGENE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-432906/46.
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Best Local Similarity
Matches 5; Conserv
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WO200151508-A1.
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3 lrpnsic 9
                                                                                                                                                                                                14-JAN-2000;
16-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09741233-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-APR-1996;
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                                                                  19-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibitor #12 of lymphocyte function associated antigen-1 and intracellular adhesion molecule (LFA-1/TCAM-1) interaction. A composition comprising a cyclic peptide inhibitor of LFA-1/ICAM-1 interaction is useful for treating haemacopoletic neoplastic disease, myocardial infarction, radiation injury, asthma, rheumatoid arthritis or lymphoma metastasis. The composition is also useful for inhibiting in a subject the interaction between LFA-1 expressed on a leukocyte and ICAM-1 expressed on another cell, preventing retinoic acid syndrome in a subject inhibiting all-trans retinoic acid, inhibiting growth of leukaemia cells, inhibiting emigration of leukocytes from blood into tissue and screening a candidate compound for binding to ICAM-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Composition comprising a cyclic peptide inhibitor of lymphocyte function associated antigen·1 and intracellular adhesion molecule interaction, for treating e.g. asthma and myocardial infarction -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents the amino acid sequence of cyclic peptide
                        Cyclic; lymphocyte function associated antigen-1; LFA-1; asthma; intracellular adhesion molecule; ICAM-1; inhibitor; leukaemia; haematucpoietic neoplastic disease; myocardial infarction; radiation injury; rheumatoid astatifitis; lymphoma metastasis; retinoic acid syndrome; all-trans retinoic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyclic; lymphocyte function associated antigen-1; LFA-1; asthma; intracellular adhesion molecule; ICAM-1; inhibitor; leukaemia; haematopoietic neoplastic disease; myocardial infarction; radiation injury; rheumatoid arthritis; lymphoma metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32; DB 22; Length 9;
Pred. No. 4.3e+05;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cyclic peptide inhibitor of LFA-1/ICAM-1 interaction #28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        retinoic acid syndrome; all-trans retinoic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SCTE-) SCI & TECHNOLOGY CORP @UNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 22; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU03751 standard; peptide; 9 AA.
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71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JAN-2001; 2001WO-US01382.
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16-JAN-2001; 2001US-0760599.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-432906/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 AA;
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3 lrpnsic 9
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Sequence

Synthetic

AAU03751;

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AAU03751 RESULT

Larson RS;

Synthetic.

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Gaps

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Length 9;

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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boyle WJ,
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                                                                                                                   Sequence
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                                                                                                                                                                                                                                             QQ
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                                                                                                          This claimed peptide is a cleavage recognition site for a HTLV-I protease. It is utilised as a linker between the A and B chains of a ricin-like protein in a novel recombinant protein. A nucleic acid (see AAT97910) encoding such a construct is obtained by PCR mutagenesis of the wild-type ricin linker sequence. The invention provides novel recombinant proteins which incorporate the A and B chains of a ricin-like toxin (preferably the A and B chains of ricin) linked by a heterologous linker sequence containing a cleavage recognition site for a retroviral protease such as HIV protease (see AAW36880-8Z), HTLV-I (see AAW36885-65). The recombinant proteins selectively inhibit or destroy mammalian cells infected with a retrovirus such as cancer cells associated with HTLV or cells associated with HTLV or cells associated from the B chain by a retroviral protease, and thus can be used to specifically target infected cells without the need for a cell binding component.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                          DNAs encoding ricin like toxins A and B - are linked via linker containing cleavage site for retroviral protease, used to inhibit or destroy mammalian cells infected with retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoding human agrin and muscle specific kinase - used in diagnosis and treatment of disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chick muscle-specific kinase (MuSK) cytoplasmic domain peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor tyrosine kinase; muscle specific kinase; MuSK; Dmk; chicken; polyclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                     DB 18; Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32; DB |
Pred. No. 85;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW26612 standard; Peptide; 18 AA.
                                                                                 Claim 5; Page 41; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                26.28;
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95US-0008657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Best Local Similarity 62.5
Matches 5; Conservative
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and related receptor
with muscle atrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glass DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-332783/30.
                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 VIPRIHPN 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW26612;
                                                                                                                                                                                                                                                                                                                                                                           Sequence
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Example 10; Page 64; 120pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fused heterologous sequences to identify potential new receptors and ligands. The present sequence represents a TNFR N-terminal peptide from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin; OPG; chimeric; fusion; dimerisation domain; autoimmune disease; inflammation; apoptosis.
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New chimeric osteoprotegerin polypeptides - contain the osteoprotegerin dimerisation domain and a heterologous sequence, useful to treat TNF and TNFR-mediated disorders
This peptide sequence comprises the first 18 amino acids of the chick muscle specific kinase (MuSK) cytoplasmic domain. It was used to raise polyclonal antibodies for MuSK. These were used in studies that demonstrated that agrin (see AAW26609) induces prominent and rapid tyrosine phosphorylation of MuSK (see also AAW26610-11).
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0
                                                                                                                                                                                                               Length 18;
                                                                                                                                                                                                            Score 32; DB 18; Length 18
Pred. No. 1.4e+02;
5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumour necrosis factor receptor N-terminal peptide #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 16; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW83548 standard; peptide; 9 AA.
                                                                                                                                                                                                               26.2%;
30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-US08631
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                                                                                                                                                                                                            Query Match 26.2
Best Local Similarity 30.8
Matches 4; Conservative
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2 lpsellldrlhpn 14
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                                                                                                                                                  18 AA;
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Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin; OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New chimeric osteoprotegerin polypeptides - contain the osteoprotegerin dimerisation domain and a heterologous sequence, useful to treat TNF and TNFR-mediated disorders
                                                                                                                                                                Tumour necrosis factor receptor N-terminal peptide #8.
                                                                                AAW83550 standard; peptide; 11 AA.
                                                                                                                                                                                                                      inflammation; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-034661/03
                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN INC.
              2 ihpqnnsic 10
                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                         WO9849305-A1
                                                                                                                                                                                                                                                                                                                                29-APR-1998;
                                                                                                                                                                                                                                                                                                                                                           01-MAY-1997;
                                                                                                                                     04-MAR-1999
                                                                                                                                                                                                                                                                                                     05-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                 Boyle WJ,
                                                                                                          AAW83550;
                                                                     AAW83550
                                                       RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a chimeric polypeptide (A1), comprising am no steeportegerin (OPG) dimerisation domain fused to a heterologous amino acid sequence. Also described are: (1) a multimer polypeptide comprising covalently associated A1 monomers; (2) an isolated nucleic acid encoding A1; (3) an expression vector comprising the nucleic acid expenses; and (4) a host cell transformed or transfected with the expression vector so that the nucleic acid is expressible. The products from the present invention are useful to treat a variety of disorders functualing those related to receptor binding. Compositions comprising tumour necrosis factor (TNE)/OPG and TNF receptor (TNFR)/OPG chimeras are used to treat TNF and TNFR-mediated disorders such as inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune diseases and disorders related to excessive apoptosis. The chimeras are also useful for detecting molecules which interact with fused heterologous sequences to identify potential new receptors and ligands. The present sequence represents a TNFR N-terminal peptide from
                                                                                                                                                                                                                                                                                                    ur necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
chimeric; fusion; dimerisation domain; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New chimeric osteoprotegerin polypeptides - contain the osteoprotegerin dimerisation domain and a heterologous sequence,
                                                                    2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31; DB 20; Length 10;
Pred. No. 1e+02;
0; Mismatches 0; Indels
                                      Score 31; DB 20; Length 9; Pred. No. 4.3e+05; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                          Tumour necrosis factor receptor N-terminal peptide #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful to treat TNF and TNFR-mediated disorders
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                                                                                                                                                                                          AAW83549 standard; peptide; 10 AA.
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77.8%;
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                        Query Match
Best Local Similarity 77.00.
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                  inflammation; apoptosis.
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| ihpqnnsic 9
9 AA;
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98WO-US08631 97US-0850188

(first entry)

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                                                       The present invention describes a chimeric polypeptide (A1), comprising an osteoprotegerin (OPG) dimerisation domain fused to a heterologous amino acid sequence. Also described are: (1) a multimer polypeptide comprising covalently associated A1 monomers; (2) an isolated nucleic acid encoding A1; (3) an expression vector comprising the nucleic acid sequence; and (4) a host cell transformed or transfected with the expression vector so that the nucleic acid is expressible. The products
                                                                                                                                                                                                                                                                                                                                                                                            autoimmune diseases and disorders related to excessive apoptosis. The chimcras are also useful for detecting molecules which interact with fused heterologous sequences to identify potential new receptors and ligands. The present sequence represents a TNFR N-terminal peptide from
                                                                                                                                                                                                                                                                       from the present invention are useful to treat a variety of disorders including those related to receptor binding. Compositions comprising tumour necrosis factor (TWF)/OPG and TWF receptor (TWFR)/OPG chimeras are used to treat TWF and TWFR-mediated disorders such as inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 1.1e+02;
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Disclosure; Page 16; 92pp; English.
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Gaps

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15 IHP--NSIC 21

inflammation; apoptosis.

Homo sapiens

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The present invention describes a chimeric polypeptide (A1), comprising an osteoprotegerin (OPG) dimerisation domain fused to a heterologous an osteoprotegerin (OPG) dimerisation domain fused to a heterologous comprising sequence. Also described are: (1) a multimer polypeptide comprising covalently associated A1 monomers: (2) an isolated nucleic acid acid encoding A1; (3) an expression vector comprising the nucleic acid sequence; and (4) a host cell transformed or transfected with the expression vector so that the nucleic cid is expressible. The products from the present invention are useful to treat a variety of disorders including those related to receptor binding. Compositions comprising tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras are used to treat TNF and TNFR-mediated disorders such as inflammation, autoimmune diseases and disorders related to excessive apoptosis. The fused heterologous sequences to identify potential new receptors and the present sequence represents a TNFR N-terminal peptide from
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                                                                                                                                                                                   Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin; OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
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                                                                                                                         Tumour necrosis factor receptor N-terminal peptide #9.
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Pred. No. 1.2e+02;
0; Mismatches 0;
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77.8%;
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Best Local Similarity 77.8;
                                                                                                                                                                                                                                                      inflammation; apoptosis.
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                                                            04-MAR-1999
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AAW83551;
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The present invention describes a chimeric polypeptide (A1), comprising am osteoprotegerin (OPG) dimerisation domain fused to a heterologous amino acid sequence. Also described are: (1) a multimer polypeptide comprising covalently associated A1 monomers; (2) an isolated nucleic acid encoding A1; (3) an expression vector comprising the nucleic acid expenses and (4) a host cell transformed or transfected with the expression vector so that the nucleic acid is expressible. The products from the present invention are useful to treat a variety of disorders from the present invention are useful to treat a variety of disorders tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras are used to treat TNF and TNFR-mediated disorders such as inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune diseases and disorders related to excessive apoptosis. The chimeras are also useful for detecting molecules which interact with fused heterologous sequences to identify potential new receptors and ligands. The present sequence represents a TNFR N-terminal peptide from
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                                                                                                                                      98WO-US08631
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Matches 7; Conservative
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                                                                   WO9849305-A1.
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WPI; 1999-034661/03.
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                                                                                                                                                                                                      The present invention describes a chimeric polypeptide (A1), comprising an osteoprotegerin (OPG) dimerisation domain fused to a heterologous amino acid sequence. Also described are: (1) a multimer polypeptide comprising covalently associated A1 amonomers; (2) an isolated nucleic acid encoding A1; (3) an expression vector comprising the nucleic acid expenses and (4) a host cell transformed or transfected with the expression vector so that the nucleic acid is expressible. The products from the present invention are useful to treat a variety of disorders from the present invention are useful to treat a variety of disorders tumour necrosis factor (TNF)/OPG and TNF receptor (TNFN)/OPG chimeras are used to treat TNF and TNFR-mediated disorders such as inflammation,
                                                                                                                                                                                                                                                                                                                                                      autoimmune diseases and disorders related to excessive apoptosis. The otherwars are also useful for detecting molecules which interact with fused heterologous sequences to identify potential new receptors and ligands. The present sequence represents a TNFR N-terminal peptide from
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chimeric; fusion; dimerisation domain; autoimmune disease;
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                                                                                                                             New chimeric osteoprotegerin polypeptides - contain the osteoprotegerin dimerisation domain and a heterologous sequence, useful to treat TNF and TNFR-mediated disorders
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                                                                                                                                                                                Disclosure; Page 16; 92pp; English.
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98WO-US08631
                        97US-0850188
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Best Local Similarity 77.80,
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inflammation; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                          the present invention.
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                                                                                                     WPI; 1999-034661/03
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                                                                                                                                                                                                                                                                                                                                                                                                                                    14 AA;
29-APR-1998;
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                                                                           Boyle WJ,
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The present invention describes a chimeric polypeptide (A1), comprising an osteoprotegerin (OPG) dimerisation domain fused to a heterologous an osteoprotegerin (OPG) dimerisation domain fused to a heterologous an osteoprotegerin (OPG) dimerisation domain fused to a heterologous comprising covalently associated A1 monomers; (2) an isolated nucleic acid acid encoding A1; (3) an expression vector comprising the nucleic acid sequence; and (4) a host cell transformed or transfected with the expression vector so that the nucleic acid is expressible. The products from the present invention are useful to treat a variety of disorders including those related to receptor binding. Compositions comprising tumour necrosis factor (TNF)/OPG and TNF receptor (TNFN)/OPG chimeras are used to treat TNF and disorders binding. Compositions comprising autoimmune diseases and disorders related to excessive apoptosis. The chimeras are also useful for detecting molecules which interact with fused heterologous sequences to identify potential new receptors and ligands. The present sequence represents a TNFR N-terminal peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diastereomer peptide; infection; therapy; excitatory neurotoxin; money bee venom; pardaxin; cytolytic activity; cancer; non-haemolytic; preservative; agricultural produce; bacterial cell lysis; agricultural pesticide; cell wall lysis.
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New chimeric osteoprotegerin polypeptides - contain the osteoprotegerin dimerisation domain and a heterologous sequence,
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Pred. No. 1.6e+02;
                                         useful to treat TNF and TNFR-mediated disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                   Disclosure; Page 16; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "D-form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "D-form
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77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diastereomer peptide 68.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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increased resistance to proteolytic degradation. Non-baemolytic, cytotoxic random copolymers of pardaxin, each has a specific spectrum of activity, allowing selection of agents for particular applications. Since these random copolymers induce total lysis of bacterial cell walls, resistance to them is unlikely to develop.
                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a diastereomer peptide of the invention. The peptides of the invention have: (a) cytolytic activity on pathogenic cells (pathogens and malignant cells not naturally present in the body); but (b) no haemolytic activity, or such activity only at a concentration significantly higher than that at which they lyse. Asthogenically the peptides, their complexes and mixtures are used to treat infections (caused by bacteria, fungi, protozoa, mycoplasma or viruses) or cancer, in human and veterinary medicine. Also, they can be used as preservatives for food, cosmetics and agricultural produce, or as agricultural pesticides. The absence of haemolytic activity (associated with disturbance of alpha-helical structures) means that the peptides have few if any toxic effects, and those that include beautiles.
                                                                                                                                                                                                                                                                                                       Peptide(s) having selective cytolytic activity - against pathogens and malignant cells, but no haemolytic activity, used for treating
                                                                                                                                                                                                                                                                                                                                                                                         Example 5; Page 47; 80pp; English.
                                                                                                                                                                                 (YEDA ) YEDA RES & DEV CO LTD.
                                                                                                   97WO-IL00066.
                                                                                                                                           96IL-0117223.
                                                                                                                                                                                                                                                                                                                                                   infections and cancer
                                                                                                                                                                                                                                                                 WPI; 1997-435088/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 AA;
                  WO9731019-A2
                                                                                                20-FEB-1997;
                                                                                                                                         22-FEB-1996;
                                                        28-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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Search completed: February 21, 2002, 16:42:59 Job time: 233 sec

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25.4%; Score 31; DB 18; Length 16; 54.5%; Pred. No. 1.7e+02; Live 2; Mismatches 3; Indels

Best Local Similarity 54.5 Matches 6; Conservative

Query Match

6 IEGHVVIPRIH 16 |: || | |:| 4 ikahvriirvh 14

oy D Sequence 12, Appl Sequence 26, Appl Sequence 26, Appl Sequence 26, Appl Sequence 28, Appl Sequence 3, Appli Patent No. 5283320

Sequence

Appl 70, 18,

Sequence 7 Sequence Sequence Sequence Sequence Sequence 8

Sequence

Sequence:

Title: Perfect :

Run on:

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Searched:

Database

Result

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SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: US/08/143,311B FILING DATE: 29-OCT-1993
US-08-476-537-12
US-08-476-537-26
US-08-485-607-25
US-08-485-607-26
US-08-475-879-12
US-08-475-879-12
US-08-817-548A-3
5283320-4
US-08-817-548A-3
US-08-627-497-18
US-08-627-497-18
US-08-838-413A-11
US-08-838-413A-11
US-08-896-933-5
US-08-896-933-5
US-08-896-933-5
US-08-841-84
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: HAYNES, BARTON F.
APPLICANT: HALE, LAURA P.
APPLICANT: PATTON, KAREN L.
APPLICANT: TELEN, MARILYN J.
APPLICANT: LIAO, HUA-XIN
TITLE OF INVENTION: AN ADHESION MOLECULE
CORRESPONDENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFF...
FILING DATE: ...
FILING DATE: ...
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,339
ATTING DATE: 30-OCT-1992
ATTING DATE: 30-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/POCKET NUMBER: 1579-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/08143311B Patent No. 5863540 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 15-MAR-1991
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-143-311B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A. ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                         US-08-143-311B-12
 (without alignments)
14.969 Million cell updates/sec
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Sequence 3, Appli
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Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 462,
Sequence 101,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 101,
Sequence 184,
Sequence 186,
                                                                                                February 21, 2002, 16:43:37; Search time 31.57 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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Compugen Ltd.
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US-09-042-107-101
US-08-467-023-184
US-08-467-023-186
US-07-854-603-12
US-08-743-168B-20
PCT-US96-10435-20
US-08-374-652C-48
US-07-994-277A-5
US-08-268-251-23
US-07-854-603-14
PCT-US93-01112-23
US-08-310-912A-54
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US-08-159-339A-462
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US-07-994-277A-4
US-07-956-700B-12
US-07-956-700B-26
                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-143-311B-12
US-08-143-311B-13
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PCT-US95-04589-54
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US-08-492-599-3
                                                                                                                                                                                                                                                      212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
             GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                    Listing first 45 summaries
                                                                    protein - protein search, using sw model
                                                                                                                                                                                  CRYGFIEGHVVIPRIHPNSIC 21
                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                               Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                      US-08-753-851-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
Match Length DB
                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 21
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Matches

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Patent No. 5726050
GENERAL INFORMATION:
APPLICANT: Rich, Alexander
APPLICANT: Herbert, Alan
TITLE OF INVENTION: Z-DNA BINDING PROTEIN AND APPLICATIONS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Revin M. Farrell, P.C.
STREET: P.O. Box 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No. 5814478enclature for this antibody is 52307K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 18;
Sequence 16, Application US/08644271

Patent No. 5814478

GENERAL INFORMATION:

APPLICANT: Valenced, et al.

TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS

TITLE OF INVENTION: AND LIGANDS

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSE: Regeneron Pharmaceuticals, Inc.

STREET: 777 Old Saw Mill Road

CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32; DB 2;
Pred. No. 47;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOCTWARE: FeatERQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/644,271
FILING DATE: 10-MAY-1996
CLASSIFCATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/008,657
FILING DATE: 15-DEC-1995
ATTONNEY,AGGNT INFORMATION:
NAME: CODERT, ROBERT J
REGISTRATION NUMBER: 36,108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: REG 195A TELECOMMUNICATION INFORMATION: TELEPHONE: 914-345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.2%;
                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 30.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 914-345-7721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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CTHER INFORMATION:

CTHER INFORMATION:

US-08-644-271-16
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                                                                                                                                                                                                      CITY: T
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0
                           Length 21;
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                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: ARLINGTON
STATE: VIRGINIA
COUNTY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMILIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                       100.0%; Score 122; DB 2;
100.0%; Pred. No. 1.1e-13;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 104; DB 2; Pred. No. 8.5e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                             APPLICANT: HAYNES, BARTON F.
PAPLICANT: HALE, LANRA P.
APPLICANT: PATYON, KAREN L.
APPLICANT: TELEN, MARILIN J.
APPLICANT: LIAO, HUA-XIN
TILLE OF INVENTION: AN ADHESION MOLECULE
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/143,311B
FILING DATE: 29-OCT-1993
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: NIXON & VANDERHYE P.C. 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 1579-50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
                                                                                                                                                                                                                                    Sequence 13, Application US/08143311B Patent No. 5863540 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/669,730 FILING DATE: 15-MAR-1991 CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.2%; Scur.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,339
FILING DATE: 30-OCT-1992
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: WILSON, MARY J. REGISTRATION NUMBER: 32,955
                                                                                                     1 CRYGFIEGHVVIPRIHPNSIC 21
                                                                                                                        FILING DATE: 15-MAR-1991
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RYGFIEGHVVIPRIHPNSI 20
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                               21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 19 amino acids
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Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                       Query Match
Best Local Similarity
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US-08-143-311B-13
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                                                                                                                                                                          Score 31; DB 5; Length 19;
Pred. No. 73;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: HLA Binding peptides and Their TITLE OF INVENTION: USES NUMBER OF SEQUENCES: 1254
CORRESPONDENCE S: 1254
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               018623-005030US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PELICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber' Ellen Lauver
REGISTRATION NUMBER: 32,762
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 462, Application US/08159339A Patent No. 6037135 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sette, Alessandro APPLICANT: Celis, Esteban
                                                                                                                                                                          25.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kubo, Ralph T.
Grey, Howard M.
LENGTH: 19 amino acids
                                                                                                                                                                        Query Match 25.4
Best Local Similarity 42.9
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 10 amino acids
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Best Local Similarity 44.4
Matches 4; Conservative
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                      ; TYPE: amino acid
; STRANDENESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US96-10455-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
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2 RYPFIVNHPKVGRV 15
                                                                                                                                                                                                                                                               2 RYGFIEGHVVIPRI 15
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US-08-159-339A-462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 19;
                                                        MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/492,599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: FARTELL, KEVIN M.
REGISTRATION NUMBER: 35,505
REREPROCE/DOCKET NUMBER: MIT-7011
TELEPHONE: (207) 363-0558
TELEPHONE: (207) 363-0528
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Kevin M. Farrell, P.C. STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/492,599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INPORMATION:
NAME: FAZTEJI, KEVID M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: MIT-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 20-JUNE-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 25.4%;
Best Local Similarity 42.9%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-492-599-3
                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 514
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Sequence 184, Application US/08467023 Patent No. 6090386
                                                      GENERAL INFORMATION:
APPLICANT: Griffeth, Irwin J.;
                                                                                                                                 Garman, Richard D;
                                                                                            Pollock, Joanne;
Bond, Julian F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                Waltham
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2 GYFSGHVI 9
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                                                                                                                                                                                         APPLICANT
                                                                                                                                                      APPLICANT
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STATE:
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APPLICANT: Rucslahti, Erkki
APPLICANT: Rucslahti, Erkki
APPLICANT: Rucslahti, Renata
APPLICANT: Rajotte, Daniel
TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
TITLE OF INVENTION: Membrane Dipeptidase
TITLE OF INVENTION: Membrane Dipeptidase
FILE REFERENCE: P-LJ 3443
CURRENT APPLICATION NUMBER: 09/042,107
EARLIER PILING DATE: 1999-02-26
EARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 452
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
LENGTH: 13
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APPLICANT: Ruoslahti, Erkki
APPLICANT: Ruoslahti, Renata
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
TITLE OF INVENTION: Tissues
FILE REPERENCE: P-LJ 2892
CURRENT FILING DATE: 1998-03-13
NUMBER OF SED ID NOS: 436
SOFTHARE: Patentin Ver. 2.0
SEQ ID NO 101
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-258-754-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-042-107-101
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                                                                                                                                 Sequence 101, Application US/09258754 Patent No. 6174687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 101, Application US/09042107
Patent No. 6232287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 24.6
Best Local Similarity 62.5
Matches 5; Conservative
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Best Local Similarity
'-has 5; Conserv?
                   : || |:|:
2 VNGHQVLPK 10
6 IEGHVVIPR 14
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| CRSGCVEG 8
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                                                                                                            US-09-258-754-101
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                                                                       APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 14; 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                       ImmuLogic Pharmaceutical Corporation, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,023 FILING DATE: June 6, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 186, Application US/08467023
Patent No. 6090386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Griffeth, Irwin J.;
Pollock, Joanne;
Bond, Julian F.;
Garman, Richard D;
               Yeung, Siu-mei H.;
Brauer, Andrew;
Exley, Mark A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 184:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yeung, Siu-mei H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.6%;
Kuo, Mei-Chang;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kuo, Mei-Chang;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Jane E. Remillard REGISTRATION NUMBER: 38
                                                                                                                                                                                                        610 Lincoln St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 24.6
Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: ImmuLogic
STREET: 610 Lincoln
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Griffet,
APPLICANT: Bollock,
APPLICANT: Bond, Ju
APPLICANT: Garman,
APPLICANT: Garman,
APPLICANT: Yeuo, Mei
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PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/743,168B
FILING DATE: 04-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/489,535
FILING DATE: 12-UUN-1995
ATTORNEY/AGENT INFORMATION:
                                        US/07/854,603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: MCDONNELL, John J
REGISTRATION NUMBER: 62,949
REFERENCE/DOCKET NUMBER: 92,7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEPA: 312-715-1234
                                                                                                                                              26,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Fitting, Thomas
REGIGSRATION NUMBER: 34,16:
REFERENCE/DOCKET NUMBER: TE
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.8%; 62.5%;
                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 23.8
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                            TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
                                        APPLICATION NUMBER: US
FILING DATE: 19901207
                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-854-603-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: La Jolla
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                TYPE: AMINO ACID
                                                             FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:|:| ||
5 GYIDGRVV 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 GFIEGHVV 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-743-168B-20
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O
                                      APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From TITLE OF INVENTION: Japanese Cedar Pollen
UNDBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: ImmuLogic Pharmaceutical Corporation, Inc. STREET: 610 Lincoln St
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 30; DB 3; Length 14; Pred. No. 76;
                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Activatable fibrinolytic and TITLE OF INVENTION: anti-thrombotic proteins NUMBER OF SEQUENCES: 40 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Dr. John J. McDonnel
STREET: Ten South Wacker Drive, Suite 3000
STRY: Chicago
STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/M9-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dawson, Keith M
APPLICANT: Edwards, Richard M
APPLICANT: Forman, Joan M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.6%;
50.0%;
Brauer, Andrew;
Exley, Mark A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 50.v.
A; Conservative
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internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GFIEGHVV 11
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2 GYFSGHVI 9
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COUNTRY: USA
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  APPLICANT:
                                                                                                                                                                                                                            COUNTRY:
                     APPLICANT
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Gaps
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Score 29; DB 1; Length 15;
Pred. No. 1.2e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/08743168B
Fatent No. 6271015
GENERAL INFORMATION:
APPLICANT: Gilula, No. 6271015ton B
APPLICANT: Cravatt, Benjamin F
APPLICANT: Lenner, Richard A
TITLE OF INVEWTION: FATTY-ACID AMIDE HYDROLASE
NUMBER OF SEQUENCES: 54
CORRESPONDENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSE: The Scripps Research Institute
STREET: 10550 No. 6271015th Torrey Pines Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                         COUNTRY:
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APPLICANT: RAMBOSEK, JOHN A.
APPLICANT: PIDDINGTON, CHRISTOPHER S.
APPLICANT: HOUGSTON, CHRISTSTINE S.
APPLICANT: CANTRELL, MICHARL A.
TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
TITLE OF INVENTION: ENZYMES IN DESIRED RATICS
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 28.5; DB 5; Length 15;
Pred. No. 1.4e+02;
3; Mismatches 2; Indels
                                                                                     DB 4; Length 15;
                                                                                Score 28.5; DB 4;
Pred. No. 1.4e+02;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: CIS-9, 10-OCTADECENOAMIDASE
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEVALAINEN, HELENA K.M.
PALOHEIMO, MARJA T.
FAGERSTROM, RICHARD B.
MIETTINEN-OINONEN, ARJA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US96/10435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/489,535
FILING DATE: 12-JUN-1995
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                              Sequence 20, Application PC/TUS9610435
GENERAL INFORMATION:
APPLICANT: The Scripps Research Ins
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 48, Application US/08374652C Patent No. 5834286 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TURUNEN, MARJA K
                                                                                     23.48;
50.08;
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50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JUN-1996
                                                                              Ouery Match 23.4
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
; FRAGMENT TYPE: internal US-08-743-168B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein FRAGMENT TYPE: internal
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5 GHTLIPFL-PNN 15
                                                                                                                                                                    8 GHVVIPRIHPNS 19
                                                                                                                                                                                             8 GHVVIPRIHPNS 19
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Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                        RESULT 13
PCT-US96-10435-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US96-10435-20
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Length 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM compatible/Compuadd 325TX
COMPRATING SYSTEM: MS-DOS/Microsoft Windows 3.1
SOFTWARE: Wordperfect for Windows 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/994,277A
                                                                  SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.4%; Score 28.5; DB 2; 46.2%; Pred. No. 1.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bedi, Gurrinder S.
APPLICANT: Genco, Robert J.
APPLICANT: Sojar, Hakimuddin T.
TITLE OF INVENTION: Fimbrial Polypeptides
NUMBER OF SEQUENCES: 12
                                                                                              7, Vt.
24-MAY-1995
11, 435
                                                                                                                                                                                                                                                                                                                                                                                                                                  1050.071001
                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/925,401
FILING DATE: 31-UL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.
REGISTRATION NUMBER: 41,264
                                                                                                                                                 FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07058
FILING DATE: 27-JUL-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/07994277A Patent No. 5536497
                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Evans, Richard T.
APPLICANT: Bedi, Gurrinder S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: single TOPOLOGY: not relevant MOLECULE TYPE: peptide 1-374-6520-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States ZIP: 14203-2391
                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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Best Local Similarity
Matches 6; Conserv
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From 226-236
(without counting the first 10 amino acids which
the leader sequence)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 23.0%; Score 28; DB 1; Length 11; Best Local Similarity 57.1%; Pred. No. 1.2e+02; Matches 4; Conservative 1; Mismatches 2; Indels
ATTORNEY/AGENT INFORMATION:

MAME: NELSON, M. Bud

REGISTRATION NUMBER: 35,300

REFERENCE/DOCKET NUMBER: 11520.0040

TELECOMMUNICATION INFORMATION:

TELEPAX: (716) 849-0349

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acid residues

TYPE: amino acid

TOPOLOGY: 1inear

MOLECULE TYPE:

DESCRIPTION: peptide

HYPOTHETICAL: no

FRACMENT TYPE: internal

PUBLICATION INFORMATION:

RELEVANT RESIDUES IN SEQ ID NO: (with
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1 IHPTILC 7
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Search completed: February 21, 2002, 16:43:37 Job time: 171 sec

us-08-753-851-15.rpr

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6
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

February 21, 2002, 17:15:00; Search time 12.69 Seconds

(without alignments)
114.052 Million cell updates/sec

US-08-753-851-15 104 1 RYGFIEGHVVIPRIHPNSI 19 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

219241 seqs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

3419

Minimum DB seq length: 0 Maximum DB seq length: 19

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

PIR\_68:\* Database :

pir1:\*
pir2:\*
pir3:\*
pir4:\* 4 3 2 1. ..

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ap (			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
П	30	28.8	1	7	I40065	shikimate 5-dehydr
7	28	26.9	Г	7	C56049	superoxide dismuta
e	27	26.0	1	7	B41868	hypothetical prote
4	27		15	7	F57789	ζŊ
S	25	4.	14	7	S12904	protein kinase (EC
9	25	24.0	18	~	A36133	hypothetical prote
7	24	23.1	13	7	A26999	carboxylesterase (
<b>ω</b>	24	23.1	16	~	A47393	neuropéptide calla
σ	24	23.1	18	Н	DRDPPP	distal-retinal-piq
10	23	22.1	12	7	C30503	Iq qamma-2b chain
	23	22.1	18	7	PN0149	
	23	22.1	18	7	140062	shikimate 5-dehydr
13	22	21.2	10	7	B61218	alpha-qliadin 6Ha
	22	21.2	12	7	PA0037	plastocyanin 2 - A
	22	21.2	13	7	PT0304	Iq heavy chain CRD
16	22		14	~	A32654	fibrinopeptide A -
17	22		17	~	S32587	L-ascorbate peroxi
18	22	21.2	18	7	B32473	histidine-rich pro
19	21	20.2	6	7	S55696	phosphoenolpyruvat
20	21	20.5	10	7	A60624	angiotensin I - Ja
21	21	20.5	1	7	A21114	gonadoliberin - ch
22	21	20.3	-	7	н37196	bradykinin-potenti
23	21	20.2		7	A90917	angiotensin precur
24	21	20.2	11	7	D60409	kassinin-like pept
25	21	20.2	11	7	S78765	ribosomal protein
26	21	20.5	11	7	PT0209	T-cell receptor al
27	21	20.5	12	7	B58503	outer membrane por
28	21	20.5	13	7	B61620 .	locustamyotropin I
29	21	20.5	14	7	S23369	T-cell receptor al

protein OF200021 - high conductance c	T cell receptor al 45k protein - piq	serum albumin - do bothropstoxin - ja	urinary tract ston	gallbladder stone	seed storage prote	large granule L4 c casein kinase II (	major allergen Myr	r-cell receptor de glutathione transf
PA0059 B53145	PH1756 S23950	B45800 A30823	B56049 A23694	A57789	PA0009	PC1317 C45133	S65709	855307
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21	21 20.5	50 50	20	200	200	0 0 7 0	50	20
30 31	33 33	34 35	36	38	40	41 42	43	45

## ALIGNMENTS

|: | : |:| | 2 FLFFHGIFPKIEP 14 4 FIEGHVVIPRIHP 16 QQ δλ

RESULT C56049

Supercylde dismutase (EC 1.15.1.1) (Fe/Mn) [similarity] - unidentified organism (frague) supercylde dismutase (EC 1.15.1.1) (Fe/Mn) [similarity] - unidentified organism (c) Species: unidentified organism (c) Species: 12-Apr-1995 #text\_change 20-Apr-2000 (c) Accession: C56049 #sequence\_revision 12-Apr-1995 #text\_change 20-Apr-2000 R.Binette, J.P.; Binette, M.B. Scanning Microsc. 8, 233-239, 1994 A.Title: Sequencing of proteins extracted from stones. A.Reference number: A56049; MUID:95215817 A.A.Statuus: preliminary A.A.Statuus: preliminary A.A.Statuus: preliminary A.A.Statuus: 1-19 4BIN> A.B.Statuus: 
Query Match 26.9%; Score 28; DB 2; Length 19; Best Local Similarity 50.0%; Pred. No. 2.5e+02; Matches 4; Conservative 2; Mismatches 2; Indels

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Gaps ö

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R;Madhusudhan, K.T.; Huang, G.; Burns, G.; Sokatch, J.R.
J. Bacteriol. 172, 565-5654, 1990
A;Title: Transcriptional analysis of the promoter region of the Pseudomonas putida br A;Reference number: A36133; MUID:91008935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochemistry 26, 4101-4107, 1987
A;Title: Purification and characterization of a carboxylesterase from the intestine o
A;Reference number: A26999; MUID:88000636
A;Accession: A26999
                                                               R;Sanghera, J.S.; Aebersold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L. FEBS. Lett. 273, 223-2256, 1990 Astrile: Identification of the sites in myelin basic protein that are phosphorylated A; Faference number: S12904; MUID:91032186
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C;Species: Pisaster ochraceus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
C;Accession: S12904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Species: Pseudomonas putida
C.Date: 30-Nov-1990 #sequence_revision 30-Nov-1990 #text_change 30-Sep-1993
C.Accession: A36133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carboxylesterase (EC 3.1.1.1), intestinal - Caenorhabditis elegans (fragmen
C;Species: Caenorhabditis elegans
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 07-Feb-1997
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Pred. No. 7.8e+02;
1; Mismatches 1; Indels
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Pred. No. 5.7e+02;
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A;Residues: 1-13 <MCG>
C;Keywords: carboxylic ester hydrolase; intestine
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80.0%;
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A;Molecule type: protein
Residues: 1-14 <SAN>
C;Keywords: phosphotransferase
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A; Residues: 1-18 <MAD>
A; Cross-references: GB:M33715
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Matches 5; Conserv
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Best Local Similarity
Matches 4; Conserv
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YGKVEG 13
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| GFLEG
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                                                                                                                                                               hypothetical protein (traEI 3' region) - Enterococcus faecalis plasmid pAD1
C; Species: Enterococcus faecalis
C; Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999
C; Accession: B41868; B37391
B; Pontius, L.T.; Clewell, D.B.
J; Bacteriol. 174, 3152-3160, 1992
A; Title: Conjugative transfer of Enterococcus faecalis plasmid pAD1: nucleotide sequence A; Reference number: A41868; MUID:92250408
A; Recension: B41868
A; Accession: B41868
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A;Reference number: A37391; MUID:91261999
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: F57789
R;Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, February 1996
A;Description: The proteins of gallbladder stones.
A;Reference number: A57789
                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Note: sequence extracted from NCBI backbone (NCBIN:99901, NCBIP:99906) R;Clewell, D.B.; Pontius, L.T.; An, F.Y.; Ike, Y.; Suzuki, A.; Nakayama, J. Plasmid 24, 156-161, 1990
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A;Genome: plasmid
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Pred. No. 2.9e+02;
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Pred. No.
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100.0%; Pre
0; }
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83.3%;
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Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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A; Residues: 1-15 <BIN>
A; Note: 9-Phe was also found
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A,Molecule type: DNA
A,Residues: 1-15 <PON>
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A; Residues: 1-15 <CLE>
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YGALEXHI 19
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A; Status: preliminary
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A; Status: preliminary
                   YGFIEGHV 9
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C; Species: Mus musculus (house mouse)
C; Date: 31-Mar-1989 #text_change 16-Aug-1996
C; Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 16-Aug-1996
C; Accession: C30503
R; Cilmore, G. L.; Bard, J. A.; Birshtein, B. K.
J. Immunol. 141, 1754-1761, 1988
R; Cilmore, G. L.; Bard, J. A.; Birshtein, B. K.
J. Immunol. 141, 1754-1761, 1988
A; Title: DNA rearrangements affecting both variable and constant regions of Ig H chain A; Reference number: A30503; MUID:88315788
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-12 <GIL>
A; Residues: 1-12 <GIL>
A; Residues: immunoglobulin
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C;Date: 30-sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PN0149
R;Odintsova, T.I.; Egorov, T.A.
Biokhimia 55, 509-516, 1990
A;Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin A;Accession: PN0149
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C;Species: Buchnera aphidicola
C;Date: 02-aug-1996 #sequence_revision 02-aug-1996 #text_change 08-oct-1999
C;Accession: 140062
R;Roubbakhsh, D; Baumann, P.
Gene 155, 107-112, 1995
A;Tile: Characterization of a putative 238-55 rRNA operon of Buchnera aphidicola (en A;Reference number: 140061; MUID:95212914
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A;Cross-references: EMBL:U10496; NID:9854711; PIDN:AAA79125.1; PID:9854712
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                                         Ig gamma-2b chain C region (F5.5.1) - mouse (fragment)
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Pred. No. 1.6e+03;
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Pred. No. 1e+03;
1; Mismatches
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A; Residues: 1-18 <0DI>
A; Experimental source: strain K-202
C; Superfamily: qiladin
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50.0%;
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30.0%;
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Best Local Similarity
Matches 3; Conserv
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Matches 4; Conserv
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3 VPVPQLQPQN 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: I40062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                          Cincession: A4739; B4739; Cd.739; Cd.; Yagi, K.J.; Tobe, S.S.; Thorpe, A. Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993

A; Title: Callatostatins: neuropeptides from the blowfly Calliphora vomitoria with sequent A; Reference number: A4739; MUID:93211980

A; Molecule type: protein
A; Residues: 1-16 cDUV.
A; Experimental source: thoracic ganglia, brains, heads
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 13-16 cDUV.
A; Experimental source: head
A; Molecule type: protein
A; Residues: 1-8 cDUJ>
A; Molecule type: protein
A; Residues: 1-8 cDUJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   distal-retinal-pigment hormone - northern shrimp
NyAlternate names: light-adapting hormone
C;Species: pandalus borealis (northern shrimp)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 23-Aug-1996
C;Accession: A01473
R;Fernlund, P.
Biochim. Biophys. Acta 439, 17-25, 1976
A;Title: Structure of a light-adapting hormone from the shrimp, Pandalus borealis.
A;Reference number: A01473; MUID:76253762
A;Residues: 1-18 cFER>
C;Comment: This peptide causes migration of the distal retinal pigment into the proximal the amount of light entering the retinulas.
C;Superfamily: pigment-dispersing hormone
C;Keywords: amidated carboxyl end; hormone
F;18/Modified site: amidated carboxyl end (Ala) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                               N:Contains: neuropeptide callatostatin 2
C;Species: Calliphora vomitoria
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999
C;Accession: A47393; B47393; C47393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
neuropeptide callatostatin 1 - bluebottle fly (Calliphora vomitoria)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Le
9.8e+02;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.1%; SCC_
100.0%; Pre
0; '
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Best Local Similarity 100..
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3 GMINSILGIPRV 14
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Best Local Similarity
Matches 5; Conserv
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||| RYGF 14
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Search completed: February 21, 2002, 17:16:49 Job time: 109 sec
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| RYGYYD 6
                                                                                                                                             1 RYGFIE 6
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                                                                                                                                                 Qγ
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CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiSpecies: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
CiAccession: PA0037
R; Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
Submitted to JIPID, July 1994
A; Reference number: PA0001
A; Reference number: PA0001
A; Reference number: protein
A; Residues: protein
A; Residues: 1-12 < KAM>A; Residues: stem
A; Experimental source: stem
                                                                                                                                                                                             R;Yamada, M; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G. D. Exp. Med. 173, 395-407, 1991
A;Title, preferential utilization of specific immunoglobulin heavy chain diversity and A;Refer fice number: Pr0222; MUID:91108337
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C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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       1,6e+03;
5; Indels
   Length 18;
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Pred. No. 1.3e+03;
3; Mismatches 2; Indels
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Pred. No. 1.5e+03;
1; Mismatches 1;
   DB 2;
                                      1; Mismatches
   Score 23;
Pred. No.
                                                                                                                                                                                                                                                                                                                                          A;Accession: B61218
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <SHE>
C;Keywords: seed; storage protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.2%;
66.7%;
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Best Local Similarity 37.5%;
Matches 3; Conservative
   22.1%;
45.5%;
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Best Local Similarity 66.7
Matches 4; Conservative
Query Match 22.1
Best Local Similarity 45.5
Matches 5; Conservative
                                                                                               2 FFLWHNVLPEI 12
                                                                       4 FIEGHVVIPRI 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 WIPRIHP 16
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A; Molecule type: DNA
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2 GXVVLP 7
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Score 22; DB 2; Length 13;
Pred. No. 1.7e+03;
2; Mismatches 1; Indels
A; Residues: 1-13 <YAM>
A; Experimental source: B lymphocyte
C; Keywords: heterotetramer; immunoglobulin
                                                                                                 21.2%;
50.0%;
                                                                                                                                       Conservative
                                                                                               Query Match
Best Local Similarity
Matches 3; Conserv
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Gaps

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. GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 21, 2002, 17:16:35; Search time 10.06 Seconds (Without alignments) 69.248 Million cell updates/sec Run on:

US-08-753-851-15 104 1 RYGFIEGHVVIPRIHPNSI 19 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

896 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 19

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	pti	P41839 calliphora	P01209 pandalus bo	P31940 homo sapien	P81555 periplaneta	P41147 pseudomonas	P80575 streptomyce				_	_	P41490 locusta mig	_		P14477 sus scrofa	Q10582 bothrops ja	P11382 rattus norv		•			_	P17441 pichia jadi	prunus se	Q10581 bothrops ja	_	-			P82651 hoplobatrac		4096 F	P35586 limulus pol
SUMMARIES	ID	ALL1_CALVO	DRPH_PANBO	UKA1_HUMAN	PVK2_PERAM	ARCD_PSEPU	AROF_STRRM	RM12_YEAST	ANGT_CHICK	BPP8_BOTIN	GON3_ONCKE	TKN3_PSEGU	LMT4_LOCMI	NEUX_HUMAN	UC08_MAIZE	FIBB_PIG	ANG2_BOTJA	NEUX_RAT	GLEM_HUMAN	ANGT_HORSE	CAT3_FASHE	LPRM_STAAU	PPK1_PERAM	TAL3_PICJA	AH3_PRUSE	ANG1_BOTJA	ANGT_BOVIN	ANGT_CRIGE	BPPB_AGKHA	MLG_THETS	TIN1_HOPTI	AH4_PRUSE	TP13_PHYRO	COCO_LIMPO
	Query Match Length DB	16 1			12 1				10 1	10 1	10 1		13 1	9	15 1	19 1	8 1	9 1	10 1	. 14 1	19 1	19 1	9 1									13 1		14 1
æ	Query	23.1	23.1	22.1	21.2	21.2	21.2	20.7	20.3	20.5	20.3	20.5	20.2	19.2	19.2	19.2	18,3	18.3	18.3	18.3	18.3	18.3	17.3	17.3	17.3	17.3	17.3	17.3	17.3	17.3	17.3	17.3	17.3	17.3
	Score	24	24	23	22	22	22	21.5	21	21	21	21	21	20	20	20	19	19	19	19	19	19	18	18	18	18	18	18	18	18	18	18	18	18
	Result No.	7	7	3	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

P19914 pseudomonas P01155 sus scrofa	P19917 pseudomonas P81266 microplitis	P29259 prunus sero	P81438 myrmecia gu	P07495 megabombus	P14313 rhizobium l	P46155 klebsiella	P80491 methanosarc		P30422 bothrops in
DCMM_PSECF HY14_PIG	DCMM_PSECH EF1A_MICCR	AH1_PRUSE	FOR1_MYRGU	BOL4_MEGPE	FIXA_RHILE	TOP1_KLEAE	FRHG_METBA	LMT3_LOCMI	BPP2_BOTIN
		Н	-	П	П	Н	7	-	-
14	15 15	16	16	17	18	18	19	6	10
17.3	17.3	17.3	17.3	17.3	17.3	17.3	17.3	16.3	16.3
18 18	18 18	18	18	18	18	18	18	17	17
34 35	36 37	38	36	40	41	42	43	44	45

# ALIGNMENTS

0; Indels Best Local Similarity 100.0%; Freq. No. 0.3e+
Matches 4; Conservative 0; Mismatches 1 RYGF 4 δ

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Penzlin H.; "Isolation of periviscerokinin-2 from the abdominal perisympathetic organs of the American cockroach, Periplaneta americana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilson S.D., Wang M., Filpula D.;
Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION. CATALYZES AN ELECTRONEUTRAL EXCHANGE BETWEEN ARGININE
AND ORNITHINE TO ALLOW HIGH-EFFICIENCY ENERGY CONVERSION IN THE
ARGININE DELMINASE PATHWAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Predel R., Rapus J., Eckert M., Holman G.M., Nachman R.J., Wang Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITATORY ACTIONS ON THE. HYPERNEURAL MUSCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas putida.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                   Periplaneta americana (American cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blattoidea; Blattidae; Periplaneta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 22; DB 1; Length 12;
Pred. No. 1e+03;
Mismatches 5; Indels
                                                                             Length 19;
                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMIDATION.
2F4D8EEE1EB05728 CRC64;
                        EF7515F79D50DE12 CRC64;
                                                                                            Pred. No. 1.1e+03;
4; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- MASS SPECTROMETRY: MW=1189.3; METHOD=MALDI
                                                                             Score 23; DB 1;
                                                                                                                                                                                                                                                                                                               (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ARGININE/ORNITHINE ANTIPORTER (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 AA.
                                                                                                                                                                                                                                                                              12 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Abdominal perisympathetic organs; MEDLINE-98326577; PubMed-9663444;
                                                                                                                                                                                                                                                                                                                                                                   PERIVISCEROKININ-2 (PEA-PVK-2).
     19
2087 MW;
                                                                             22.1%;
25.0%;
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33.3%;
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                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 21.2
Best Local Similarity 33.3
Matches 4; Conservative
                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                  8 HVVIPRIHPNSI 19
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1 GSSSGLISMPRV 12
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     19
19 AA;
                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ATCC 4359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-303;
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20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                  20-AUG-2001
                                                                                                                                                                                                                                                                              PVK2_PERAM P81555;
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P41147;
     NON_TER
SEQUENCE
                                                                                                                                                                                                                                          RESULT 4
PVK2_PERAM
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                                                                                                                Matches
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m SQ}
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                                                                                                                                                                                                                  Pandalus borealis (Northern red shrimp).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea; Pandaloidea;
Pandalidae; Pandalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF EPIDERMAL KERATINOCYTES (SPOT 1118)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Microsequences of 145 proteins recorded in the two-dimensional gel protein database of normal human epidermal keratinocytes."; Electrophoresis 13:960-969(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 7.24, ITS MW IS: 23.5 KDA.
Aarhus/Ghent-2DPAGE; 1118; IEF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                 Biochim. Biophys. Acta 439:17-25(1976).

-!- FUNCTION: CAUSES THE MIGRATION OF THE DISTAL RETINAL PIGMENT INTO THE PROXIMAL END OF THE PIGMENT CHROMATOPHORE CELLS AND THUS DECREASES THE AMOUNT OF LIGHT ENTERING THE RETINULAS.

-!- SIMILARITY: TO THE PDH OF OTHER ARTHROPODS.
                                                                                                                                                                                                                                                                                                                                                                            "Structure of a light-adapting hormone from the shrimp, Pandalus
                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
PIGMENT-DISPERSING HORMONE (PDH) (LIGHT ADAPTING DISTAL RETINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Keratinocytes;
MEDLINE=93162043; PubMed=1286667;
Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
Vandekerckhove J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 24; DB 1; Length 18;
Pred. No. 7.3e+02;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMIDATION.
B2346B6D0178650E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 AA.
                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                              MEDLINE=76253762; PubMed=952951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 18
18 AA; 1903 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 41./۰
دم 5; Conservative
                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                  PIGMENT HORMONE) (DRPH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
13
17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A01473; DRDPPP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 GFIEGHVVIPRI 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GMINSILGIPRV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hormone; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
11 RYGF 14
                                                                                                                                                                                                                                                                                                                                                               Fernlund P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (FRAGMENTS).
                                                                                        DRPH_PANBO
P01209;
                                                                                                                                                                                                                                                                                                                                                                                                  borealis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UKA1_HUMAN
P31940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                              SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
UKA1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNSURE
                                                     RESULT 2
DRPH_PANBO
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HELD THE STANK STA

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Gaps

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Takel Y., Hasegawa Y.;
"Vasopressor and depressor effects of native angiotensins and inhibition of these effects in the Japanese quail.";
Gen. Comp. Endocrinol. 79:12-22(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ANGIOTENSINOGEN (CONTAINS: ANGIOTENSIN I; ANGIOTENSIN II) (FRACMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                      "Extended N-terminal sequencing of proteins of the large ribosomal subunit from yeast mitochondria."; FEBS Lett, 284:51-56(1991). PIR; S17261; S17261.
                                                                                                                                                                                                                                                                                                                                                                                                 Grohmann L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin
                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                        01-JUN-1994 (Rel. 29, Created)
1-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L12 (YML12) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakayama T., Nakajima T., Sokabe H.;
"Comparative studies on angiotensins. 3. Structure of fowl angiotensin and its identification by DNS-method.";
Chem. Pharm. Bull. 21:2085-2087(1973).
                                                                                                                                                                                                                                                                                                  Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 AA; 1851 MW; 74BCD9FEDDDB3900 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 21.5; DB 1;
Pred. No. 1.6e+03;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 AA.
                                                                                                                     15 AA
                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=Chicken;
MEDLINE=74127845; PubMed=4361802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES-C.c.japonica;
MEDLINE=90284684; PubMed=2191893;
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-91285106; PubMed-2060626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribosomal protein; Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 20.7
Best Local Similarity 46.2
Matches 6; Conservative
                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031, 93934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGD; L0002687; MRPL12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:| || || || 6 EVE---VIVRENP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 FIEGHVVIPRIHP 16
                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SERPINAS OR AGT
|| | | |
13 GFFEVH 18
                                                                                                                                                                                                                                                                                                                                                                                                                            Kitakawa M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANGT_CHICK
ID ANGT_CHICK
AC P01018;
                                                                                                                   RM12_YEAST
P36522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus.
                                                                              RESULT 7
RM12_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
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                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lisb-sib.ch).
                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PHOSPHO-2-DEHYNDON-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15) (PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE) (DAHP SYMTHETASE) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3-deoxy-D-arabino-heptulosonate-7-phosphate synthase in Streptomyces coelicolor A3(2), Streptomyces rimosus and Neurospora crassa."; Microbiology 142:1973-1982(1996).

-i- CATALITIC ACTIVITY: 7-PHOSPHO-2-DEHYDRO-3-DEOXY-D-ARABINO-HEPTONATE + OFTHOPHOSPHATE = PHOSPHOENOLPYRUVATE + D-ERYTHROSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- PATHWAY: FIRST ŚTÉP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN THE BIOSYNTHESIS OF AROMATIC ANTINO ACIDS (THE SHIKIMATE PATHWAY).
-i- SUBUNIT: HOMODIMBR (BY SIMILARITY).
-i- PTM: THE N-TERMINUS IS BLOCKED.
-i- SIMILARITY: BELONGS TO CLASS-II DAHP SYNTHETASE FAMILY.
InterPro: IPR002480; DAHP_SYNTH_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces rimosus.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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0
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                                                                                                                                                                                                                                                                             Transport; Amino-acid transport; Transmembrane; Inner membrane
                (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE ARCD/CADB/GERAB/LYSI FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                  Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 22; DB 1; Length 18;
Pred. No. 1.5e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                     16 AA; 1644 MW; 90B48A7C8FAA9705 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7FE627E713C871BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  Score 22; DB 1; 1
Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01474; DAHP_synth_2; 1.
Aromatic amino acid biosynthesis; Lyase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE, AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                  21.2%;
30.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.2%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2209 MW;
                                                                                                                                                                                                                                                           EMBL; U07185; AAA16963.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-ISOLATE 4018;
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YGFIEGHVVI 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 YGLYDGFLTL 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1927;
                                                         PERMEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GFIEGH 8
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P80575;
                                                                                                                                                                                                                                                                                                  NON_TER
SEQUENCE
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SEQUENCE
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AROF\_STRRM

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Matches

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Gaps

3;

Indels

Length 15;

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01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GONADOLIBERIN III (GONADOTROPIN-RELEASING HORMONE III) (GNRH-III) (LH-
                                                                                                                                                                                                                                                                                                                                                                                       Carolsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G., Chang J.P., Rivier J.E., Sherwood N.M.;
"Primary structure and function of three gonadotropin-releasing hormones, including a novel form, from an ancient teleost, herring."; Endocrinology 141:505-512(2000).
-i- FUNCTION: STIMULATES THE SECRETION OF BOTH LUTEINIZING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
Roberts J.D., Melchiorri P., Erspamer V.;
"Six novel tachykinin- and bombesin-related peptides from the skin of
the Australian frog Pseudophryne guntheri.";
Peptides 11:299-304(1990).
--- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
                                                                                                                                                                                                                                      SPECIES-O.keta;
MEDICINE-83195140; PubMed-6341999;
Sherwood N., Eiden L., Brownstein M., Spiess J., Rivier J., Vale W.;
"Characterization of a teleost gonadotropin-releasing hormone.";
Proc. Natl. Acad. Sci. U.S.A. 80:2794-2798(1983).
                                                                                                                 Clupea pallasii (Pacific herring).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8018, 30724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.2%; Score 21; DB 1; Length 10; 50.0%; Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMIDATION.
284B3233786B45A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                        SPECIES-C.pallasii; TISSUE-Brain, and Pituitary; MEDLINE-20114351; PubMed-10650929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE GNRH FAMILY.
PIR; A21114; A21114.
InterPro; IPR002012; GNRH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence upoly Nory-2000 (Rel. 39, Last annotation to RASSININ-LIKE PERPIDE K-III (PG-KIII)
                                                                                                     Oncorhynchus keta (Chum salmon), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Skin;
MEDLINE=90287814; PubMed=2356157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOLLICLE-STIMULATING HORMONES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hormone; Amidation; Hypothalamus.
MOD_RES 10 10 AMIC
SEQUENCE 10 AA; 1230 MW; 284B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudophryne guentheri (Frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00446; GnRH; 1.
PROSITE; PS00473; GNRH; 1.
                                                                    RH III) (LULIBERIN III).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                          SEQUENCE, AND FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                        SEQUENCE
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                                                                                  GNRH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TKN3_PSEGU
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Cintra A.C.O., Vleira C.A., Giglio J.R.;
Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";
J. Protein Chem. 9:221-227(1990).
--- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE ANGIOTEMENIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.

IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
PPIR; H37196; H37196
               CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL BALANCE OF BODY FLUIDS.
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                        -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
-!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
PIR; A01250; A01250.
CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
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01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
BRADYKININ POTENTIATING PEPTIDE S5,1 (ANGIOTENSIN-CONVERTING
                                                                                                                                                                                                                                                                                                                    Score 21; DB 1; Length 10;
Pred. No. 1.3e+03;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.2%; Score 21; DB 1; Length 10; 100.0%; Pred. No. 1.3e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bothrops insularis (Island jararaca) (Queimada jararaca)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                    ANGIOTENSIN II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 AA.
                                                                                                                                                                                                                     ANGIOTENSIN I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                InterPro; IPR000215; Serpin.
PROSITE; PS00284; SERPIN; PARTIAL.
VASOCONSTRICTOR; Plasma; Serpin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                    20.2%;
                                                                                                                                                                                                                                                      10 10
10 AA; 1232 MW;
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                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 50.0
Matches 3; Conservative
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                                                                                                                                                    PIR; A60624; A60624
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Best Local Similarity
Matches 3; Conserv
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P20367; P81751;
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5 VHPFSL 10
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HPN 7
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P30426;
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NON_TER
SEQUENCE
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GON3_ONCKE
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BPP8_BOTIN
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01-JUL-1989 (Rel. 11, Last annotation update)
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IARRHP 6
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UC08_MAIZE
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EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND SECRETAGGGGES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
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Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
Acridomorpha; Acridoidea; Acrididae; Locusta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.2%; Score 21; DB 1; Length 13; 42.9%; Pred. No. 1.6e+03; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 11;
1.4e+03;
                                                                                                                                                                                                                                                                                                           PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                               3DBA7C37C9CB1457 CRC64;
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20861943824D6698 CRC64;
                                                                                -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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04, Last sequence update)
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Locusta migratoria (Migratory locust).
                                                                                                                                                                                                                                                                                                                                        AMIDATION
                                                                                                                                                                                     Pfam; PF02202; Tachykinin; 1.
SMART; SM00203; TK; 1.
PROSITE; PS00267; TACHYKININ; 1.
Tachykinin; Neuropeptide; Amidation.
                                                                                                                                    Interpro; IPR003580; Protachykinin.
Interpro; IPR002040; Tachykinin.
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                                                                                                          PIR; D60409; D60409.
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Best Local Similarity
Matches 3; Conserv
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1 RLHONGM 7
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20-MAR-1987
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P41490;
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P04277;
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SEQUENCE
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NEUX_HUMAN
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Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C., Pernollet J.-C., Zivy M., de Vienne D.; The maize two dimensional gel protein database: towards an integrated
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NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                         Shively J.E., Walsh J.H.; "The amino acid sequence of kinetensin, a novel peptide isolated from pepsin-treated human plasma: homology with human serum albumin, neurotensin and angiotensin.";
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NEUROTENSIN-RELATED PEPTIDE (NRP) (KINETENSIN).
Homo sapiens (Human), Bos taurus (Bovine), and
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=87194805; PubMed=2437111;
Carraway R.E., Mitra S.P., Cochrane D.E.;
Carraway R.E., Mitra S.P., Cochrane D.E.;
Structure of a biologically active neurotensin-related peptide obtained from pepsin-treated albumin(s).";
J. Biol. Chem. 262:5968-5973(1987).
-1- FUNCTION: REGULATION OF FAT DIGESTION, LIPID ABSORPTION, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: STRUCTURALLY WITH NEUROTENSIN AND ANGIOTENSIN I. STRONG SEQUENCE HOMOLOGY WITH RAT NRP.
                                                                                                                                                                                                                                           SPECIES-Human;
MEDLINE-86242180; PubMed-3087352;
Mogard M.H., Kobayashi R., Chen C.F., Lee T.D., Reeve J.R. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 159)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C804DB4761F4140D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun. 136:983-988(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES-Human, Bovine, and Rabbit;
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                                                                                                                                                      NCBI_TaxID=9606, 9913, 9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1172 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BLOOD FLOW (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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PIR; A26693; A26693
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Best Local Similarity
Matches 4; Conserv
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-1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

-1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOBEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBEL FOR THE FORMATION OF THE SOFT CLOT.

INTERPROP PROSITE: PSO0514; FIBRINGSOR_C DOMAIN; PARTIAL.

Blood coagulation; Plasma; Sulfation.

MOD RES
                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
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Pred. No. 2.7e+03;
1; Mismatches 3; Indels
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15 15 15
15 AA; 1785 MW; 1978BlD6AB4DDF8D CRC64;
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01-JAN-1990 (Rel. 13, Last sequence update)
01-JAN-1990 (Rel. 13, Last annotation update)
FIBRINOPEPTIDE B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 AA.
                                                                                                                         h 19.2%;
Similarity 42.9%;
3; Conservative
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Best Local Similarity 50.0
Matches 2; Conservative
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Best Local Similarity
Matches 3; Conserv
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8 YPVVPGH 14
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PKVH 15
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Search completed: February 21, 2002, 17:19:31 Job time: 176 sec

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09twh heliothis v
09bdd6 ovis aries
09qv20 mus sp. per
042416 gallus gall
086578 sigma virus
09xsq4 gorilla gor
09xsp5 pan troglod
09r5p6 legionella
09t5p6 legionella
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Q39829 glycine max
Q9x6x7 salmonella
Q106721 homo sapien
Q9uce4 homo sapien
O82685 gerbera hyb
Q67605 squash leaf
                                              Oguca4 homo sapien
O19716 homo sapien
P82671 spinacia ol
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
BUCCALIN B, BUCB.
Aplysia californica (California sea hare)
Bukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
Aplysidae; Aplysia.
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95079448; pubmed=7527301;
Okada H., Yoshida J., Seo H., Wakabayashi T., Sugita K., Hagiwara M.;
"Anti-(glioma surface antigen) monoclonal antibody G-22 recognizes
overexpressed CD44 in glioma cells.";
Cancer Immunol. Immunother. 39:313-317(1994).
SEQUENCE 12 AA; 1337 MW; 2E0F6CE9D9D2CIE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                   Q9xsp2
Q9nr93
Q99374
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100.0%; Pred. No. 0.0015;
ive 0; Mismatches 0; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
85 KDA GLIOMA MEMBRANE PROTEIN/CD44 HOMOLOG.
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099XSP6
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099XSP6
09XSP7
09XSP6
09XSP2
09NR93
099374
09UCA4
019716
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 SEQUENCE
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QgucnO homo sapien
Qgpry8 triakis scy
Qgr4c4 agrobacteri
095795 homo sapien
P79480 cervus elap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oguc29 homo sapien
Ogtwm2 aplysia cal
O44610 buchnera ap
Oguc28 homo sapien
Ogucf4 homo sapien
Ogucf2 homo sapien
OS2135 enterococcu
P92072 euhadra her
P82600 aedes aegyp
Ogucn0 homo sapien
                                                               ; Search time 22.04 Seconds
(without alignments)
126.097 Million cell updates/sec
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                    Compugen Ltd
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          GenCore version 4.5 Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                          473505 seqs, 146272329 residues
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                                                                 February 21, 2002, 17:16:15
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Maximum Match 100%
Listing first 45 summaries
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P92072
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Gapop 10.0 , Gapext 0.5
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Q9UC28
Q9UCF4
Q9UC82
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sp_unclassified:*
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sp_human:*
sp_invertebrate:*
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sp_phage:*
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length: 19
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Homo sapiens (Human).
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Matches 5; Conserv
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Best Local Similarity
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3 VPAIHP
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MEDLINE=95212914; PubMed=7535281;
Roubbakhsh D., Baumann P.;
"Characterization of a putative 238-5S rRNA operon of Buchnera aphidicola (endosymbiont of aphids) unlinked to the 16S rRNA-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEXITNE-95079448; PubMed=7527301;
Okada H., Yoshida J., Seo H., Wakabayashi T., Sugita K., Hagiwara M.;
"Anti-(giloma surface antigen) monoclonal antibody G-22 recognizes
overexpressed CD44 in glioma cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                        MEDLINE-95083478; PubMed-7991459;
Vilim F.S., Cropper E.C., Rosen S.C., Tenenbaum R., Kupfermann I.,
Weiss K.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                             "Structure, localization, and action of buccalin B: a bioactive
                                                                                                                                                      .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 30; DB 2; Length 16;
Pred. No. 3.3e+02;
3; Mismatches 5; Indels
                                                                                                                                 Length 11;
                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Buchnera.
                                                                                               692253F9C9C86B44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 AA; 1891 MW; 72A8175598D30DF1 CRC64;
                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-MAY-2000 (TrEMBLrel. 13, Last annotation
85 KDA GLIOMA MEMBRANE PROTEIN/CD44 HOMOLOG.
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EMBL; U10499; AAA79128.1; -.
NON_TER 1
                                                                          peptide from Aplysia.";
Peptides 15:959-969(1994).
SEQUENCE 11 AA; 1153 MW;
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Best Local Similarity 38.5%;
Matches 5; Conservative
                                                                                                                                29.8%;
71.4%;
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044610;
01-NOV-1996 (TrEMBLrel. 01
01-NOV-1996 (TrEMBLrel. 01
01-NOV-1998 (TrEMBLrel. 05
SHIKIMATE DEHYDROGENASE (F
                                                                                                                               Query Match 29.8
Best Local Similarity 71.4
Matches 5; Conservative
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NCBI_TaxID=6500;
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                      SEQUENCE
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"Sequencing of proteins extracted from stones.";
Scanning Microsc. 8:233-239(1994).
-!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
-!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
FAMILY.
                                                                                                                                                                            Gaps
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MEDLINE=93285747; PubMed=8509158;
Kim Y.J., Zhou Z., Hurtado J., Wood D.L., Choi A.S., Pescovitz M.D.,
Warfel K.A., Vandagriff J., Davis J.K., Kwon B.S.;
"IDDM patients' sera recognize a novel 30-kb pancreatic autoantigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Catarrhini; Hominidae; Homo.
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                                                                                                              27.9%; Score 29; DB 4; Length 17; 100.0%; Pred. No. 5.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 28; DB 4; Length 18;
Pred. No. 7.9e+02;
Cancer Immunol. Immunother. 39:313-317(1994). SEQUENCE 17 AA; 1788 MW; 7806F51C97A3E217 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 AA; 2162 MW; AD703A074F3C9655 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunol. Invest. 22:219-227(1993).
SEQUENCE 18 AA; 1826 MW; 38105D1037CA6837 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         QUCCF4;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
CHYMOTRYPSINOGEN HOMOLOG (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                       18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seque
01-UN-2001 (TrEMBLrel. 17, Last annot.
22 RDA STONE MATEIX PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.9%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   related to chymotrypsinogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P17670; 1IDS.
InterPro; IPR001189; SOD_MI.
Pfam; PF00081; sodfe; 1.
Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                         5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Gaps

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Insect Blochem. Mol. Biol. 26:309-317(1996).

-!- FUNCTION: INVOLVED IN THE FORMATION OF A RIGID AND INSOLUBLE EGG CHORION BY CATALYZING CHORION PROTEIN CROSSLINKING THROUGH DITYROSINE FORMATION.

-!- CATALYTIC ACTIVITY: DONOR + H(2)O(2) = OXIDIZED DONOR + 2 H(2)O.

-!- COPACYOR: BINDS HEME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- ENZYME REGULATION: EXTREMELY RESISTANT TO DENATURATING AGENTS, SUCH AS SDS AND ORGANIC SOLVENTS.
-i- SUBCELLULAR LOCATION: IN THE CHORION LAYER OF THE MATURE EGGS.
-i- MISCELLANEOUS: HAS HIGHEST ACTIVITY AT PH 8.0 WITH GUALACLE AS A
                                                                                                                                                                                                                                                                                                                 Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Han Q., Li G., Li J.; "Purification and characterization of chorion peroxidase from Aedes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Li J., Hodgeman B.A., Christensen B.M.; "Involvement of peroxidase in chorion hardening in Aedes aegypti."; Insect Biochem. Mol. Biol. 26:309-317(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 9 N-LINKED (GLCNAC. . ) (POTENTIAL).
19 AA: 2172 MW; 022F95BA72E14998 CRC64;
                                                                                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0MR-2010 (TrEMBLrel. 16, Last annotation update)
01-MR-2010 (TrEMBLrel. 16, Last annotation update)
CHORION PEROXIDASE (EC 1.11.1.7).
Aedes aegypti (Yellowfever mosquito).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.0%; Score 26; DB 5; Length 19; 33.3%; Pred. No. 1.7e+03; Live 4; Mismatches 2; Indels
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oxidoreductase; Glycoprotein; Peroxidase; Heme; Chorion CARBOHYD 9 N-LINKED (GLCNAC...) (PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
7;
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                                                                                                                                                                  19 AA
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-LIVERPOOL / BLACKEYE; TISSUE-OVARY;
MEDLINE-97056259; PubMed-8900599;
                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-LIVERPOOL / BLACKEYE; TISSUE-OVARY; MEDLINE-20326865; Pubmed=10871050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aegypti eggs.";
Arch. Biochem. Biophys. 378:107-115(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 33.3
Matches 3; Conservative
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSFERRIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REDUCING AGENT
                                    11 IPRIHPNSI 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 IPRIHPNSI 19
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                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7159;
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                                                        :|:: |:|:
1 VPQLSPHSL
3;
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SEQUENCE.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION.
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                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                              P82600
P82600;
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Matches
                                                                                                                             RESULT
P82600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitochondrion.
Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
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Yamazaki N., Ueshima R., Terrett J.A., Yokobori S., Kaifu M.,
Segawa R., Kobayashi T., Numachi K., Ueda T., Nishikawa K.,
Watanabe K., Thomas R.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 27; DB 2; Length 15;
Pred. No. 9.2e+02;
0; Mismatches 1; Indels
                                  Length 19;
                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 8; Length 9;
                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
PLASHID PADI SEX PHEROMONE INHIBITOR (IADI) DETERMINANT
Enterococcus faecalis (Streptococcus faecalis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases. EMBL; 271697; CAA96373.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 AA; 1874 MW; 0D9D07E3079E3559 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
THPASE SUBUNIT 8 (FRAGMENT).
Euhadra herklotsi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        977 MW; 25BBB1F775B736C7 CRC64;
                                Score 28; DB 4; Ler
Pred. No. 8.3e+02;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 26; DB 8;
Pred. No. 4.7e+05;
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                                                                                                                                                                                                                                          15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicacea; Bradybaenidae; Buhadra.
NCBI_raxID=58912;
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33.3%;
                                  26.9%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.0%;
ilarity 83.3%;
Conservative
                                                                                                                                                                                                                                    Q52135
Q52135;
01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 03,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M62888; AAA98040.1;
                                Query Match 26.9
Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                 NCBI_TaxID=1351;
                                                                                                          2 YGFIEGHV 9
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Enterococcus

RESULT

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SEQUENCE Plasmid

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Gaps

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01-MAY-1997

P92072

RESULT

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NON\_TER SEQUENCE

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Gaps

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6; Indels

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                  01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24; DB 4; Length 1/, Pred; No. 3.2e+03;
                                                                                                                                                                                                                                                                                                                      Blazkova M., Kankova K.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF065211; AAD15888.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                 38C7EE8959E00D72 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
         Pred. No. 3.2e+03;
                    4; Mismatches
                                                                                                                                           17 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                           PRT;
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9 9
17 17
17 AA; 1727 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.1%;
50.0%;
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55.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03, 01-AUG-1998 (TrEMBLrel. 07,
        28.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 17
17 AA; 2022 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cervidae; Cervinae; Cervus.
NCBI_TaxID=9860;
                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cervus elaphus (Red deer)
                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                             4 FIEGHVVIPRIHPN 17
                                                              |: | :|:
3 FLPGXPEVPAEYPS 16
                                                                                                                                                                                                                                         Homo sapiens (Human).
     Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 IPRIHPNS 18
                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : |: |||
2 VARVLPNS 9
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                              Receptor
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VARIANT
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P79480;
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                                                                                                                RESULT 13
095795
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MEDLINE-92375195; PubMed-1380674; Chicz R.M., Urban R.G., Lane W.S., Gorga J.C., Stern L.J., Vignall D.A., Strominger J.L.; Vignall D.A., Strominger J.L.; Predominant naturally processed peptides bound to HLA-DR1 are derived from MHC-related molecules and are heterogeneous in size."; SEQUENCE 17 A4; 2035 MW; A7DEDA39A2538A88 CRC64;
                                                                                                                                                                                                                                                                                                                                                        Triakis scyllium (Leopard shark) (Triakis scyllia).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hammer A., Stolz A., Knackmuss H.;
"Purification and characterization of a novel type of protocatechuate 3.4-dioxygenses with the ability to oxidize 4-sulfocatechol.";
Arch. Microbiol. 166:92-100(1996).
SEQUENCE 17 AA: 1812 MW; ECA688148553EDF2 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
PROTOCATECHUATE 3,4-DIOXYGENASE TYPE II BETA SUBUNIT (EC 1.13.11.3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Rhizobium.
NCBI_TaxID=358;
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Takei Y., Hasegawa Y., Watanabe T.X., Nakajima K., Hazon N.;
"A novel manjotensin I isolated from an elasmobranch fish.";
J. Endocrinol. 139:281-285(1993).
SEQUENCE 10 AA; 1284 MW; 20F02FD761E04B47 CRC64;
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                                                                                                                          24.0%; Score 25; DB 4; Length 17; 33.3%; Pred. No. 2.2e+03; ive 3; Mismatches 5; Indels
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Last annotation update)
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Best Local Similarity 33 3.
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Best Local Similarity 80.0
Matches 4; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
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                                                                                                                       SECUENCE FROM N.A. Swarbrick P.A., Crawford A.M.; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases. EMBL; U63083; AAB37783.1; -.
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TISSUB-GRANULAR DORSAL CLAND;

MEDLINE=20408845; PubMed=10951191;

MEDLINE=20408845; PubMed=10951191;

MA ROZEK T., Wegener K.L., Bowle J.H., Olver I.N., Carver J.A.,

Mallace J.C., Tyler M.J.;

Mallace J.C., Ty
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                                                                                           P82396;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
AUREIN 3.3/3.3.1.
Litoria raniformis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
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66.7%; Pred. No. 3.2e+03;
tive 1; Mismatches 1;
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Best Local Similarity
Matches 4; Conserv
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NCBI_TaxID=116057;
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SEQUENCE
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RESULT
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Search completed: February 21, 2002, 17:19:15 Job time: 180 sec

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; Search time 23.85 Seconds
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59.010 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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522463 seqs, 74073290 residues US-08-753-851-15 104 1 RYGFIEGHVVIPRIHPNSI 19 BLOSUM62 Gapop 10.0 , Gapext 0.5 Perfect score: Scoring table: Sequence: Searched: Title:

193517 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 19

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

\$\text{\$1DS8\gagadata/geneseqy/Aniscseqy}\$\text{\$1DS8\gagadata/geneseqy/Aniscseqy}\$\text{\$1DS8\gagadata/geneseqy/Anisg.} DAT: \*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description		CD44 peptide CD44-	HTLV-I protease cl	Chick muscle-speci	Diastereomer pepti	Antipathogenic pep	Antipathogenic pep	Hepatitis B virus-	Immunogenic peptid	Angiogenic vascula	Japanese cedar pol	Japan cedar pollen
	ID		AAR53485	AAW36883	AAW26612	AAW35207	AAW82923	AAB17458	AAY38164	AAY45732	AAB23536	AAR53696	AAR97942
	DB	;	15	18	18	18	19	21	15	20	21	15	17
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øP	Query Match		100.0	30.8	30.8	29.8	29.8	29.8	28.8	28.8	28.8	28.8	28.8
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Japan cedar pollen Human leptin recep Peptide #6043 enco Peptide #6043 enco Antigenic peptide purified cis 9,10-Farty acid amide h EFRH containing per Tomato ACC synthas Human SNP associat CD66 peptide Coff Calmodulin inhibit HLA class In superrype Protein SEQ ID NO: Peptide #8096 enco Peptide SEQ ID HIV peptide SEQ ID HIV peptide SEQ ID HIV peptide SEQ ID Kb-binding random Human leucocyte an HTW-II protease C Reactive peptide w Porphyromonas qinq	
17 AAR97943 21 AAV5842 22 AAM15842 22 AAM32006 10 AAP90252 118 AAW57399 22 AAB87799 22 AAB87799 22 AAB8174 22 AAB8174 22 AAG888 22 AAG8862 22 AAG8862 22 AAM23969 22 AAM2396 22 AAM2396 22 AAM2396 22 AAM2396 22 AAM2396 22 AAM2396 21 AAM49228 21 AAM49228 21 AAM49228 22 AAM2396 22 AAM2396 22 AAM2396 22 AAM2396 23 AAM2396 24 AAM2396 25 AAM2396 27 AAM2396 28 AAM2396 29 AAM2396 21 AAY89879 21 AANB1871	
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# ALIGNMENTS

Cell adhesion molecule; CD44; antiinflammatory; rheumatoid; arthritis; tumor cell metastasis; autoimmune disease; AAR53485 standard; peptide; 19 AA. 93WO-US10412. (first entry) CD44 peptide CD44-12. immunosuppressive. Homo sapiens 29-OCT-1993; 01-DEC-1994 WO9409811-A. 11-MAY-1994. AAR53485; AAR53485 

92US-0973339. 30-OCT-1992;

Patton KL, Telen MJ; Liao H, Hale LP, Haynes BF, (UYDU-) UNIV DUKE.

WPI; 1994-167121/20.

Use of CD44 protein and new peptide derivs - for developing prods for inflammation, immune-mediated tissue damage and tumour cell metastasis Length 12;

DB 18; 48;

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30.8%;
62.5%;
                                                                                    Conservative
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and related receptor
with muscle atrophy
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15-DEC-1995;
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                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNAs encoding ricin like toxins A and B - are linked via linker containing cleavage site for retroviral protease, used to inhibit or destroy mammalian cells infected with retrovirus
                        The peptide can be used for treating inflammation and immune-mediated tissue damage such as occurs in the course of autoimmune diseases, e.g. rheumatoid arthritis. It can also be used for determining metastatic potential or to treat or prevent tumor cell metastasis. This peptide corresponds to AA 76-96 of the CD44
                                                                                                                                                                                                                                                                                                                                                                                                                    Ricin; toxin; antiviral; virucide; retrovirus; protease; HTLV-I;
                                                                                                                                                                                          0;
                                                                                                                                                                Length 19;
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                                                                                                                                                            100.0%; Score 104; DB 15;
100.0%; Pred. No. 7.2e-11;
tive 0; Mismatches 0;
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 Claim 4; Page 14; 83pp; English.
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Matches 19; Conserv
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                                                                                            protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                     Chick muscle-specific kinase (MuSK) cytoplasmic domain peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chick muscle specific kinase (MuSK) cytoplasmic domain. It was used to raise polyclonal antibodies for MuSK. These were used in studies that demonstrated that agrin (see AAW26609) induces prominent and rapid tyrosine phosphorylation of MuSK (see also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor tyrosine kinase; muscle specific kinase; MuSK; Dmk; chicken; polyclonal antibody.
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Score 32; DB
Pred No. 48;
2; Mismatches
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Pred. No. 78;
5; Mismatches
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Gaps

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This sequence represents a diastercomer peptide of the invention. The peptides of the invention have: (a) cytolytic activity on pathogenic cells (pathogens and malignant cells not naturally present in the body); but (b) no haemolytic activity, or such activity only at a concentration significantly higher than that at which they lyse pathogens. The peptides, their complexes and mixtures are used to treat infections (caused by bacteria, fungi, protozoa, mycoplasma or viruses) or cancer, in human and veterinary medicine. Also, they can be used as preservatives for food, cosmetics and agricultural produce, or as preservatives for food, absence of haemolytic activity (associated with disturbance of alpha-helical structures) means that the peptides have few if any toxic effects, and those that include D-aa will have increased resistance to proteolytic degradation. Non-haemolytic, allowing selection of agents for particular applications. Since these random copolymers induce total lysis of bacterial cell walls, resistance to them is unlikely to develop.
                                                                                                                                                                                                                                                                                                                                                                                                            /note= "D-form residue"
                                                                                                                                                                                                                                                                                                 'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                 /note= "D-form residue"
                                                                                                                                                                                      /note= "D-form residue"
                                                                                                                                                                                                                 "D-form residue"
                                                                                                                                                                                                                                            note= "D-form residue"
                                                                                                                                                                                                                                                                      'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                             "D-form residue"
                                                                                                                                                                                                                                                                                                                                                        note= "D-form residue"
                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 5; Page 47; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96IL-0117223.
            (first entry)
                                     Diastereomer peptide 68
                                                                                                                                                                                                                  'note=
                                                                                                                                                                                                                                                                                                                             'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-435088/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oren 2, Shai Y;
                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                              Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9731019-A2
         14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-AUG-1997
                                                                                                                                  Synthetic
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specification describes a non-haemolytic, cytolytic agent, which is a peptide, a complex of bundled peptides, a mixture of peptides or a random peptide copolymer. The agent has a selective cytolytic activity on pathogenic cells. The agent is selected from a cyclic derivative of a peptide which has a net positive charge greater than 1, comprises L-amino acid residues and/orn D-amino acid residues and comprises an alpha-halix breaker moiety, or a peptide (or cyclic derivative of this) which (comprises L-amino acid residues and D-amino acid residues, has a net
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a corresponding amino acid sequence comprising only L-amino acid residues is not found in nature. The cytolytic agents may be used for treatment of cancer or for treatment of several diseases caused by pathogens. Including bacterial, fungal, viral, mycoplasma and protozoan infections. They may be used in both human and veterinary medicine. They may also be used as disinfectants for destruction of microorganisms, i.e. in solutions for wetting contact lenses, as preservatives, e.g., in the bactericides or for preservation of agricultural products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present peptide is used to produce the agents of the invention. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         positive charge greater than 1 and has an amino acid sequence such that
                                                                                                                                                                                                                                                                                                                                                                                   Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution; preservative; pesticide; fungicide; bactericide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New non-haemolytic cytolytic agent useful in treating cancer or infections - is a peptide comprising a moiety which disrupts the continuity of an alpha-helical structure
Length 16;
                                       Indels
                                   3;
DB 18;
                Pred. No. 1e+02;
                                     2; Mismatches
Score 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; Page 46; 126pp; English.
                                                                                                                                                                                                                       AAW82923 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (YEDA ) YEDA RES & DEV CO LTD
29.8%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-IL00066.
                                                                                                                                                                                                                                                                                                       (first entry)
                                       Conservative
                                                                                                                                                                                                                                                                                                                                               Antipathogenic péptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-594464/50.
                                                                           5 IEGHVVIPRIH 15
                                                                                                      |: || | |:|
4 ikahvriirvh 14
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oren Z, Shai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-FEB-1997;
                                                                                                                                                                                                                                                                                                       19-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9837090-A1
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                               AAW82923;
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                                                                                                                                                                                  S
                                       Matches
                                                                                                                                                                                                   AAW82923
                                                                             οy
                                                                                                                     αd
                                                                                                                                                                                                                                                               Diastereomer peptide; infection; therapy; excitatory neurotoxin; money bee venom; pardaxin; cytolytic activity; cancer; non-haemolytic; preservative; agricultural produce; bacterial cell lysis; agricultural pesticide; cell wall lysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide(s) having selective cytolytic activity - against pathogens and malignant cells, but no haemolytic activity, used for treating infections and cancer
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Gaps

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29.8%; Score 31; DB 19; Length 16; 54.5%; Pred. No. 1e+02; ive 2; Mismatches 3; Indels

Query Match Best Local Similarity 54... اتام 6; Conservative

5 IEGHVVIPRIH 15

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4 ikahvriirvh 14

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|: || | |:| 4 ikahvriirvh 14

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AAB17458;

AAB17458

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The sequence is a specific example of a group of new immunogenic peptides having an HLA-A3.2, HLA-A1, HLA-A11 or HLA-A24.1 binding motif. For example, the peptides having an HLA-A3.2 binding motif each have 9-10 residues and contain, from the N-terminus to the C-terminus, (a) a first conserved residue selected from L, M, I, V, S, Y, T, F, C, G, D and E and (b) a second conserved residue of K, R, Y, H or F, where the first and second conserved residue of separated by 6-7 residues. The peptides are capable of binding selected MHC molecules and inducing an immune response. They can be used to treat and/or prevent viral infection and cancer, e.g. prostate cancer, lymphoma, hepatitis or AIDS. They can also be used to produce antibodies for use as diagnostic or therapeutic agents. The peptides can also be used as diagnostic agents.
                                                                                                                                                                                                                                              Immunogen; HLA; human leukocyte antigen; binding motif; antiviral; MHC; major histocompatability complex; viral infection; anticancer; prostate cancer; lymphoma; hepatitis; AIDS; diagnostic; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide which specifically binds selected MHC allele - used to induce an immune response for treatment or prevention of viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.8%; Score 30; DB 15; Length 10;
                                                                                                                                                                                                Hepatitis B virus-derived HLA-binding peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 83;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sette A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infection or cancer, or for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 107; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY45732 standard; Peptide; 10 AA.
                                              AAY38164 standard; Peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Celis E, Grey HM, Kubo RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-0027746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93WO-US07421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.48;
                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1994-065403/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CYTE-) CYTEL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                     Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 IEGHVVIPR 13
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2 vnghqvlpk 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      WO9403205-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-MAR-1993;
07-AUG-1992;
                                                                                                                                                  29-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                       7-FEB-1994.
                                                                                               AAY38164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY45732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                         AAY38164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(Li)C-F1, -(Li)C-F1-(L2)d-P2.

(Li)c-P1-(L2)d-P2-(L3)e-P^3, or -(Li)C-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; Li, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and b, c, d, e, and f = are each independently linkers; and b, b. c, d, e, and f = are each independently linkers; and b, b. c, d, e, and f = are each independently linkers; and bost colls from the present invention can have cytostatic, antiasthmatic, thrombollytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention are useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

The use of an FC domain (rather than a Fab domain) can provide a longer while of the present incorporate functions such as FC receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 condences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                          autoimmune disease; Oyfostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO: TPO: CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoiethi; thrombopoiethi, interleukin 1; eytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                        Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .,
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                                                                                                                                                                                                                       Antipathogenic peptide sequence SEQ ID NO:562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                           asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 39; Page 392; 608pp; English.
                                                                  AAB17458 standard; Peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0105371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0428082
                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 IEGHVVIPRIH 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-1998;
                                                                                                                                                                    31-OCT-2000
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04-MAY-2000

Synthetic.

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Gaps

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2; Indels

01-DEC-1999 (first entry)

Sequence

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Angiogenic vasculature homing peptide; proteoglycan; NG2; tumour; drug targeting; cytotoxic; chemotherapeutic agent.
Angiogenic vasculature homing peptide SEQ ID 13
                                                                                                                                WO200048464-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANY ANY 45390 to ANY 48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukcoyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes CC HLA-A2.1, Al, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell cresponse against the antigen from which the peptide is derived. Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound commandly induced by an antigen in the form of a peptide fragment bound are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) corporate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or individuals susceptible or otherwise at risk of viral infection or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful
                 Immunogenic peptide having a human leukocyte antigen binding motif #343
                                                  Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New immunogenic peptides with HLA binding motif, useful in treatment
                                                                                                                                                                                                                                                                                                                                                                                                                   Southwood S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Grey HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and diagnosis of cancers and viral diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  Kubo RT, Sidney J, Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB23536 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.8%;
44.4%;
                                                                                                                                                                                                                                                                                                     98WO-US05039
                                                                                                                                                                                                                                                                                                                                          98WO-US05039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 40; 150pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                vaccine; immunisation
                                                                                                                                                                                                                                                                                                                                                                               (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-551214/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : || |:|:
2 vnghqvlpk 10
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                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                           W09945954-A1
                                                                                                                                                                                                                                                                                                     13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                          13-MAR-1998;
                                                                                                                                                                                                                                                                16-SEP-1999.
                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                   Sette A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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peptides, which interact with proteoglycan NG2. The invention includes a method for trargeting anglogenic vasculature in a tumour in vivo, and a method for inhibiting anglogenesis in a tumour comprising administering one of the anglogenic vasculature homing peptides linked to a moiety such as a drug or cytotoxic agent. The peptides exhibit cytostatic activity, and are used for targeting drugs, cytotoxic agents or chemotherapeutic agents to tumours or tissues or other organs associated with anglogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                     for
                                                                                                                                                                                                                                                                                                                                                                                                    Sequences AAB23524-B23539 represent angiogenic vasculature homing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                     New angiogenic vasculature homing peptides and conjugates e.g.
                                                                                                                                                                                         Stallcup WB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Japanese cedar pollen allergen Cry j IIB fragment.
                                                                                                                                                                                       Ruoslahti EI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 30;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeund S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR53696 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 58; 86pp; English
                                                                                                                                                                                         Arap W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brauer A, Kuo M, Pollock J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cedar pollinosis; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IMMU-) IMMULOGIC PHARM CORP
                                             16-FEB-2000; 2000WO-US03864.
                                                                                           99US-0250700
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                                                                                                                                                                                                                                                                                                        drugs to tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                       Burg MA, Pasqualini R,
                                                                                                                                           (BURN-) BURNHAM INST
                                                                                                                                                                                                                                  WPI; 2000-558237/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGHVVIPR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 dahvlvpr 8
                                                                                         16-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vasculature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1995
24-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9411512-A
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                                                                                                                                                                                                                                                                                                           targeting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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pollinosis

Sequence

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AAR97871-R97960 are overlapping peptides used for the epitope mapping of the Japan cedar pollen allergen Cry j II. Cry j II and allergenic peptides of it are useful in the diagnosis, prevention and treatment of Sugi pollinosis, the allergic reaction to Japan cedar pollen. Significant regions of the allergic were identified using the overlapping peptides of the full epitope derived from a Cry j II antigen-specific T cell line. Anino acids 66-80 (AAR97884) and 186-200 (R978908) of the full mature 460 amino acid allergen are the most
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Japan cedar pollen allergen Cry j II epitope – comprises at least part of specified 460 amino acid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human leptin receptor intracellular peptide EC-2 residues 473-487
                                                                                                                                                                                                                                                                                                                      Japan cedar pollen mature allergen Cry j II amino acids 361-375.
                                                                                                                                                                                                                                                                                                                                                        Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;
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     Length 15;
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Score 30; DB 17; Length 15
Pred. No. 1.4e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30; DB 17; I
Pred. No. 1.4e+02;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                           Sugi pollinosis; diagnosis; treatment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       allergenic of the 90 peptides tested.
                                                                                                                                                                                                       AAR97943 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY57842 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Fig 5; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MILK PROD CO LTD.
 28.8%;
50.0%;
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50.0%;
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93JP-0276773.
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                                                                                                                                                                                                                                                                                 (first entry)
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                                        4; Conservative
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                 Best_Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity
Matches 4; Conserv
                                                                          3 GFIEGHVV 10
                                                                                                               gyfsghvi 15
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                                                                                                                                                                                                                                                                                 16-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-NOV-1993;
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                                                                                                                                                                                                                                             AAR97943;
   Query Match
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                                                                                                                                                                                       AAR97943
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                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                           The sequence is of a Japanese cedar pollen allergen Cry j IIA fragment. The protein and fragments can be used for diagnosis and treatment of Japanese cedar pollinosis and to identify similar sequences in other plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Japan cedar pollen allergen Cry j II epitope – comprises at least part of specified 460 amino acid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Japan cedar pollen mature allergen Cry j II amino acids 356-370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Allergen; epitope; overlapping peptide; Cry j II; cedar pollen; Sugi pollinosis; diagnosis; treatment.
                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                             Allergenic Cry j II protein and fragments from Japanese cedar
pollen – used to diagnose, treat and prevent Japanese cedar
                                                                                                                                                                                                                                                                                                                                   Length 14;
                                                                                                                                                                                                                                                                                                                               Score 30; DB 15; Length 14
Pred. No. 1.3e+02;
2; Mismatches 2; Indels
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                                                                                                                        Disclosure; Page 38; 89pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR97942 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MEIP ) MEIJI MILK PROD CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; Fig 5; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                               28.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94JP-0134868.
93JP-0276773.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Best Local Similarity 50.0
امرو 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cryptomeria japonica
           WPI; 1994-183513/22
                                                                                                                                                                                                                                                                          14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      3 GFIEGHVV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                          gyfsghvi 9
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05-NOV-1993;
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AAR97942;

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**AAR97942** RESULT

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Sequence

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The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs
                                                                                                                                                                                                                                                                                                                                                                   can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printer specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide #6043 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                         analyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 30; DB 22; Length 16
Pred. No. 1.7e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                           Claim 27; SEQ ID No 24108; 487pp; English.
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                                                                                                                                                  Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM32006 standard; Protein; 18 AA.
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                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                  Chen W,
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.8%;
40.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0207456.
2000US-0608408.
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2000US-0236359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Best Local Similarity 40.0.
                                                                                                                                                  Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanzel DK,
                                                                                                                                                                                    WPI; 2001-488901/53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                     cervical cancer.
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                    21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAY-2000;
   30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM32006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    angiogenesis-inducing stimulus by administering an agent (1) that modulates a leptin, or leptin receptor, mediated angiogenic response to that stimulus. The method may be used to treat diseases controlled by angiogenesis including wound healing, tumours and tumour metastasis, diabetic microangiopathy, retinal neovascularisation, neovascularisation of adipose tissue and fat metabolism, revascularisation of necrotic tissue, enhancement or vascularisation in microvascular transplants and ovarian follicle maturation. The present sequence represents a peptide based on the human leptin receptor, given in an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     method has been developed for modulating a response in a subject to an
                                                                                                                                                                                                                                                                                                                                                                                            Modulating an angiogenesis-inducing stimulus in wound healing, used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide #5716 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; microarray; gene expression; cervical epithelial cell;
                                      regulation; ischaemia; leptin; tumour; metastasis; fat metabolism; diabetic microangiopathy; neovascularisation.
                      Human; leptin receptor; modulation; angiogenesis; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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Pred. No. 1.4e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 39; 89pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM19282 standard; Protein; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.8%;
75.0%;
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26-MAY-2000; 2000US-0207456
                                                                                                                                                                                                       99WO-US11209
                                                                                                                                                                                                                                           98US-0086354
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                                                                                                                                                                                                                                                                                                                                                                                                             treating, e.g. tumors
                                                                                                                                                                                                                                                                                                                   Sierra-Honigmann RM;
                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-086576/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                               (UYYA ) UNIV YALE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                             Homo sapiens
                                                                                                                               W09959614-A1
                                                                                                                                                                                                       20-MAY-1999;
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                                                                                                                                                                   25-NOV-1999
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Sequence

AAM19282;

AAM19282 RESULT

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Probe;

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Gaps

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Length 18;

WPI; 2001-488897/53.

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                                                                                                                        The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                         Gaps
                                             .;
0
                                                                                                                                                                                                                                                                                   Query Match 28.8%; Score 30; DB 22; Length 18; Best Local Similarity 40.0%; Prèd. No. 1.7e+02; Matches 4; Conservative 3; Mismatches 3; Indels
                                                                                           Claim 27; SEQ ID No 32275; 654pp; English.
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6 gwvsghadlp 15
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                                                                                                                                                                                                                                       18 AA;
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δ
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Search completed: February 21, 2002, 17:16:11 Job time: 191 sec

1120, Ap 3, Appli 2, Appli

Sequence Sequence Sequence Sequence Sequence Sequence 15, Sequence 15, Sequence 15,

Sequence

Appl i

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence

Sequence

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SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                      -08-159-339A-1120
                               US-07-888-943-3
US-08-100-691-2
US-08-100-691-2
US-08-297-494-15
US-08-297-510-15
US-08-455-526-15
US-08-455-526-15
US-08-452-2698-9
US-08-452-2698-9
US-09-139-491-15
US-09-139-491-15
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            3-US95-09261-5
                                                                                                                                                                                    US-08-492-599-2
US-08-031-538-44
                                                                                                                                                                 -09-294-923-9
                                                                                                                                                                                                                                                                                                                                APPLICANT: HAYNES, BARTON F.
APPLICANT: HALE, LAURA P.
APPLICANT: PATTON, KAREN L.
APPLICANT: TELEN, MARILYN J.
APPLICANT: LIAO, HUA-XIN
TITLE OF INVENTION: AN ADHESION MOLECULE
CORRESPONDENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/143,311B
FILING DATE: 29-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,339
FILING DATE: 30-OCT-1992
CLASSIFICATION: 436
APPLICATION NUMBER: 07/669,730
FILING DATE: 15-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1579-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                             Sequence 13, Application US/08143311B Patent No. 5863540 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               E: NIXON & VANDERHYE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 157
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: peptide US-08-143-311B-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 22201-4714
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                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
STREET: 11
                                                                                                                                                                                                                                                                                     US-08-143-311B-13
16, Appl
3, Appli
3, Appli
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34.287 Million cell updates/sec
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                                                                               ; Search time 12.47 Seconds
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.: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/becTUS_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-143-311B-13
US-08-644-271-16
US-08-64-271-16
US-08-159-339A-462
US-08-159-339A-462
US-08-467-023-184
US-08-467-023-184
US-08-77-023-184
US-08-77-023-184
US-08-77-023-184
US-08-77-18-20
US-08-77-18-20
US-08-77-18-20
US-08-268-251-23
US-08-268-251-23
US-08-268-251-23
US-08-268-251-23
US-08-310-912A-54
US-08-310-912A-54
US-08-310-912A-54
US-08-310-912A-54
US-08-310-912A-54
US-09-301-085-54
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US-09-338-876-15
US-09-248-588-47
US-08-665-966-4
                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-436-420-16
US-07-854-603-10
                                                                                                                                                                                                              212252 seqs, 22503292 residues
                                                                              February 21, 2002, 17:14:40
                                                         OM protein - protein search, using sw model
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                                                                                                                                                    1 RYGFIEGHVVIPRIHPNSI 19
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
                                                                                                                              US-08-753-851-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
Match Length
                                                                                                                                                                                                                                                            length: 0
length: 19
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Maximum DB seq
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GENERAL INFORMATION:

APPLICANT: Rich Alexander
APPLICANT: Herbert, Alan
TITLE OF INVENTION: Z-DNA BINDING PROTEIN AND APPLICATIONS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATE: Massachusetts Institute of Technology
TITLE OF INVENTION: Z-DNA BINDING PROTEIN AND APPLICATIONS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. BOX 999.
CITY: York Harbor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 19;
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/492,599
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US96/10455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTATION NUMBER: 35,505
REPERENCE/DOCKET NUMBER: MIT-7011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application PC/TUS9610455 GENERAL INFORMATION:
Sequence 3, Application US/08492599
Patent No. 5726050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEPAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 42.55
- Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: peptide US-08-492-599-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                               as
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                                                                                                                                                                                                                                               ZIP: 03911
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PCT-US96-10455-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: YO STATE: M COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
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                                    Length 19;
                                                                       Indels
                                                                                                                                                                                                                               | Sequence 16, Application US/08644271
| Patent No. 5814478
| GENERAL INFORMATION:
| APPLICANT: Valenzuela, et al.
| TILE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS
| TILE OF INVENTION: AND LIGANDS
| NUMBER OF SEQUENCES: 32
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Regeneron Pharmaceuticals, Inc.
| STREET: 777 Old Saw Mill Road
| CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                 Score 104; DB 2;
Pred. No. 2e-11;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 29;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FASTSEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/644,271
FILING DATE: 10-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/008,657
FILING DATE: 15-DEC-1995
ATTORNEY,AGENT INFORMATION:
NAME: CODERT, ROBERT 36,108
REGISTRATION NUMBER: 36,108
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: 36,108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7721
                             Query Match 100.0%; S. Best Local Similarity 100.0%; P. Matches 19; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.8%;
30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                          1 RYGFIEGHVVIPRIHPNSI 19
                                                                                                                            1 RYGFIEGHVVIPRIHPNSI 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 30.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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COTHER INFORMATION:
COTHER INFORMATION:
US-08-644-271-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: NY COUNTRY: U
                                                                                                                                                                                                                         US-08-644-271-16
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US-08-492-599-3
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Japanese Cedar Pollen
261
                                                                                                                                                                             Length 10;
                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: ImmuLogic Pharmaceutical Corporation, Inc. 610 Lincoln St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                           DB 3;
32;
                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 30; DB
Pred. No. 47;
                                                                                                                                                                             Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 184, Application US/08467023 Patent No. 6090386 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Griffeth, Irwin J.;
Pollock, Joanne;
Bond, Julian F.;
Garman, Richard D;
Kuo, Mei-Chang;
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Brauer, Andrew;
Exley, Mark A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Powers, Steven P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.8%;
50.0%;
                              10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 14 amino acids
                                                                                                                                                                           Query Match 28.8
Best Local Similarity 44.4
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
           SEQUENCE CHARACTERISTICS:
                                                                 single
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CORRESPONDENCE ADDRESS:
                                                                                                      peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
                            ; LENGTH: 10 amino a
; TYPE: amino acid
; STRANDEDNESS: sing
; TOPOLOGY: linear
; MOLECULE TYPE: peptil
US-08-159-339A-462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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Best Local Similarity
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2 VNGHOVLPK 10
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FRAGMENT TYPE:
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COUNTRY: US
ZIP: 02154
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STREET: 61
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US-08-467-023-184
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
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Pred. No. 45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kubo, Ralph T.
APPLICANT: Kubo, Howard M.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32.7762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                         ATTORNEY AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: MIT-7011 WO
TELEPHONE: (207) 363-0558
TELEPHONE: (207) 363-0558
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION UNBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/159,339A FILING DATE: 29-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 462, Application US/08159339A Patent No. 6037135 GENERAL INFORMATION:
APPLICATION NUMBER: 08/492,599
FILING DATE: 20-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 462;
                                                                                                                                                                                                                                                                                                                                                                                    Query Match 29.8%;
Best Local Similarity 42.9%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                             LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: peptide PCT-US96-10455-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Two Embarcac
CITY: San Francisco
STATE: CA
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                          FILING DATE: 2
CLASSIFICATION:
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APPLICANT: Dawson, Keith M
APPLICANT: Edwards, Richard M
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| S GYIDGRVV 12
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                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                   COUNTRY:
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APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From TITLE OF INVENTION: Japanese Cedar Pollen
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 14;
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                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS: ADDRESS: ImmuLogic Pharmaceutical Corporation, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       025.6 USD2 (IMI-028CPD2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,023 FILING DATE: June 6, 1995 CLASSIFICATION: 424 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30; DB 3
Pred. No. 47;
2; Mismatches
 Mismatches
                                                                                                                                                Sequence 186, Application US/08467023 Patent No. 6090386
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US-07-854-603-12
; Sequence 12, Application US/07854603
; Patent No. 5637492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                Griffeth, Irwin J.;
Pollock, Joanne;
Bond, Julian F.;
Garman, Richard D;
Kuo, Mei-Chang;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Jane E. Remillard
REGISTATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
INFORMATION FOR SEC ID NO: 186:
SEQUENCE CHARACTERISTICS:
2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                  Yeung, Siu-mei H.;
Brauer, Andrew;
Exley, Mark A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.8%;
ilarity 50.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                610 Lincoln St
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4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 4; Conserv
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                                GFIEGHVV 10
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2 GYFSGHVI 9
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2 GYFSGHVI 9
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CITY: W
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Matches
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                                                                                                                                                                                                                                                                                                SOFTWARE: PATIENT F. COSTINGTONS SOFTWARE: PATIENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
              TITLE OF INVENTION: Activatable fibrinolytic and TITLE OF INVENTION: anti-thrombotic proteins NUMBER OF SEQUENCES: 40 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: The Scripps Research Institute
10550 No. 6271015th Torrey Pines Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gilula, No. 6271015ton B
APPLICANT: Cravatt, Benjamin F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: FATTY-ACID AMIDE HYDROLASE
UNMBER OF SEQUENCES: 54
CORRESPONDENCES: ADDRESS:
ADDRESSE: The Scripps Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
75;
                                                                                                                      Ten South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                         PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20, Application US/08743168B Patent No. 6271015
                                                                                                   Dr. John J. McDonnel
                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                        26,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.98;
62.58;
                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,
REFERENCE/DOCKET NUMBER:
Joan M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 62.5
                                                                                                                                                                                                                                                                                                                                                                      19901207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-07-854-603-12
                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 10550 No. CITY: La Jolla STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMINO ACID
  Forman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                STREET: Ten overty: Chicago
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APPLICANT: TURUNEN, MARJA K.
APPLICANT: RAMBOSEK, JOHN A.
APPLICANT: RAMBOSEK, JOHN A.
APPLICANT: PIDDINGTON, CHRISTINE S.
APPLICANT: HOUSTON, CHRISTINE S.
APPLICANT: HOUSTON, CHRISTINE S.
TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
TITLE OF INVENTION: BNZYMES IN DESIRED RATIOS
NUMBER OF SEQUENCES: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
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                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,652C
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07058
FILING DATE: 27-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jamieson, Gordon A
APPLICANT: Dedman, John R
APPLICANT: Kaetzel, Marcia A
TITLE OF INVENTION: Calmodulin-Binding Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 28.5; DB 2;
Pred. No. 1.2e+02;
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ER: 1050.071001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/925,401
FILING DATE: 31-01L-1992
CLASSIFICATION: 435
ATTOCNEV AGENT INFORMATION:
NAME: REED, GRANT E.
REGISTRATION NUMBER: 41,264
REFERNCE/DOCKET NUMBER: 1050.071001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                          PALCHEIMO, MARJA T.
FAGERSTROM, RICHARD B.
MIETTINEN-OINONEN, ARJA S.
                        NEVALAINEN, HELENA K.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 23, Application US/08268251
; Patent No. 5585475
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: single TOPOLOGY: not relevant; MOLECULE TYPE: peptide US-08-374-652C-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 27.4
Best Local Similarity 46.2
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RYGFI-EGHVVIP 12
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  GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
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                                          APPLICANT:
APPLICANT:
                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                          STATE:
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Pred. No. 91;
3; Mismatches 2; Indels.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10435 FILING DATE: 12-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: CIS-9, 10-OCTADECENOAMIDASE
NUMBER OF SEQUENCES: 32
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                       NAME: FILLING, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSI 485.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 aming acids
                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/489,535
FILING DATE: 12-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/489,535
FILING DATE: 12-JUN-1995
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application PC/TUS9610435 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-374-652C-48; Sequence 48, Application US/08374652C; Patent No. 5834286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 27.4%;
Best Local Similarity 50.0%;
Matches 6; Conservative
04 - NOV - 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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Best Local Similarity 50.0.
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; FRAGMENT TYPE: internal
US-08-743-168B-20
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internal
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5 GHTLIPFL-PNN 15
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| GHTLIPFL-PNN 15
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                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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FRAGMENT TYPE:
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Gaps
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PCT-US93-01112-23
; Sequence 23, Application PC/TUS9301112
; Sequence 23, Application PC/TUS9301112
; GENERAL INFORMATION:
APPLICANT: Jamieson, Gordon A
APPLICANT: Reatzel, Marcia A
TITLE OF INVENTION: Calmodulin-Binding Peptides
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                    Score 28; DB 1; 1 Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01112
FILING DATE: 19930208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/831,219
FILING DATE: 06-FEB-1992
ATONEX/AGENT INFORMATION:
NAME: Green, Grant D
REGISTRATION NUMBER: 31,259
                                                                    92,338
                 NAME: MCDONNELL, 26,949
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,3:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELERAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Chiron Corporation 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 23:
         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                    Query Match 26.9
Best Local Similarity 50.0
Matches 4; Conservative
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LENGTH: 15 amino acids
                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
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GY: linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                                                                                                                              US-07-854-603-14
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Patent No. 5637492
GENERAL INFORMATION:
APPLICANT: Dawson, Keith M
APPLICANT: Edwards, Richard M
APPLICANT: Edwards, Richard M
TITLE OF INVENTION: Activatable fibrinolytic and
TITLE OF INVENTION: anti-thrombotic proteins
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Dr. John J. McDonnel
STREET: Ten South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/854,603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 28; DB 1; Pred. No. 1.1e+02; Pred. No. 1.1e+02; Pred. No. 1.1e+02; Nismatches 0
                                                                                                                                                     COMFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/251
                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/831,219
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: Chiron Corporation
STREET: 4560 Horton Street
CIIY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 27.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-206
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 15 amino acids
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Best Local Similarity
Matches 4; Conserva
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STREET: Ten
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                                                                                                                      USA
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10 YLEGHV 15
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                                                                                               STATE: C. COUNTRY:
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APPLICANT: Katagiri, Fumiaki
APPLICANT: Katagiri, Fumiaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindrinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RES2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION
NUMBER OF SEQUENCES: 208
                        Gaps
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Pred. No. 1.2e+02;
2; Mismatches 1; Indels
                            Indels
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ZIF: 0110-2904
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,912A
FILING DATE: September 22, 1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/227,360
FILING DATE: APPLI 13, 1994
ATTORNEY/AGENT INFORMATION:
ANNELS AREA TO THE T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INCOMPANDER: Lech, Karen F.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/254001
TELEPHONE: (517) 542-8906
TELEPHONE: (617) 542-8906
TELER: 100254
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C. STRRET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                    US-08-310-912A-54
; Sequence 54, Application US/08310912A
; Patent No. 5981730
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ausubel, Frederick M.
Staskawicz, Brian J.
Brent, Andrew F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 26.9%;
Best Local Similarity 57.1%;
Matches 4; Conservative
                    4; Conservative
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; MOLECULE TYPE: protein
US-08-310-912A-54
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4 RVHPSKI 10
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10 YLEGHV 15
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Matches
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Search completed: February 21, 2002, 17:16:30 Job time: 110 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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OM protein - protein search, using sw model

Run on:

February 21, 2002, 17:18:50 ; Search time 12.71 Seconds
(without alignments)
65.926 Million cell updates/sec

US-08-753-851-16 61 Title:

1 LTYNTSQYDTY 11 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

219241 segs, 76174552 residues Searched: 1324 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 11

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

pir1:\* pir2:\* pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

	Description	endosperm protein,	perisulfakinin - A	chlorophyll a/b-bi	Ig heavy chain CRD	amine oxidase (cop		tumor-associated a	tumor-associated a	glucose-6-phosphat	adipokinetic hormo	alpha-peptide/algi	placental lactogen	T-cell receptor al	fructose-bisphosph	mannose receptor -	Ig heavy chain CRD	leucosulfakinin -	T-cell receptor be	heavy	Ig heavy chain V r	cosulfakin	gluconokinase (EC	polyferredoxin - M	polygalacturonase	leucosulfakinin II	T-cell receptor be	corazonin - Americ	glycoprotein H-a -	T-cell receptor be
SUMMARIES	ID	\$70334	A60656	PW0002	PT0243	A32428	PC1316	S43971	S43972	S11078	A24244	PU0037	A47364	S23373	A28924	S39374	PT0291	GMROL	PH0919	PT0311	836850	GMROL2	S74176	S62208	C61440 .	B60656	PT0215	805002	A40795	PT0214
	DB	7	7	7	7	~	7	7	7	~	7	~	7	7	7	7	~	7	7	~	7	-	~	~	~	7	7	7	7	7
	Length	6	11	6	10	11	7	80	œ	80	6	10	10	11	9	10	10	11	11	œ	6	10	10	10	10	10	10	11	11	11
æ	Query Match	32.8	32.8	31.1	29.5	29.5	27.9	27.9	27.9	27.9	27.9	27.9	27.9	27.9	26.2	26.3	26.2	26.2	9	24.6	4	4	4	24.6	4	4	4	4	₹	₹*
	Score	20	20	19	18	18	17	17	17	17	17	17	17	17	16	16	16	16	16	15	15	15	15	15	15	15	15	15	15	15
	Result No.	-	7	e	4	'n	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59

68kDa neurofilamen	beta-D-galactosida	phenol 2-monooxyge	hypothalamic hepta	dissimilatory sulf	calsequestrin, car	hypothetical prote	calliFMRFamide 1 -	Ig heavy chain CRD	enamelin i - bovin	pyrimidine synthes	T-cell receptor ga	peptidylglycine mo	T-cell receptor be	hypertrehalosemic/	probable glucose-6
160434	S53436	A37832	NYPG7	S63493	A61230	G85802	A41978	PT0270	S10784	865913	G41946	A42266	PH0937	A31571	S18396
7	7	~	1	7	~	N	~	~	~	~	~	7	7	7	7
11	11	4	7	<b>&amp;</b>	σ	6	6	6	6	6	σ	6	6	10	10
24.6	24.6	23.0	23.0	23.0	23.0	23.0	23.0	23.0	23.0	23.0	23.0	23.0	23.0	23.0	23.0
15	15	14	14	14	14	14	14	14	14	14	14	14	14	14	14
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

```
c. Species: Secale cereale (rye)
C. Species: 1998 #1ext_change 17-Apr-1998
R. Species: S70334
R. Species: S70334
R. Socher, A.; Calero, M.; Soriano, F.; Mendez, E.
B. Biochim. Blophys. Acta 1295, 13-22, 1996
A. Title: Identification of major rye secalins as coeliac immunoreactive proteins.
A. Reference number: S70334
A. Status: preliminary
A. Molecule type: protein
A. Molecule type: protein
A. Residues: 1-9 <ROC>
                                                                                                                                                                                                                                                                                                                                                                                                    ö
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0
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                                                                                                                                                                                                                                                                                                                                                    32.8%;
57.1%;
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 TSQYDTY 11
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RESULT

perisulfakinin - American cockroach
perisulfakinin - American cockroach
perisulfakinin - American cockroach
c;Species: Periplaneta americana (American cockroach)
c;Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 11-Jul-1997
C;Accession: A6055
R;Veenstra, J.A.
Neuropeptides 14, 145-149, 1989
A;Fitle: Isolation and structure of two gastrin/CCK-like neuropeptides from the Ameri
A;Reference number: A60556; MUID:90137190
A;Accession: A60556
A;Molecule type: protein
A;Residues: 1-11 <VEE>
C;Comment: This neuropeptide stimulates hindgut contractions.
C;Comment: This neuropeptide stimulates hindgut contractions.
C;Keywords: amidated carboxyl end; neuropeptide; sulfoprotein
F;CABinding site: sulfate (Tyr) (covalent) #status experimental
F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Gaps .; 0 32.8%; Score 20; DB 2; Length 11; 60.0%; Pred. No. 1e+03; tive 1; Mismatches 1; Indels Conservative Best Local Similarity Matches 3; Conserv Query Match

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7 QYDTY 11 Ω δ

|:| | 2 QFDDY 6

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Page

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Gaps

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Indels

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large granule L3 chain - horseshoe crab (Tachypleus tridentatus) (fragment)
C;Species: Tachypleus tridentatus
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C;Accession: PC1316
R;Shigenaga, T.; Takayenoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.; J. Biochem. 114, 307-316, 1993
A;Title: Separation of large and small granules from horseshoe crab (Tachypleus tride A;Reference number: PC1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: S43971
R;Mandelboim, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenstein, M.; Eisenbach, L.
Nature 369, 67-71, 1994
A;Title: CTL induction by a tumour-associated antigen octapeptide derived from a muri
A;Reference number: S43971; MUID:94217811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 1-7 <SHI>
C;Comment: This protein participates in immobilization of invading microbes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumor-associated antigen MUT1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Oct-1994 #sequence_revision 17-Nov-1995 #text_change 18-Aug-2000
                   Pred. No. 2.4e+03;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17; DB 2; I
Pred. No. 2.2e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 < MAN.
C;Superfamily: unassigned animal peptides
100.0%; Prt
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumor-associated antigen MUT2 - mouse
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80.0%;
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75.0%;
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                   Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 3; Conserv
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1 TSQPD 5
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NTAQ 7
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7 TYN
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S43972
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S43971
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                                                                                                                                                                                                                                                                                                                                     A;Accession: Pw0002
A;Molecule type: protein
A;Residues: 1-9 <LAR>
C;Superfamily: chlorophyll a/b-binding protein
C;Keywords: chloroplast; grana; light-harvesting complex; membrane adhesion; membrane px
                                                                                     Chlorophyll a/b-binding protein 31K - green alga (Dunaliella tertiolecta) (fragment)
N;Alternate names: photosystem II light-harvesting chlorophyll 31K protein
S;Species: Dunaliella tertiolecta
C;Species: Dunaliella tertiolecta
C;Species: Dunaliella tertiolecta
C;Accession: PW0002
E;Accession: PW0002
E;Accession: PW0002
A;Accession: PW0002
A;Ascession: PW0002
A;Ascession: PW0002
A;Ascession: PW0002
A;Ascession: PW00040; WUID:91065528
A;Reference number: JW0040; WUID:91065528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; van der Meer, R.A.; van Wassenaar, P.D.; van Brouwershaven, J.H.; Duine, J.A.
Blochem. Blochys. Res. Commun. 159, 726-733, 1989
A;Title: Primary structure of a pyrrologuinoline guinone (PQQ) containing peptide isolat
A;Reference number: A32428; MUID:89193662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Accession: A32428
A; Molecule type: protein
A; Residues: 1-7, 'K', 9-11 <VAN>
A; Residues: 1-7, 'K', 9-11 <VAN>
A; Residue the modified residue thought by the authors to be pyrrologuinoline guinone coval C; Keywords: oxidoreductase; quinoprotein; topaquinone
F; 8/Modified site: topaquinone (Tyr) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G. J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Reference number: PT0222; MUID:91108337
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amine oxidase (copper-containing) (EC 1.4.3.6) - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 12-Oct-1989 #sequence_revision 31-Dec-1993 #text_change 06-Sep-1996
C;Accession: A32428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 2.2e+05;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.5%; Score 18; DB 2; I
50.0%; Pred. No. 2.1e+03;
iive 2; Mismatches 1;
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A; Molecule type: DNA
A; Residues: 1-10 < YAM>
A; Experimental source: B lymphocyte
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.1%;
75.0%;
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Best Local Similarity 75.09
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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1 AQYD 4
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4 YDSSGY
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Gaps

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Length 7;

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R; Mandelboim, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenstein, M.; Eisenbach, L. Nature 369, 67-71, 1994
A; Title: CTL induction by a tumour-associated antigen octapeptide derived from a muri A; Reference number: S43971; MUID:94217811
A; Accession: S43972
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-8 < MAN>
                                                        ö
                                                                                                                                                                                                                                                                                                                                               C;Species: Mus musculus (house mouse)
C;Date: 20-Oct-1994 #sequence_revision 17-Nov-1995 #text_change 18-Aug-2000
C;Accession: S43972
                                                           Gaps
                                                           ;
0
     Length 8;
Score 17; DB 2; Le
Pred. No. 2.2e+05;
1; Mismatches 0;
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DB 2; Length 11;

29.5%; Score 18;

Query Matech

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Gaps

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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S23373
E;Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eich Eur. J. Immunol. 21, 2749-2754, 1991
A;Title: Blased T cell receptor V(alpha) region repertoire in the synovial fluid of r A;Accession: S23373
                          RiFujiyama, K.; Maki, H.; Kinoshita, S.; Yoshida, T. submitted to JiPtD, October 1994
A: Description: High gene expression in E. coli of recombinant alginate lyase as a fus A; Reference number: PU0037
A; Reference number: PU0037
A; Rocession: PU0037
A; Molecule type: protein
A; Residues: 1-10 < PUJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mouse placental lactogen-I gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    placental lactogen-I precursor - mouse (fragment)
C;Species: Mus sp. (mouse)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No. 3.2e+03;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: A47364
R; Shida, M.M.; Ng, Y.K.; Soares, M.J.; Linzer, D.I.
Mol. Endocrinol. 7, 181-188, 1993
A; Title: Trophoblast specific transcription from the A; Reference number: A47364; MUID:93225959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.9%; Score 17; DB 2; I
llarity 75.0%; Pred. No. 3.5e+03;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                  Score 17; DB 2; 1
Pred. No. 3.2e+03;
1; Mismatches 1;
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A;Molecule type: DNA
A;Residues: 1-10 <RES>
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     C; Accession: PU0037
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N.Alternate names: Hez-AKH
C.Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
C.Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
C.Accession: A2424
R.Ja48 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997
C.Accession: A2424
R.Ja46e, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway Blochem. Bloophys. Res. Commun. 135, 622-628, 1986
A;Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helic A;Reference number: A24244
A;Accession: A24244
A;Accession: A24244
A;Molecule type: protein
A;Residues: 1-9 <JAF>
C;Superfamily: adipokinetic hormone
C;Superfamily: adipokinetic darboxyl end: corpora cardiaca; hormone; neuropeptide; pyroglutamic F;1/Modified site: pyrrolidone carboxylic acid (GIn) #status experimental
                                                                                                                                                                                                                                                                                                       RESULT 9
$11078
glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - yeast (Pichia jadinii) (fragment)
glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - yeast (Pichia jadinii) (fragment)
glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - yeast (Pichia jadinii) (fragment)
G.Species: 91chia jadinii, Candida utilis
G.Species: 91chia jadinii, Candida utilis
G.Species: 18-69
G.Species: 18-69
A.Title: Fast atom bombardment mass spectrometry and chemical analysis in determinations
A.Reference number: $11074; MUID:90353571
A.Recession: $11078
A.Recidue: 1-8 e&cgec
A.Residues: 1-8 e&cgec
A.Residues: 1-8 e&cgec
A.Recidue type: protein
A.Recidue type: protein
C.Keywords: acetylated amino end; oxidoreductase; pentose phosphate pathway
F:1/Modified site: acetylated amino end (Ser) #status experimental
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                                                                               Score 17; DB 2; Length 8; Pred. No. 2.2e+05;
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C; Superfamily: unassigned animal peptides
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A;Accession: A28924
A;Molecule type: protein
A;Residues: 1-9 <LAK>
C;Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; liver; per
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arch. Biochem. Biophys. 306, 391-401, 1993
A'Itle: The mannose receptor and the cation-dependent form of mannose 6-phosphate recept
A'Reference number: S39374; MUID:94029009
A'Accession: S39374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-10 <MES>
C; Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II
C; Keywords: membrane protein; receptor
                                                                                                              Rilacko, A.G.; Brox, L.W.; Gracy, R.W.; Horecker, B.L.
J. Biol. Chem. 245, 2140-2141, 1970
A; Title: The carboxyl-terminal structure of rabbit liver aldolase (aldolase B).
A; Reference number: A28924; MUID:70166720
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fructose-bisphosphate aldolase (EC 4.1.2.13) B, hepatic - rabbit (fragment) C;Species: Oryctolagus cuniculus (domestic rabbit) C:Date: 2B-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 07-Feb-1997 C;Accession: A28924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mannose receptor - bovine (fragment)
C;Species: Bos primiganius taurus (cattle)
C;Date: 18-Feb-1994 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Accession: 539374
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0; Mismatches 1; Indels
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Best Local Similarity 75.0%;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

February 21, 2002, 17:20:26; Search time 10.02 Seconds (without alignments) 40.251 Million cell updates/sec Run on:

US-08-753-851-16 61 1 LTYNTSQYDTY 11

Perfect score: Title:

Sequence:

Scoring table:

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100059 seqs, 36664827 residues Searched:

Total number of hits satisfying chosen parameters:

388

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Venstra J.A.;
"Isolation and structure of two gastrin/CCK-like neuropeptides from the American cockroach homologous to the leucosulfakinins.";
Neuropeptides 14:145-149(1989).
-i- FUNCTION: STIMULATES HINDGUT CONTRACTIONS.

TISSUE-Corpora cardiaca; MEDLINE-90137190; PubMed-2615921;

SEQUENCE.

01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-FBB-1996 (Rel. 33, Last annotation update)
01-FBB-1996 (Rel. 33, Last annotation update)
PERISULFAKININ (PES. 28.-1).
Periplaneta americana (American cockroach).
Periplaneta americana (American cockroach).
Periplaneta americana (American cockroach).
Peryota: Metazoa: Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota: Meoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blattoidea: Blattidae; Periplaneta.

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                       "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas."; Eur. J. Biochem. 250:727-734(1997).
-!- FUNCTION: MAY ACT AS A NEUROFRANSMITTER OR NEUROMODULATOR.
-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
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SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Cerebral ganglion, and Thoracic ganglion;
MEDLINE-98121193; PubMed-9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpe A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF PLASMA (SPOT 12) (FRAGMENT).
                                                                                                                                                                                                                                                                                                  Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
NCBI_TaxID=6759;
                                                                                                           Score 20; DB 1; Length 11; Pred. No. 3.3e+02; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.9%; Score 17; DB 1; Length 9; 75.0%; Pred. No. 1e+05; Live 0; Mismatches 1; Indels
                                                                 AMIDATION.
884E0680E86B5AAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 AA; 927 MW; 832D79CDCB46D861 CRC64;
                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                    9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuropeptide; Amidation; Multigene family.
                                                      SULFATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                     PRT;
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MEDLINE-93092937; PubMed-1459097;
         PIR; A60656; A60656.
InterPro; IPR001651; Gastrin.
PROSITE; PS00259; GASTRIN; 1.
Hormone; Amidation; Sulfation.
                                                                                                             32.8%;
60.0%;
                                                                            11 AA; 1445 MW;
                                                                                                                                    3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Conservative
                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                            Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                         CARCINUSTATIN 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                         7 QYDTY 11
                                                                                                                                                                      |:| |
2 QFDDY 6
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P30090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 TSQY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 TGQY 5
                                                                                                                                                                                                                                   AL11_CARMA
P81814;
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                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE.
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                                                      MOD_RES
                                                                   MOD_RES
                                                                                                                                                                                                              RESULT 3
AL11_CARMA
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UPA4_HUMAN
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Krajniak K.G.;
"The identification and structure-activity relations of a
cardioactive FMRFamide-related peptide from the blue crab Callinectes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                  "Plasma protein map: an update by microsequencing.";
Electrophoresis 13:707-714(1992).
-!- MISCELLANEOUS: ON THE 20-76EL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 4.8, ITS MW IS: 40.5 KDA.
-!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
                                                                                                                                                                                                 ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptides 12:1295-1302(1991).
-!- FUNCTION: CARDIOACTIVE PEPTIDE.
-!- SIMILARITY: BELONGS TO THE FARP (EMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Callinectes.
NCBI_TaxID-6763;
Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16; DB 1; Length 9; Pred. No. 1e+05;
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                                                                                                                                                                                                                                                                                                                                                     10 AA; 1067 MW; 269492EB05A1A457 CRC64;
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SEQUENCE 9 AA: 1159 MW; 134F0729D5A4045B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17; DB 1;
Pred. No. 1e+03;
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13-AUG-1987 (Rel. 05, Last sequence update)
10-NOV-1995 (Rel. 32, Last annotation update)
LEUCOSULFAKININ-I (LSK-I).
Leucophaea maderae (Madeira cockroach).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 AA.
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0; Mismatches
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MEDLINE=92270479; Pubmed=1815216;
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01-0CT-1994 (Rel. 30, Last sequ
01-NOV-1995 (Rel. 32, Last anno
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75.0%;
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuropeptide; Amidation.
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 3; Conserv
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SEQUENCE

MOD\_RES

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PRT;
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MEDLINE=87048769; PubMed=3778455;
                                                                                                                                                                                                                     MEDLINE=94282319; PubMed=8012595;
                                                                                                                                                                                                                                                                                            Microbiology 140:741-752(1994).
                                                                                                                                                                                                                                                                                                                                                        Heat shock; Complete proteome.
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                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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Best Local Similarity
                                                                                                                    Bacillus subtilis.
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6 GXVD 9
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P09039;
                GS09_BACSU
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                              P80243;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
01-FEB-1996 (Rel. 33, Last annotation update)
NEOSULFAKININ-I (NEB-SK-I).
Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
Eukartyota: Metazoa: Arthropoda; Tracheata: Hexapoda: Insecta:
Pterygota: Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea: Sarcophagidae: Sarcophaga.
                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                             OF
                                                                                               Nachman R.J., Holman G.M., Haddon W.F., Ling N.;
"Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and cholecystckinin.";
Science 234:71-73(1986).
-!- FUNCTION: CHANGE THE FREQUENCY AND AMPLITUDE OF CONTRACTIONS C THE COCKROACH HINGUT. INHIBITS MUSCLE CONTRACTION OF HINDGUT.
-!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
                                                                                                                                                                                                                                                                                                                                      Score 16; DB 1; Length 11; Pred. No. 1.8e+03; 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                              AMIDATION.
7E4E0680E86B5AAB CRC64;
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8B0A0691E86B5AAA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 AA.
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                                                                                                                                                                                                                                                              SULFATION.
                         Blaberoidea; Blaberidae; Leucophaea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neuropeptide; Amidation; Sulfation.
                                                                                    MEDLINE-86315858; PubMed-3749893;
                                                                                                                                                                                                 PIR; A01622; GMROL,
InterPro; IPR001651; Gastrin.
PROSITE; PS00259; GASTRIN; 1.
Hormone; Amidation; Sulfation.
                                                                                                                                                                                                                                                                                                                                        26.2%;
40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.6%;
50.0%;
                                                                                                                                                                                                                                                                             MOD_RES 11 11
SEQUENCE 11 AA; 1459 MW;
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                                                                                                                                                                                                                                                                                                                                      Query Match 26.2
Best Local Similarity 40.0
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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Best Local Similarity
Matches 2; Conserv
                                        NCBI_TaxID=6988
                                                                                                                                                                                                                                                                                                                                                                                              7 QYDTY 11
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2 QFEDY 6
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P41492;
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SARBU

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MOD\_RES SEQUENCE

SEQUENCE.

-!- INDUCTION: BY HEAT SHOCK, SALT STRESS, OXIDATIVE STRESS, GLUCOSE LIMITATION AND OXYGEN LIMITATION.
Subtilist; BG19022; yzzF. Gaps Voelker U., Engelmann S., Maul B., Riethdorf S., Voelker A., Schmid R., Mach H., Hecker M.; "Analysis of the induction of general stress proteins of Bacillus subtilis."; Nachman R.J., Holman G.M., Cook B.J., Haddon W.F., Ling N.; Leucosulfakinin-II, a blocked sulfated insect neuropeptide with homology to cholecystokinin and gastrin "; Biochem. Biophys. Res. Commun. 140:357-364(1986). ; 0 Periplaneta americana (American cockroach). Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea; Blaberidae; Leucophaea. Length 10; 10 AA; 1168 MW; 99766442D5A2C05A CRC64; Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus. NCBL\_TaxID=1423; 01-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) GENERAL STRESS PROTEIN 9 (GSP9) (FRAGMENT). 01-NOV-1988 (Rel. 09, Created) 01-FCB-1994 (Rel. 28, Last sequence update) 01-NOV-1995 (Rel. 32, Last annotation update) LGUCOSULFAKININ-II (LSK-II). Leucophaea maderae (Madeira cockroach), and SPECIES=P.americana; TISSUE=Corpora cardiaca; MEDLINE=90137190; PubMed=2615921; 10 AA 10 AA. PIR; A26335; GMROL2 PIR; B60656; B60656 

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Gaps

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CALLIFWRFANIDE 1.
Calliphora vomitoria (Blue blowfly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Calliphora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chang R. C.C., Hung W.-Y., Arimura A., Redding T.W., Coy D.H.,
Saffran M., Kong A., Hamilton J.W., Cohn D.V., Schally A.V.;
"Isolation, structure and synthesis of a heptapeptide with in vitro
ACTH-releasing activity from porcine hypothalamus.";
PIR; A01417; NYPG7.
                Flengsrud R., Skjeldal L.;
"Two-dimensisbonal get electrophoresis separation and N-terminal
"Two-dimensishonal get electrophoresis sequence analysis of proteins from Clostridium pasteurianum W5.";
Electrophoresis 19:802-806(1998).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5.0, ITS MW IS: 75.9 KDA.
NON_TER 6
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MEDLINE=92196111; PubMed=1549595;
Buve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
Rehfeld J.F., Thorpe A.;
"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.0%; Score 14; DB 1; Length 7; 50.0%; Pred. No. 1e+05;
                                                                                                                                                                               Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (Pig).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;

NCBI_TaxID=9823;
                                                                                                                                6 AA; 657 MW; 605B1DC1A45A8000 CRC64;
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                                                                                                                                                                                 Score 14; DB 1;
Pred. No. 1e+05;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                               01, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
                                                                                                                                                                                                                 2; Mismatches
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 MEDLINE=98291870; PubMed=9629918;
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01, Last seq
                                                                                                                                                                               23.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             957 MW;
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HYPOTHALAMIC HEPTAPEPTIDE.
                                                                                                                                                                                                                 2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                             (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=27454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 YDTY 11
                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986
21-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FARI_CALVO
ID FARI_CALVO
AC P41856;
                                                                                                                                                                                                                                                 4 NTSQ 7
                                                                                                                                                                                                                                                                               2 NTAE 5
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                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                             HY7_PIG
P01153;
                                                                                                                                                                                                                                                                                                                                12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3
                                                                                                                                                                                                               Matches
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HY7_PIG
   δy
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                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEBS Lett. 250:231-234(1989).
-1- FUNCTION: CARDIOACTIVE PEPTIDE. CORAZONIN IS PROBABLY INVOLVED
IN THE PHYSIALOGGICAL REGULATION OF THE HEART BEAT.
PIR; S05002; S05002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolation and structure of corazonin, a cardioactive peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clostridium pasteurianum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
                                                                 SULFATION (IN L.MADERAE, BUT NOT IN P.AMERICANA).
                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Periplaneta americana (American cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blattoidea; Blattidae; Periplaneta.
NCBI_TaxID=6978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 15; DB 1; Length 11; Pred. No. 2.7e+03; 0; Mismatches 1; Indels
                                                                                                                                                                Length 10;
                                                  PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMIDATION.
C7CFF32D6415AB46 CRC64;
                                                                                                 AMIDATION.
9B4F5391E86B5AAA CRC64;
                                                                                                                                                                  Score 15; DB 1; I Pred. No. 2.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
UNKNOWN PROTEIN CP 6 FROM 2D-PAGE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1989 (Rel. 12, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-89325572; PubMed-2753132;
                                                                                                                                                                                                ..
                                Amidation; Sulfation
InterPro; IPR001651; Gastrin.
                  PS00259; GASTRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.68;
75.08;
                                                                                                 10
1255 MW;
                                                                                                                                                                  24.6%;
60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 24.6
Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                  3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE.
IISSUE=Corpora cardiaca;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the American cockroach."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                 10
10 AA;
                                                                                                                                                                Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBL TAXID=1501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Veenstra J.A.;
                                                                                                                                                                                                                              7 QYDTY 11
                                                                                                                                                                                                                                                              S
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                                                                                                                                                                                                                                                                                                                                            CORZ_PERAM
P11496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 TSQY 8
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P81351;
                                                                                                                                                                                                                                                              1 QSDDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 TFQY
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                                                                                                                                                                                                                                                                                                                                                                                                                               CORAZONIN.
                                Hormone; A
MOD_RES
MOD_RES
                                                                                                 MOD_RES
SEQUENCE
                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                               RESULT 10
CORZ_PERAM
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UN06_CLOPA
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Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Heliothinae; Helicoverpa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Heart;
MEDLINE=95203287; PubMed=7895732;
Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
"The human myocardial two-dimensional gel protein database: update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Electrophoresis 15:1459-1465(1994).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 6.0, ITS MW IS: 55.3 KDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                        -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                      0
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O
                                                   Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
-!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
SALIVARY GLAND OF CALLIPHORA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (Rel. 31, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF HEART (SPOT 5603) (FRAGMENT).
neuropeptides (designated calliFMRFamides) from the blowfly
                                                                                                                                                                                                                                                                                                                                                        Score 14; DB 1; Length 9; Pred. No. 1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 14; DB 1; Length 9;
Pred. No. 1e+05;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                 AMIDATION.
29D00699CAB6C6C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 AA; 1104 MW; 8874B1BB5B01B2CA CRC64;
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01-FEB-1994 (Rel. 28, Last annotation update)
HYPERTREHALOSAEMIC HORMONE (HEZ-HRTH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1995 (Rel. 31, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.0%;
16.7%;
                                                                                                                                                                                                                                                                                                                                                             23.0%;
60.0%;
                                                                                                                                                                                                                                                 9 9
9 AA; 1169 MW;
                                                                                                                                                                                                                     Neuropeptide; Amidation. MOD_RES 9
                                                                                                                                                                                                                                                                                                                                                             Query Match 23.0
Best Local Similarity 60.0
Matches 3; Conservative
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TISSUE=Corpora cardiaca;
                                  Calliphora vomitoria.";
                                                                                                                                                                                              PIR; A41978; A41978.
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Best Local Similarity
Matches 1; Conserv
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1 FDVTEY 6
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P40929;
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SEQUENCE
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P16353;
                                                                                                                                                                       FAMILY
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SEQUENCE
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Search completed: February 21, 2002, 17:23:23 Job time: 177 sec

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                                                                                                                                                    23.0%; Score 14; DB 1; Length 10; 40.0%; Pred. No. 3.6e+03; Live 3; Mismatches 0; Indels
                                                                                                               PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                     AMIDATION.
8E70367865A5B9D1 CRC64;
MEDLINE-88326324; PubMed-3415690;
                                                                                                                             10 AA; 1096 MW;
                                                                                    InterPro; IPR002047; AKH.
PROSITE; PS00256; AKH; 1.
Neuropeptide; Amidation.
MOD_RES 1 1 1
MOD_RES 10 10
SEQUENCE 10 AA; 1096 MW;
                                                                                                                                                                      Conservative
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Best Local Similarity
Matches 2; Conserv
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US-08-753-851-16 61 1 LTYNTSQYDTY 11

Perfect score:

Title:

Run on:

Sednence:

**BLOSUM62** 

Scoring table:

Searched:

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Q9trr7 oryctolagus
Q9dyw4 human immun
Q9t2w0 saccharomyc
Q9uge4 homo sapien
Q70140 human immun
                                                                                            087471 haemophilus
P8725 saccharomyc
Q9t2y3 begonia for
Q9t2y3 begonia for
Q9t2y2 capra hircu
P9641 capra hircu
P9642 cacrobacter
Q63056 rattus norv
P96319 desulfovibr.
Q9arj6 candidatus
Q9tx2 bos taurus
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desulfovibr.
candidatus
                                                                            litoria cit
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           oreochromis
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                                                                                                                                                                                                                                            077912 oreochromis
                                                                                                                                                                                                                                                                                                                           077899;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS II B LOCUS 14 (FRAGMENT)
Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
Cichlidae, Oreochromis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A. MEDINE-9849519; MEDINE-9815113; PubMed-9649539; Malaga-Trillo E., McAndrew B., Vincek V., Zaleska-Rutczynska Z., Sueltmann H., Figueroa F., Klein J.; Linkage relationships and haplotype polymorphism among cichlid Mhc
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                                                                           P82088
P82089
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                    09tvf1
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2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                         AA
                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                        11
        O78121
Q9TVF1
Q9TRR7
Q9DYW4
Q9T2W0
                                                        Q9UGE4
Q70140
P82089
P82089
P82089
O87471
Q9T273
Q9T273
Q9G417
Q9G417
Q9G417
Q9G3056
P9G319
Q9R1Y6
Q9AIY6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                class II B loci.";
Genetics 149:1527-1547(1998).
EMBL; AF050009; AAC41348.1; -.
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88
110
110
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110
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Best Local Similarity
1 LTYNTSQYD 9
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SEQUENCE
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077902 oreochromis
077903 oreochromis
077904 oreochromis
077916 oreochromis
077917 oreochromis
077921 pseudotroph
091902 borrelia bu
083978 influenza a
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P8209 litorea cit
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rattus norv
                                                                          (without alignments)
73.003 Million cell updates/sec
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077900 oreochromis
077901 oreochromis
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS II B LOCUS 14 (FRAGMENT).
Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Cichlidae; Oreochromis.
                                                                                                                                                                                                                                                                                                                                 "Linkage relationships and haplotype polymorphism among cichlid Mhc class II B loci.";
                                                                                                                                                                                                                                                                               MEDLINE-98315113; PubMed-9649539;
Malaga-Trillo E., McAndrew B., Vincek V., Zaleska-Rutczynska Z.,
Sueltmann H., Fiqueroa F., Klein J.;
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Pred. No. 8.5e+02;
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EMBL; AF050012; AAC41351.1; -.
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EMBL; AF050013; AAC41352.1; -.
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                                                            Oreochrones inloticus (Nile Lilapia) (Tilapia nilotica).

Bukaryota, Metazoa, Chordta, Craniata, Vertebrata; Euteleostomi,

Actinopterygii, Neopterygii, Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii, Percomorpha; Perciformes; Labroidei;

Cichlidae; Oreochromis.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Cacthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
Cichlidae; Oreochromis.
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MEDIINE-98315113; PubMed-9649539;
Malaga-Trillo E., McAndrew B., Vincek V., Zaleska-Rutczynska Z.,
Sueltmann H., Figueroa F., Klein J.;
"Linkage relationships and haplotype polymorphism among cichlid Mhc
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MEDILINE-98315113; PubMed-9649539;
Malaga-Trillo E., McAndrew B., Vincek V., Zaleska-Rutczynska Z.,
Sueltmann H., Figueroa F., Klein J.;
"Linkage relationships and haplotype polymorphism among cichlid Mhc
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11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;
01-NOV-1998 (TrEMBLrel. 08, Created)
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS II B LOCUS 14 (FRAGMENT):
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MHC CLASS II B LOCUS 14 (FRAGMENT).
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Genetics 149:1527-1547(1998).
EMBL; AF050010; AAC41349.1; -.
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Genetics 149:1527-1547(1998).
EMBL; AF050011; AAC41350.1; -.
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
Cichlidae; Oreochromis.
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98315113; PubMed-9649539; Malaga-Trillo E., McAndrew B., Vincek V., Zaleska-Rutczynska Z., Suelfmann H., Figueroa F., Klein J.; Linkage relationships and haplotype polymorphism among cichlid Mhc class II B loci.
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS II B LOCUS 14 (FRAGMENT).
Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
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Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
Cichlidae; Oreochromis.
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS II B LOCUS (4 (FRAGMENT).
Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
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Genetics 149:1527-1547(1998).
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Genetics 149:1527-1547(1998).
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01-NOV-1998 (TrEMBLrel.
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NCBI_TaxID=8128;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS II B. LOCUS 14 (FRAGMENT).
Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
Guechromis metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Cichlidae; Oreochromis.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS II B LOCUS 14 (FRAGMENT).
Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Cichlidae; Oreochromis.
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-98315113; PubMed=9649539;
Malaga-Trillo E., McAndrew B., Vincek V., Zaleska-Rutczynska Z.,
Sueltmann H., Figueroa F., Klein J.;
"Linkage relationships and haplotype polymorphism among cichlid Mhc
class II B loci.";
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Genetics 149:1557-1547(1998).
EMBL; AF050015; AAC41354.1; -.
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MEDILNE-9831513; Pubmed-9649539;
MEDILNE-98315110 E., McAndrew B., Vincek V., Zaleska-Rutczynska Z.,
Sueltmann H., Figueroa F., Klein J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.1%; Score 22; DB 7; Length 11; 44.4%; Pred. No. 8.5e+02; Live 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;
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44.48;
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                                                                          PRELIMINARY;
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3 MTYRLSRCD 11
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SEQUENCE PROM N.A.

Caetano A.R., Shiue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
Bowling A.T., Murray J.D.;

"A comparative gene map of the horse (Equus caballus).";
Genome Res. 9:1239-1249(1999).

EMBL; AF134056; AAF31299.1; -.
                                                                                                                                                                                                                                                                                                                                                                             synthesized from cloned DNA in in the nucleus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
INFLUENZA A/UDORN/72 (H3N2), NUCLEOPROTEIN (SEG 5), 3' CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 21; DB 12; Length 10;
Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                  Influenza A virus.
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
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                            Indels
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Pred. No. 4.7e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 19; DB 6; Le
Pred. No. 2.7e+03;
3; Mismatches 2;
                                                                                                                                                    10 AA
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                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=A/UDORN/72 (H3N2);
MEDLINE=83112211; PubMed=6296449;
Lin B.C., Lai C.J.;
"The influenza virus nucleoprotein simian virus 40 vector is detected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Last an ALCOHOL DEHYDROGENASE 3 (FRAGMENT).
                                                                                                                                                    PRT;
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EMBL; J02171; AAA43469.1; -
NUCLEOPTOLEIN; Ribonucleoprotein.
NON_ET SEQUENCE 10 AA; 1173 MW; 87876
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37.5%;
            80.08;
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50.0%;
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Best Local Similarity 37.5
Matches 3; Conservative
                           Conservative
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           Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 3; Conserv
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4 NAEEYD 9
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MFC CLASS II B LOCUS 14 (FRAGMENT).
MFC CLASS II B LOCUS 14 (FRAGMENT).
Escudotropheus sp. 'Pseudotropheus tropheops complex'.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Acanthomorpha; Acanthopterygii; Teleostei; Euteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
NCBI_TaxID=51796;
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"Evidence of past recombination events among the genes encoding the Erp antigens of Borrelia burgdorferi.";
Microbiology 144:0-0(0).
EMBL; AF022480; AAC35445.1; -.
Plasmid. 8 8
SEQUENCE 8 AA; 985 MW; E8B41B41A735B446 CRC64;
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-98315113; PubMed=9649539;
Malaga-Trillo E., McAndrew B., Vincek V., Zaleska-Rutczynska Z.,
Sueltmann H., Figueroa F., Klein J.;
"Linkage relationships and haplotype polymorphism among cichlid Mhc
class II B loci.";
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01-MXY-2000 (TrEMBLrel. 13, Last sequence update)
01-MXY-2000 (TrEMBLrel. 13, Last annotation update)
PLASMID CP32-3, POSSIBLE PARTITION PROTEINS, COMPLET
Borrelia burgdorferi (Lyme disease spirochete).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spirochaetales; Spirochaetaceae; Borrelia
         Pred. No. 8.5e+02;
2; Mismatches 3;
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MEDLINE-98361033; PubMed-9695920;
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EMBL; AF050034; AAC41373.1; -.
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ilarity 44.4%;
Conservative
           44.48;
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11 AA; 1349 MW;
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        Best Local Similarity 44.4
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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                                                                 3 MTYRLSRCD 11
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3 MTYRLSRCD 11
                                                   1 LTYNTSQYD 9
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Q9R9C2;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wabnitz P.A., Bowie J.H., Tyler M.J.; "Caerulein-like peptides from the skin glands of the Australian blue montains tree frog Litoria citropa. Part 1. Sequence determination
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MEDLINE-98141813; PubMed=9473273;
Peale F.V., Mason K., Hunter A.W., Bothwell M.;
"Multiplex display polymerase chain reaction amplifies and resolves related sequences sharing a single moderately conserved domain.";
Anal. Biochem. 256:158-168(1998).
EMBL; U26148; AAC06186.1; -.
                                                                                                                                                                                                                                                                                                                                                                   Litoria citropa (Australian blue mountains tree frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia, Batrachia, Anura, Neobatrachia, Bufonoidea, Hylidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amphibian skin; Hypotensive agent; Amidation; Sulfatation.
MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
MOD_RES 4 4 SULFATATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19; DB 13; Length 11; Pred. No. 2.9e+03; 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMIDATION.
10DAB8867861A86B CRC64;
                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
CAERQLEIN 3.2/3.2Y4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=SKIN SECRETION;
MEDLINE=20057701; PubMed=10589099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            u1-AUG-1998 (TrEMBLrel. 07, Cr
01-AUG-1998 (TrEMBLrel. 07, La
01-NOV-1998 (TrEMBLrel. 08, La
ENGRAILED-3 (FRAGMENT).
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Best Local Similarity
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NCBI_TaxID=94770;
                           4 NTSQYDTY 11
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1 NTAQVEPW 8
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01-AUG-1998
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073588
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Search completed: February 21, 2002, 17:23:06 Job time: 180 sec

Mouse PAF receptor HLA binding peptid HLA binding peptid Arabidopsis thalia Antigenic site of

Claudin-2 cyclic c Potato patatin pro HOX7, a hexose oxi S. peregrina cyste Cladosporium herba Peanut Ara h 2 mou Mouse immunoglobul

Mealworm encapsula

Mouse immunoglobul IgE binding epitop Mouse IgE epitope C. histolyticum CH

Immunogenic peptid HER2/NEU DR 3a mot

Dopamine receptor

Leukocyte adhesion Prostate specific Oligopeptide 36 cl

Total number of

Searched:

Minimum DB Maximum DB

Database

score:

Perfect

Sequence:

OM protein

Run on:

Scoring table:

Leukocyte adhesion Ara h 2 linear IqE Human Leukocyte An Potato patatin pro

Urokinase-type

Human urokinase-ty

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Cell adhesion molecule; CD44; antiinflammatory; rheumatoid; arthritis; tumor cell metastasis; autoimmune disease;
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AAW19636
AAW15949
                                          AAB06537
AAB83062
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AAW20074
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AAR89619
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AAB27534
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AAU06346
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AAW74276
                          AAG83833
                                   AAW97549
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                                                                                                                                                                                                                                                                                                                                                                 AAR53486 standard; peptide; 11 AA
 93WO-US10412
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                                                                                                                                                                                                                                                                                                                                                                                                                      CD44 peptide CD44-13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunosuppressive.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-OCT-1993;
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AAR53486;
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 RESULT
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34.351 Million cell updates/sec
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                                                           February 21, 2002, 17:16:50; Search time 23.72 Seconds
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                                                                                                                                                                                                                                                                                  /SIDS8/gcgdata/geneseqy/geneseqp/AA1982.DAT:*
/SIDS8/gcgdata/geneseqy/geneseqp/AA1983.DAT:*
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        GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                            hits satisfying chosen parameters:
                                                                                                                                                          522463 seqs, 74073290 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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61
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Match Length
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Non-covalently int Interleukin-1 type

Peptide of the spe

Interleukin-1 type HJ loop peptide Kl

Use of CD44 protein and new peptide derivs - for developing prods for inflammation, immune-mediated tissue damage and tumour cell metastasis Telen MJ; Patton KL, Liao H, Hale LP, Haynes BF, WPI; 1994-167121/20.

Interleukin-1 type Peptide binding in Interleukin-1 type IL-1 antagonist pe

AAW68880 AAY10049 AAB17876

Human immunoglobul Light chain CDR3 p Amino acid sequenc

AAG88313 AAW24776 AAW80146 AAY40428 AAW15948

100.0 45.9 44.3 42.6 42.6 42.6 42.6 42.6 42.6

61 28 27 26 26 26 26 26 26 26

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Saccharomyces cere HER2/NEU DR superm CD44 peptide CD44-Determinant site o

AAR53486 AAP50473

Score

Result Š.

15: 17: 18: 20:

AAG85437

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cerevisiae; complementary peptide; peptide identification;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to the identification of complementary peptides by analysis of protein and nucleotide sequence databases from higher eukaryotic genomes, excluding human and plants. The specific complementary peptides interact with their relevant target proteins encoded in the eukaryote genome. The peptides may be used as reagents and drugs for drug discovery and as lead ligands for drug design and development. The present sequence is a complementary peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying complementary peptides by analysis of protein and nucleotide sequence databases, useful in drug design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HER2/NEU DR supermotif binding peptide core sequence #13.
                                                                                      Saccharomyces cerevisiae peptide, SEQ ID NO: 386
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 83; 488pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.38;
57.18;
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                                                                                                                                      drug discovery; drug design
                                                   11-SEP-2001 (first entry)
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                     Saccharomyces
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Synthetic.
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                   AAG85437;
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                                                                                                                                                                                                                                       Gaps
                                                          diseases, e.g. rheumatoid arthritis. It can also be used for determining metastatic potential or to treat or prevent tumor cell metastasis. This peptide corresponds to AA 107-117 of the CD44 protein sequence.
                                                mediated tissue damage such as occurs in the course of autoimmune diseases, e.g. rheumatoid arthritis. It can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The synthetic peptide sequence is useful as an antigen in the production of vaccines, antiviral agents, diagnostic reagents, e for the detection and therapy of infectious and immune diseases.
                                                                                                                                                                                                                                     0;
                                  peptide can be used for treating inflammation and immune-
                                                                                                                                                                                                    Length 11;
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Pred. No. 6.7e-05;
0; Mismatches 0;
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59;
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55.6%; Pred. No.
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Claim 4; Page 14; 83pp; English.
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100.0%;
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Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
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Gaps

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1; Indels

22; Length 10;

17-APR-1997.

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candipleur; (4) an isolated nucleic acid encoding a perture compitation, (5) and (5) an isolated nucleic acid encoding (11). (1) has cytostatic and immunostimulant activities, and can be used in vaccines. (1), (11) are useful for inducing cellular immune responses for the prevention and treatment of cancer. (1) and (11) are useful for monitoring or evaluating an immune response to a tumour-associated antigen when incubated with a T lymphocyte to (1) or (11). Epitope based vaccines mean that immunosuppressive epitopes that may be present in whole antigens may be avoided. Selected epitopes may be combined to enhance immunogenicity. The possible pathological side effects caused by infectious agents or whole protein antigen is eliminated. The vaccine provides the ability to direct and focus an immune response to multiple provides the ability to direct and focus an immune response to multiple selected antigens from the same pathogen. Epitope-based anti-tumour vaccines provides the opportunity to combine epitopes derived from the same pathogen. Epitope-based anti-tumour vaccines provides the opportunity to combine epitopes derived from the same pathogen. Epitope-based provides the ability to direct and focus and immune response to multiple tumour-associated molecules addressing the problem of frumour-associated molecules addressing the problem of tumour-associated molecules address
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes isolated prepared HER2/neu epitopes (I). Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is culture in vitro and binds to a complex of an epitope (I), bound to human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I) and a second epitope and the peptide is less than 50 contiguous amino acids that have 100% identity with a native peptide sequence of HER2/neu; (3) a vaccine composition (II) comprising (II) and a pharmaceutical excipient; (4) an isolated nucleic acid encoding a peptide comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ņ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumour variability and reducing the likelihood of tumour escape due to antigen loss. AAG88266 to AAG89121 represent amino acid sequences used the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                       An isolated prepared \ensuremath{\mathsf{HER2}}\xspace/\ensuremath{\mathsf{her}}\xspace/\ensuremath{\mathsf{her}}\xspace for the prevention and treatment of cancer-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig; affinity constant; human; antigen; hybridoma; B cell; transgene; transgenic; mouse; CD4; antibody; autoimmune; inflammatory;
                                                                                                                                                                            Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 26.5; DB 22; Length 9;
Pred. No. 4.3e+05;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunoglobulin light chain CDR3 region peptide.
                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 166; 199pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW24776 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.5%;
11-DEC-2000; 2000WO-US33591
                                                      99US-0458299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 43.4
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transplant rejection.
                                                                                                                   (EPIM-) EPIMMUNE INC.
                                                                                                                                                                                                                                                              WPI; 2001-374995/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LTYNTSQYDTY 11
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2 vtynt---dtf 9
                                                         10-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9713852-A1
                                                                                                                                                                         Fikes J,
Keogh E;
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A novel composition has been developed which comprises an immunoglobulin (Ig) having an affinity constant (Ka) of at least 2 multiply 10000000000 M-1 for binding to a predetermined human antigen. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complementarity determining region; CDR3; transgenic non-human animal; human heterologous antibody; heavy chain; light chain transgene; neutrophil efflux; reperfusion injury; CD4 binding; autoimmune reaction; inflammatory response; transplant rejection; acid induced lung injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              of multiple isotypes by undergoing isotype switching. These animals produce a first Ig type that is necessary for antigen-stimulated B-cell maturation and can switch to encode and produce one or more subsequent
                                                                                                                                                                                                                                                                                                                          present sequence represents a human light chain CDR3 region peptide which forms part of an immunoglobulin comprising a Vkil5 segment, and the present light chain CDR3 region. The anti-CD4 antibodies may be used in therapeutic and diagnostic applications, especially for the treatment of human diseases. These antibodies reduce activity of CD4 cells and reduce undesirable autoimmune reactions, inflammatory response and transplant rejection. Transpenic animals are capable of producing heterologous antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                              Novel anti-CD4 antibody produced by transgenic mice - used in the treatment of auto-immune disease etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acute adult respiratory distress syndrome, ARDS; vasculitis; septic shock; allergic reaction; asthma; cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 26; DB 18;
Pred. No. 4.3e+05;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Light chain CDR3 peptide from clone 4D1.
                                                                                                                                                                                                                                               Claim 60; Page 287; 396pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW80146 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.6%;
80.0%;
                              96WO-US16433
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                                                             95US-0544404
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Chimeric - Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 heterologous isotypes.
                                                                                               (GENP-) GENPHARM INT
                                                                                                                               Kay RM, Lonberg N;
                                                                                                                                                            WPI; 1997-235888/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 QYDTY 11
                              10-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 qydsy 6
                                                             10-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW80146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db
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Ball WJ;

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The specification describes transgenic animals that are capable of producing a heterologous antibody. The antibodies are isolated form a hybridoma, comprising B cells, that is obtained from a transgenic mouse having a genome comprising a human heavy chain transgene and a human light chain transgene. The B cells are fused to immortalized cells
                                                                                                                                                                                                                                                                                                   suitable for generating a hybridoma, which produces a detectable amount of an immunoglobulin that specifically binds digoxin or Shinga-like toxin. B cells from transgenic animals can be used to apenerate hybridomas expressing monoclonal high affinity human sequence antibodies. Antibodies produced from the transgenic animals of the invention can be used to treat human diseases, e.g. autoimmune diseases, cancer, infectious disease, transplant rejection, blood disorders such as coagulation disorders and other diseases. The present sequence represents a VDJ joint of a heterologous antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interleukin-1 type I receptor inhibitor peptide(s) and compounds - used to antagonise the activity of IL-1, for treatment of e.g. AIDS, rheumatoid arthritis, chronic hepatitis B, etc.
                                                                                                                        Novel transgenic non-human animals used to produce heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interleukin-1 type I receptor binding peptide.
                                                                                                                                                                            Example 41; Page 307; 484pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barrett RW, Bovy PR,
Leahy EM, Pottorf RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW15948 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AFFY-) AFFYMAX TECHNOLOGIES NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IL-1RtI; agonist; antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-US09835.
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                                                    Fishwild DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
                  (GENP-) GENPHARM INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-042846/04.
                                                                                       WPI; 1999-551219/46.
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 QYDTY 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUN-1995;
                                                    Lonberg N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baldwin D,
Jacobs JW,
                                                                                                                                           antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a light chain complementarity
determining region (CDR) 3 peptide. It is part of the antibody of
the invention. The specification describes transgenic non-human
animals, especially a mouse, which are capable of producing a human
heterologous antibodies of multiple isotypes by undergoing isotype
switching. The transgenes are capable of functionally rearranging a
transgenes. The transgenes are capable of functionally rearranging a
heterologous diversity (D) gene in a variable-diversity-junction (V-D-J)
recombination. The transgenes include a heavy chain transgene comprising
at least one V D and J gene segment, and one constant region gene
segment. The immunoglobulin (Ig) light chain transgene comprises at least
one V and J gene segment and one constant region gene segment. The gene
segments are heterologous to the transgenic animal. The antibody can be
used to prevent efflux of neutrophils from vasculature. It can also be
used to treat reperfusion injury. Ob binding antibodies are used to
reduce undesirable autoimmune reactions inflammatory responses and
rejection of transplanted organs. The anti-IL-8 antibodies can reduce
tissue damage and prolong survival in animal models of acute adult
respiratory distress syndrome (ARDS) and acid induced lung injury. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 septic shock, allergic reactions (e.g. asthma) and cystic fibrosis. note: mouse and human parts of the sequence are not defined in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transgenic mouse; human heavy chain transgene; digoxin; human light chain transgene; immortalized cell; immunoglobulin; Shinga-like toxin; autoimmune disease; cancer; infectious disease; transglant rejection; blood disorder; coagulation disorder.
                                                                                                          - used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of the VDJ joint of a heterologous antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transgenic animal; heterologous antibody; hybridoma; B cell;
                                                                                                      Hybridoma producing antibody specific for interleukin-8 - prevent efflux of neutrophils from vasculature, and treat reperfusion injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.6%; Score 26; DB 19; Length 9; 80.0%; Pred. No. 4.3e+05; Live 1; Mismatches 0; Indels
                                                                                                                                                                            Example 41; Page 306; 452pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY40428 standard; Peptide; 9 AA.
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(GENP-) GENPHARM INT.
                                                                    WPI; 1998-333306/29
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Matches 4; Conserv
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2 qydsy 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY40428;
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                                   Kay RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY40428
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Gaps

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Score 26; DB 20; Length 9; Pred. No. 4.3e+05; 1; Mismatches 0; Indels

42.6%; 80.0%;

1; Mismatches

Dharanipragada R; Tomlinson RC, Yanofsky SD;

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                                                                             The patent discloses, inter alia, new peptides of 11-40 amino acids in length which bind to the IL-1 type I receptor and which comprise the generic sequence 223-N-224-239-225-225-227-228-229-230-240, in which 223 is D or Y; 224 is D, S or T; 239 is S, T or A; 225 is S or Y; 224 is D, Q. E or V; 238 is N, S, K, H or W; 229 is F or L; 230 is D, N, S or L; and 240 is L, I, Q, M or A. These peptides may be used in the treatment of a variety of IL-1 related disorders including atherosclerosis, renumatoid arthritis, osteoporosis, HIV infection and AIDS, bacterial infection, respiratory distress syndrome, acute myelogenous leukeemia, graft versus host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease, coal miner pneumoconiosis, alcoholic cirrhosis, cuprophane haemodialysis, cardiopulmonary bypass, chronic hepatitis B, tuberculosis, obstructive jaundice, Paget's disease and osteomalacia, IDDM, Kawasaki's disease, inflammatory bowel disease, sepsis, toxic shock and luteal phase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a specifically claimed example of the new peptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antagonist; interleukin-1; IL-1; IL-1 type I receptor; IL-1RtI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.6%; Score 26; DB 18; Length 11; 50.0%; Pred. No. 1.3e+02; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jacobs JW, Leahy EM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide binding interleukin-1 type I receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Columns 159-160; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AFFY-) AFFYMAX TECHNOLOGIES NV. (HMRI ) HOECHST MARION ROUSSEL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovy PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA.
Claim 17; Page 70; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW68880 standard; peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0465391.
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Yanofsky SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treatment; IL-1 disorder
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Best Local Similarity
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2 nsswydsf 9
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01-FEB-1995;
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Pottorf RS,
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The invention relates to new peptides which which bind to the interleukin-1 type I receptor (IL-IRtI). These include 'lead' peptides identified using random peptide diversity generating systems (e.g. 'peptides on phage' and 'peptides on plasmids' systems) and derivatives of the 'lead' peptides which have a similar structure or shape as the lead compounds but which differ with respect to susceptibility to hydrolysis or proteolysis and/or with respect to biological properties. In particular, peptides are claimed which are 11,to 40 amino acids in length, which bind to the IL-IRtI with an IC50 standard of no more than 2.5 mM and which comprise the sequence: 223-124-225-225-227-228-229-230-240 where: 233 is Dor Y: 224 is D, Os E or V: 228 is N, S, K, H or W: 229 is F or L: 230 is D, N, S or L; and 240 is L, I, Q, M or A.
IL-1, e.g. atherosclerosis, arthritis, osteoporosis, AIDS, bacterial infections, respiratory distress syndrome, acute myelogenous leukaemia, graft-versus-host disease, pneumoconiosis, cirrhosis, cuprophane haemodialysis, cardiopulmonary bypass, hepatitis B, thermal injury, reticulohisticoytosis, sarcoidosis, tuberculosis, obstructive jaundice, Paget's disease, osteomalacia, diabetes, Kawasaki's disease, inflammatory bowel disease, sepsis, toxic shock and luteal phase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interleukin-1 type I receptor; IL-1RtI; inflammatory bowel disease; rheumatoid arthritis; osteoarthritis; psoriasis; encephalitis; glomerulonephritis; respiratory distress syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                              Score 26; DB 19; Length 11;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interleukin-1 type I receptor binding peptide #370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                          42.6%;
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Best Local Similarity 50.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                               11 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-ri-(X2)b, where F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L1)c-P1-(L2)d-P2.
-(L3)c-P2-(L3)d-P2.(L3)e-P3. or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3
                                                                                                                                                                                                                                                                                                                        Gaps
These peptides are useful as agonists/antagonists for the study of IL-IRtI mediated activities (e.g. as labels and probes), for the identification of new IL-1 receptor blockers, and for the identification, diagnosis and treatment/prevention of diseases with
                                                                                 an inappropriate production or response to 11-1, e.g. rheumatoid arthritis, osteoarthritis, psoriasis, inflammatory bowel disease, encephalitis, glomerulonephritis, and respiratory distress syndrome. The present sequence is a specifically claimed example of the above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoictin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                        ó;
                                                                                                                                                                                                                                                                              Length 11;
                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                           Score 26; DB 20;
Pred. No. 1.3e+02;
3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IL-1 antagonist peptide sequence SEQ ID NO:980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Page 538; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB17876 standard; Peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                           42.6%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0105371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                    4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune diseases
                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                               11 AA;
                                                                                                                                                                                                                                                                                                                                                             4 NTSQYDTY 11
                                                                                                                                                                                                                                                                                                                                                                                                   nsswydsf 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200024782-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB17876;
                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                  Matches
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                                           useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
activities. DNAs, vectors and host cells from the present invention can
                         be used for producing pharmaceutical compositions. The compositions are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the complementarity determining region (CDR) 3 of the light chain hypervariable region of an antibody recognising the platelet activating factor (PAF) receptor. The variable region of mouse anti-PAF receptor monoclonal antibody is useful for the preparation of chimeric antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin light chain; hypervariable region; PAF; CDR; antibody; platelet activating factor receptor; murine; chimeric; anti-PAF; complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polypeptide comprising variable region of antibody recognising PAF receptor - useful for the preparation of chimeric antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse PAF receptor antibody light chain hypervariable region CDR3
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                                                                                                                                                                                                                                                                                                      Score 26; DB 21; Length 11; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 9;
                                                                                                                                                                                                                                                                                                                                                        1; Indels
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Pred. No. 4.3e+05;
                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW59175 standard; Protein; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 10; 14pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SUME ) SUMITOMO ELECTRIC IND
                                                                                                                                                                                                                                                                                                    42.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.0%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                          4; Conservative
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                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                              11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         4 NTSQYDTY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 nsswydsf 9
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2 qynty
                                                                                                                                                                                                                                 Seguence
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                                                                                                                                                                                                                                                                                                         Query Match
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AAW59175
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AAY07198;

AAY07198

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The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically biological sample isolated from product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions. Characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                  Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.0%; Score 25; DB 20; Length 10; 57.1%; Pred. No. 1.8e+02; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen Y, Gout I, Gure A, O'Hare M, Obata Y, Old Pfreundschuh M, Sahin U, Scanlan MJ, Stockert E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 16; Page 760; 787pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG83833 standard; Peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LUDW-) LUDWIG INST CANCER RES
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97US-0061599.
97US-0061765.
97US-0948705.
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                                    (first entry)
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                                                                          HLA binding peptide.
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                                                                                                                                                                 prostate cancer.
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                                                                                                                                                                                                                                                                                                                                                                                       17-JUL-1997;
10-OCT-1997;
10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                             WO9904265-A2
                                    02-JUL-1999
                                                                                                                                                                                                                                                                                                                              15-JUL-1998;
                                                                                                                                                                                                                                                                                     28-JAN-1999.
                                                                                                                                                                                                                                                                                                                                                                      22-JUN-1998
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AAY07153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic and sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, remal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                                Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products {\bf x}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 25; DB 20; Length 10;
Pred. No. 1.8e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Obata Y, Old LJ; , Stockert E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for the diagnosis, monitoring or treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O'Hare M, O'
Scanlan MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 16; Page 767; 787pp; English.
                AAY07198 standard; Peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0102322.
97US-0896164.
97US-0061599.
97US-0948705.
97GB-0021697.
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                                                                                                                                                                                                                                                                                                                                                                                       98WO-US14679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen Y, Gout I, Gure A,
Pfreundschuh M, Sahin U,
                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-132448/11.
                                                                                                                                     HLA binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10 AA;
                                                                                                                                                                                                                          prostate cancer.
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3 ynxtgyd
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                                                                                               02-JUL-1999
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Gaps

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11-SEP-2001 (first entry)

AAY07153 standard; Peptide; 10 AA.

RESULT 14

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AAY07153 ID AAY0 XX

Matches

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The present invention relates to a set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of plant genomes. The present sequence is one such peptide from Arabidopsis thaliana. The peptides of the present invention are useful in an assay to identify a peptide, especially a peptide pesticide or herbicide. The peptides are also useful for tools for agricultural research and
                                                                                                                                                                                                                                                                                                                       A set of peptide ligands for agricultural research and development of therapeutic agents comprise specific complementary peptides to proteins encoded by genes of plant genomes .
                                            Plant; peptide pesticide; peptide herbicide; agricultural research.
            Arabidopsis thaliana peptide ligand #473.
                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Page 97; 201pp; English.
                                                                                                                                                                     13-DEC-2000; 2000WO-GB04781.
                                                                                                                                                                                                 13-DEC-1999; 99GB-0029469
                                                                                                                                                                                                                                                              Roberts GW, Heal JR;
                                                                         Arabidopsis thaliana
                                                                                                                                                                                                                               (PROT-) PROTEOM LTD.
                                                                                                                                                                                                                                                                                           WPI; 2001-381629/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 AA;
                                                                                                       WO200142279-A2.
                                                                                                                                     14-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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Search completed: February 21, 2002, 17:20:02 Job time: 192 sec

0;

Gaps

ó:

Query Match
41.0%; Score 25; DB 22; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 3; Indels

1 LTYNTSQYDT 10 |||:|: | 1 ltysttddst 10

QY Dp

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Sequence 564, App
Sequence 602, Appl
Sequence 1, Appl 1
Sequence 1421, Ap
Sequence 1997, Ap
Sequence 3140, Ap
Sequence 2197, Appl
Sequence 2191, Appl
Sequence 216, Appl
Sequence 216, Appl
                                                                                                                                                                                                                                                                                                                  Sequence 216, App
Sequence 280, App
Sequence 280, App
Sequence 280, App
Sequence 280, App
Sequence 28, App
Sequence 126, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/973,339
FILING DATE: 19921030
US-09-793-451-152
US-09-793-411-248
US-09-793-411-602
US-09-793-411-607
US-09-793-411-607
US-09-458-299-1421
US-09-458-299-1421
US-09-458-299-1397
US-09-458-299-1397
US-09-458-299-1253
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US-09-458-299-12191
US-09-458-299-1046
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US-09-458-299-1913
US-09-458-299-1913
US-09-458-299-1913
US-09-458-299-1913
US-09-458-299-1913
US-08-728-4638-216
US-08-728-463-216
US-08-728-463-216
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US-09-751-181-28
US-09-751-181-28
US-09-185-908-126
US-09-434-355-126
US-09-434-355-126
US-09-438-299-517
US-09-458-299-517
US-09-458-299-561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: HALE, LAURA P.
APPLICANT: HALE, LAURA P.
APPLICANT: PATTON, KAREN L.
TITLE OF INVENTION: AN ADHESION MOLECULE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/07973339 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: WEST AR., WILLIAM K.
REGISTRATION NUMBER: 2057
REFERENCE/DOCKET NUMBER: 954:
TELECHONE: 202-661-3000
TELEPHONE: 202-6944
    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D.C.
: U.S.A.
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: WAS
STATE: D.
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
US-07-973-339-14
 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Appl
Sequence 14, Appl
Sequence 16, Appl
Sequence 14, Appl
Sequence 800, App
Sequence 1422, Ap
Sequence 1422, Ap
Sequence 1998, Ap
                                                                                            February 21, 2002, 17:19:20 ; Search time 90:49 Seconds (without alignments) 33.752 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                Pending_Patents_AA_Main:*

1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/USOG_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
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7: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
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17: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
18: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
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                4.5
Compugen Ltd
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US-08-04-068-16
US-08-143-311A-14
US-08-753-851-16
US-08-959-784-14
US-09-458-299-1800
US-09-458-299-1828
US-09-458-299-1938
US-09-458-299-1399
                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                       3148936 seqs, 277657034 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
             GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                           Maximum Match 100%
Listing first 45 summaries
                                                                           protein - protein search, using sw model
                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                               US-08-753-851-16
61
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                                                                                                                                                                                             1 LTYNTSQYDTY 11
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length: 11
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Match
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100.0
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100.0
47.5
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229 229 229 229

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Result Š.

Minimum DB seq Maximum DB seq

Database

Perfect score:

Run on:

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Scoring table: Sequence:

Searched:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                    APPLICANT: HALE, LAURA P.
APPLICANT: PATTON, KAREN L.
APPLICANT: TELEN, MARLIYN J.
APPLICANT: LIAO, HUA-XIN
TITLE OF INVENTON: AN ADHESION MOLECULE
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: WEINBERG, J. BRICE
APPLICANT: HAYNES, BARTON F.
TITLE OF INVENTION: AN ADHESION MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/143,311A FILING DATE: 29-OCT-1993
                                                                                                                                                                                                                                                                                                                                                    E: NIXON & VANDERHYE P.C. 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                             Sequence 14, Application US/08143311A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 436
APPLICATION NUMBER: 07/669,730
FILING DATE: 15-8-1991
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,339
FILING DATE: 30-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
US-08-753-851-16
Sequence 16, Application US/08753851
CENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGIETRATION NUMBER: 32,955
REFRENCE/CDCKET NUMBER: 1579
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                         HAYNES, BARTON F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 703-810-400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 200797 NIXN UR INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                             1 LTYNTSQYDTY 11
        1 LTYNTSQYDTY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LTYNTSQYDTY 11
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                         CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                    VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                             В
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                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                        100.0%; Score 61; DB 3; Length 11; 100.0%; Pred. No. 0.00046;
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100.0%; Score 61; DB 4; Length 11;
Best Woocal Similarity 100.0%; Pred. No. 0.00046;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/047,068

FILING DATE: 16-APR-1993

CLASSIFICATION: 424

PRIOR APPLICATION NUMBER: US 07/945,581

FILING DATE: 16-SEP-1992

PRIOR APPLICATION NUMBER: US 07/682,518

FILING DATE: 05-APR-1991

PRIOR APPLICATION NUMBER: US 07/682,518

FILING DATE: 05-APR-1991

PRIOR APPLICATION NUMBER: US 07/669,730

FILING DATE: 15-ABR-1991

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/08047068
GENERAL INFORMATION:
APPLICANT: WEINBERG, J. BRICE
APPLICANT: HAYNES, BARTON F.
TITLE OF INVENTION: AN ADHESION MOLECULE
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NNRTH GLEBE ROAD, 8TH FLOOR
                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (703) 816-4100
TELERAX: (703) 816-4100
TELERX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 11; Conservative
                                                              TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-973-339-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                              1 LIYNISQXDIY 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
US-08-047-068-16
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                                                                                                                                                                                                        Query Match
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TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO TITLE OF INVENTION: HER2/neu USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS FILE REFERENCE: 018623-014800US CURRENT APPLICATION NUMBER: 02/99/458,299 CURRENT FILING DATE: 2001-09-17
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                                                          SOFTWARE PATENTIAN STATES SOFTWARE SOFTWARE PATENTIAN DATA:
APPLICATION NUMBER: US/08/959,784
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/143,311
FILING DATE: 29-0CT-1993
APPLICATION NUMBER: 07/973,339
FILING DATE: 30-0CT-1992
APPLICATION NUMBER: 07/669,730
FILING DATE: 15-MAR-1991
ATTOMEX/AGENT IRFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 61; DB 13; 100.0%; Pred. No. 0.00046;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR PILING DATE: 1993-06-04
PRIOR PILING DATE: 1993-06-04
PRIOR PILING DATE: 1993-05-05
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NUMBER OF SEQ ID NOS: 4570
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 800
                                                                                                                                                                                                                                                                                                    NAME: WILSON, MARY J.
REISTRATION NUMBER: 32,955
RESPERENCE/POCKET NUMBER: 1579-50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 800, Application US/09458299 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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Sette, Alessandro
Sidney, John
Southwood, Scott
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ORGANISM: Artificial Sequence
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Celis, Esteban
Keogh, Elissa
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: peptide US-08-959-784-14
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STRANDEDNESS: si
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APPLICANT:
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                                                                                                                                                                              SOFTWARE: Patentin PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
FILING DATE:
CLASSTORM DATE:
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GENERAL INFORMATION:
APPLICANT: HAYNES, BARTON F.
APPLICANT: HALE, LAURA P.
APPLICANT: TELEN, MARLIXN J.
APPLICANT: LIAO, HUA-XIN
TILLE OF INVENTION: AN ADHESION MOLECULE
NUMBER OF SEQUENCES: 28
                                         E: NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD, 8TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/047,068
FILING DATE: 16-APR-1993
APPLICATION NUMBER: US 07/945,581
FILING DATE: 16-SEP-1992
PRIOR APPLICATION NUMBER: US 07/682,518
FILING DATE: 09-APR-1991
PRIOR APPLICATION NUMBER: US 07/669,730
APPLICATION NUMBER: US 07/669,730
APPLICATION NUMBER: US 07/669,730
FILING DATE: 15-WAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32,955
FR: 1579-21
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ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                            NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 11; Conservative
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  NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22201-4714
COMPUTER READABLE FORM:
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                                                                                 CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                        U.S.A.
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                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                         ADDRESSEE:
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US-08-959-784-14
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Gaps

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TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO TITLE OF INVENTION: HER2/neu USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 29; DB 18; Length 11;
Pred. No. 2.5e+02;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Artificially Synthesized Peptide US-09-458-299-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-09-458-299-1399
                                          TILE REFERENCE: 018623-014800US
CURRENT APPLICATION NUMBER: US/09/458,299
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1994-11-10
PRIOR FILING DATE: 1994-03-04
PRIOR PILING DATE: 1994-03-04
PRIOR PILING DATE: 1994-03-04
PRIOR FILING DATE: 1993-06-04
PRIOR FILING DATE: 1993-06-04
PRIOR FILING DATE: 1993-06-04
PRIOR FILING DATE: 1993-06-04
PRIOR PILING DATE: 1993-06-04
PRIOR FILING DATE: 1993-06-05
NUMBER OF SEQ ID NOS: 4570
SOFTWARE: FESTERE OF WINDOWS VERSION 4.0
SEQ ID NO 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/458,299
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1994-03-04
PRIOR PILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR FILING DATE: 1993-06-04
PRIOR FILING DATE: 1993-06-04
PRIOR PLILNG DATE: 1993-03-05
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1399, Application US/09458299 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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Sette, Alessandro
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Best Local Similarity 40.0
کید 4; Conservative
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APPLICANT: Celis, Esteban
APPLICANT: Keogh, Elissa
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1 VTYNTDTFES 10
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                                                                                                                                                            Gaps
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                                                                                                           Score 29; DB 18; Length 11;
Pred. No. 2.5e+02;
4; Mismatches 2; Indels
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; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-09-458-299-800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Artificially Synthesized Peptide US-09-458-299-1422
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Pred. No. 2.5e+02;
4; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1994-03-04
PRIOR PRIOR DATE: 1994-03-04
PRIOR PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR PRILING DATE: 1993-06-04
PRIOR FILING DATE: 1993-06-04
PRIOR FILING DATE: 1993-06-04
PRIOR FILING DATE: 1993-03-05
NUMBER OF SEQ ID NOS: 4570
SEQ ID NO 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/458,299 CURRENT FILING DATE: 2001-09-17
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                                                                                                             47.5%;
40.0%;
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Sette, Alessandro
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Sette, Alessandro
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Chesnut, Robert
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Chesnut, Robert
Celis, Esteban
Keogh, Elissa
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APPLICANT: Keogh, Elissa
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Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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1 VTYNTDTFES 10
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1 VTYNTDTFES 10
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT: Daniel E.H. Afar
APPLICANT: Cazelle S. Rastegar
APPLICANT: Gazelle S. Rastegar
APPLICANT: Gazelle S. Habert
APPLICANT: Rene S. Hubert
APPLICANT: Rene S. Hubert
APPLICANT: Hary Faris
APPLICANT: Hary Faris
APPLICANT: Hary Faris
APPLICANT: Mary Paris
APPLICANT: Mary Baris
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APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
FILE REFERENCE: 129.2USU2
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 60/184,558
PRIOR APPLICATION NUMBER: 60/184,558
PRIOR APPLICATION NUMBER: 60/218,856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 9;
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83.3%; Pred. No. 2.9e+06;
                                                                                                                                                                                              Score 27; DB 21;
Pred. No. 2.9e+06;
0; Mismatches 1
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APPLICANT: Gazelle S. Rastegar
APPLICANT: Steve Chappell Mitchell
APPLICANT: Rene S. Hubert
APPLICANT: Pla M. Challita-Eid
APPLICANT: Mary Faris
TITHE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 564, Application US/09793451; GENERAL INFORMATION:
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; GENERAL INFORMATION:
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Best Local Similarity 83.3°
""hea 5; Conservative
                                                                                                                                                                                                                                                                         Conservative
   ; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-248
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ORGANISM: homo sapiens
US-09-793-451-564
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Best Local Similarity
..... 5; Conserva
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2 THQYDT 7
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Sequence 2. **Ji . 440

Sequence 3. **Sequence 3
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APPLICANT: Gazelle S. Rastegar
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
APPLICANT: Rene S. Hubert
APPLICANT: Pia M. Challita-Eid
APPLICANT: Mary Faris
APPLICANT: May Faris
TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
FILE REFERENCE: 129-20802
TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
FILE REFERENCE: 129-20802
CURRENT APPLICATION NUMBER: US/09/793,451
CURRENT FILING DATE: 2001-02-26
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 752
SOFTWARE: FastSEQ for Windows Version 4.0
   Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 9;
                                                                           Indels
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Score 28; DB 18;
Pred. No. 3.4e+02;
3; Mismatches 2.
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Pred. No. 2.9e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 248
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 152, Application US/09793451
GENERAL INFORMATION:
APPLICANT: Arthur B. Raitano
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                                       44.48;
   Query Match 45.9
Best Local Similarity 44.4
Matches 4; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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; ORGANISM: homo sapiens
US-09-793-451-152
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1 TYNTDTFES 9
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4 THQYDT 9
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Search completed: February 21, 2002, 17:22:18 Job time: 178 sec
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TITE OF INVENTION: INDOCING CELLULAR IMMUNE RESPONSES TO
TITLE OF INVENTION: HERZ/neu USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 018623-014800018
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APPLICANT: MAY FAILS
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
FILE REFERENCE: 129.2USU2
CURRENT APPLICATION NUMBER: US/09/793.451
CURRENT FILING DATE: 2000-02-24
PRIOR PAPLICATION NUMBER: 60/184,558
PRIOR FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 752
SOFTWARE FELING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 752
SOFTWARE FELING DATE: PASLEC FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                Score 27; DB 21; Length 10;
Pred. No. 5.1e+02;
0; Mismatches 1; Indels
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Pred. No. 5.1e+02;
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PRIOR FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 752
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 602
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Daniel E.H. Afar
Gazelle S. Rastegar
Steve Chappell Mitchell
Rene S. Hubert
Pia M. Challita-Eid
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 607, Application US/09793451
GENERAL INFORMATION:
APPLICANT: Arthur B. Raitano
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Sette, Alessandro
Sidney, John
Southwood, Scott
Chesnut, Robert
Celis, Esteban
Keogh, Elissa
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                                                                                                                                                                                                Query Match 44.3
Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                 ; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-602
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; ORGANISM: homo sapiens
US-09-793-451-607
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3 THQYDT 8
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.4%; Score 26.5; DB 18;
illarity 54.5%; Pred. No. 2.9e+06;
Conservative 2; Mismatches 0;
CURRENT APPLICATION NUMBER: US/09/458,299
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR FILING DATE: 1993-11-29
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR APPLICATION NUMBER: US 08/077,146
                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 4570
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence FEATURE:
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Best Local Similarity
Matches 6; Conserv
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1 VTYNT---DTF 8
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Sequence 14, Appl Sequence 730, App Sequence 957, App Sequence 951, App Sequence 8, Appli Sequence 1, Appli Sequence 383, App Sequence 1839, App

US-09-572-270B-471 US-09-692-170B-4 US-09-692-170B-4 US-09-692-170B-14 US-09-572-270B-730 US-09-572-270B-730 US-09-572-404B-951 US-09-572-404B-951 US-09-572-404B-2585 US-09-458-302A-88 US-09-458-302A-1390 US-09-667-365-139 US-09-667-365-140

Sequence 138, Sequence 139,

Sequence Sequence

Sequence

US-09-667-365-141 US-09-667-365-572

ALIGNMENTS

3, Appli 4, Appli

Sequence

Seguence Sequence Sequence

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Sequence 216, Application US/09724965
Sequence 216, Application US/09724965
GENERAL INFORMATION:
GENERAL INFORMATION:
Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CUKRENT APPLICATION DATA:

PAPLICATION INDRER: US, 09/724,965
FILING DATE: 28-Nov-2000
CLASSIFECATION: CURNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/32,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/32,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/095,3131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: US 07/904,068
                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 417
                                                                                                                                                                                                                                                                                                                                          US-09-724-965-216
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4, Appl
7, Appl
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2605, Ap
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156, App
                                                                                                        (without alignments)
38.262 Million cell updates/sec
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Sequence 348, App
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Sequence 1500, Ap
Sequence 50, Appl
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                                                                                          February 21, 2002, 17:19:35; Search time 13.59 Seconds
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(ggn2_6/ptodata/1/paa/USO6_NEW_COMB.pep:*

(ggn2_6/ptodata/1/paa/USO6_NEW_COMB.pep:*

(ggn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*

(ggn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*

(ggn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*

(ggn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*

(ggn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*
                                                                                                                                                                                                                                                                        45562
            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-824-053-14
US-09-824-053-14
US-09-620-405B-488
US-10-007-805-488
US-10-007-805-488
US-09-674-507-5
US-09-674-507-5
US-09-677-365-124
US-09-667-365-188
US-09-667-365-1052
US-09-667-365-1052
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US-09-948-939-36
US-09-311-784A-375
US-09-508-413A-12
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5-09-667-365-604
5-09-667-365-1052
5-09-667-365-1500
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T-US01-28124A-76
-09-749-873-120
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US-09-572-270B-473
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-09-828-708-53
                                                                                                                                                                                                                                            235865 seqs, 47271153 residues
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                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                 protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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61
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Match Length
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length: 11
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Maximum DB
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Producing Heterologous Antibodies

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METHOD OF PRODUCING SAME AND USE OF SUCH ENZYME
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TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A
METHOD OF PRODUCING SAME AND USE OF SUCH ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                              TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.3%; Score 24; DB 5;
80.0%; Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/824,053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 20006-1109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/669,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-824-053-7
                                                                                                                                                   Hunton & Williams
                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Hunton & Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Stanislaus Aksman
REGISTRATION NUMBER: 28,562
REFERENCE/DOCKET NUMBER: <U
                                                                                                                                                                       STREET: 1900 K Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1900 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 03-Apr-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 20006-1109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 955-1926
TELEFAX: (202) 778-2201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/09824053 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                            Ole Cai Hansen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS
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                                                                                                                                                     ADDRESSEE:
      GENERAL INFORMATION:
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Matches 4; Conserv
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TITLE OF INVENTION: Complementary peptide ligands from plant genomes
FILE REFERENCE: Plant patent
CURRENT APPLICATION NUMBER: US/09/572,270B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 1144
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 473
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                                                                                                                                                                                                                                                                                        NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 26; DB 5; Pred. No. 2.1e+05;
                                                                                                                                                            FILING DATE: 29-AUG-1990
APPLICATION NUMBER: WO PCT/US92/10983
FILING DATE: 29-AUG-1991
APPLICATION NUMBER: WO PCT/US91/06185
FILING DATE: 29-AUG-1991
                                                                          FILING DATE: 17-DEC-1991
APPLICATION NUMBER: US 07/575,962
FILING DATE: 31-AUG-1990
APPLICATION NUMBER: US 07/574,748
                     07/853,408
                                    FILING DATE: 18-MAR-1992
APPLICATION NUMBER: US 07/810,279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 216:
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Pred. No. 8
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                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
FILING DATE: 23-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-824-053-7; Sequence 7 Application US/09824053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.6%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 42.6
Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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; OTHER INFORMATION:
US-09-572-270B-473
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Gaps
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                                    APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: DIAGNOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
CURRENT APPLICATION NUMBER: US/09/620,405B
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 495
SOFTWARE: FastSEQ for Windows Version 3.0
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REPERSONCE: 210121,470CID
CURRENT APPLICATION NUMBER: US/10/007,805
CURRENT FILING DATE: 2001-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Score 23; DB 5; Length 9; Pred. No. 2.1e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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NUMBER OF SEQ ID NOS: 593
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 488, Application US/10007805; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 25, Application US/10020269; GENERAL INFORMATION: APPLICANT: Mitchell, William M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xu, Jiangchun
Harlocker, Susan L.
Hepler, William T.
Henderson, Robert A.
Fanger, Gary R.
Vedvick, Thomas S.
McNeill, Patricia D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dillon, Davin C.
Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                             37.78;
62.58;
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62.58;
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Best Local Similarity 62.5
Matches 5; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CRCANISM: Homo sapiens
US-10-007-805-488
                                                                                                                                                                                                                                                                                        TYPE: PRT
CORGANISM: Homo sapiens
US-09-620-405B-488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Jiang, Yuqiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LTYNTSOY 8
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2 LTKRASOY 9
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LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/09186949A
GENERAL INFORMATION:
FAPPLICANT: Murgita, Robert A.
TITLE OF INVENTION: Treating and Diagnosing Cancers
TITLE OF INVENTION: Treating and Diagnosing Cancers
FILE REPERENCE: 06727/004002
CURRENT APPLICATION NUMBER: US/09/186,949A
CURRENT FILING DATE: 1998-11-05
FRIOR FILING DATE: 1996-12-03
FRIOR FILING DATE: 1996-12-03
FRIOR FILING DATE: 1995-01-24
                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Stanislaus Aksman
REGISTRATION NUMBER: 28,562
REFERENCE/DOCKET NUMBER: <unknown>
TELECCOMMUNICATION INFORMATION:
TELEPHONE: (202) 955-1926
TELEFRAX: (202) 778-2201
                                  APPLICATION NUMBER: US/09/824,053
FILING DATE: 03-Apr-2001
CLASSIFICATION: UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/669,304
FILING DATE: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-824-053-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acid
                   CURRENT APPLICATION DATA:
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55.6%;
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US-09-186-949A-17
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                                                                                                                                                                                                                                                                                                                TELEX: None
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Best Local Similarity
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Best Local Similarity
Matches 5; Conserv
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2 QYQTY 6
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US-09-572-404B-2605
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LENGTH: 10
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APPLICANT: WAGNACHI, HILDARI,
APPLICANT: KATAOKA, Jiro
APPLICANT: KTTAMOYO, Katsuhiko
TITLE OF INVENTION: A Novel Glutaminase, its Gene and a Method of Producing It
FILE REFERENCE: 19943802-822-10-0-PCT
CURRENT APPLICATION NUMBER: US/09/674,507
CURRENT APPLICATION NUMBER: JP 10/134080
PRIOR APPLICATION NUMBER: JP 10/258974
PRIOR APPLICATION NUMBER: JP 10/292443
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-10-14
PRIOR FILING DATE: 1998-10-14
PRIOR FILING DATE: 1999-03-30
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TITLE OF INVENTION: SEQUENCES
FILE REFERENCE: VDB98-01
CURRENT APPLICATION NUMBER: US/10/020,269
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/025,596
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-18
PRIOR PELION NUMBER: EARLIER FILING DATE: 1996-03-18
PRIOR FILING DATE: EARLIER FILING DATE: 1996-08-14
NUMBER OF SEQ ID NOS: 118
SOFTWARE: FASTSEQ for Windows Version 3.0
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Pred. No. 2.1e+05;
1; Mismatches 1
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LOCATION: (4)..(4)
OCHER INFORMATION: Xaa = Thr or Gly
NAME/KEY: MISC_FEATURE
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66.78;
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
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60.0%;
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Best Local Similarity 66.7
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Best Local Similarity 60.0
Matches 3; Conservative
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3 STSDYD 8
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LENGTH: 11
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OTHER INFORMATION: sequence located in TFCOUP1 OR NR2F1 OR ERBAL3 OR EAR3 at 194-0THER INFORMATION: may interact with Sequence 2606 in this patent.
US-09-572-404B-2605
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APPLICANT: KAMABA, TAKABA
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING G2 CELL CYCLE
TITLE OF INVENTION: ARREST AND SENSITIZING CELLS TO DNA DAMAGING AGENTS
FILLE REFERENCE: 087533/02/56411
CURRENT APPLICATION NUMBER: 05/09/667,365
CURRENT APPLICATION NUMBER: 05/09/09-21
NUMBER OF SEQ ID NOS: 1948
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 124
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GENERAL INFORMATION:
APPLICANT: SUGANUMA, MASASHI
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING G2 CELL CYCLE
TITLE OF INVENTION: ARREST AND SENSITIZING CELLS TO DNA DAMAGING AGENTS
FILE REPERENCE: 087533/027641
CURRENT APPLICATION NUMBER: US/09/667,365
                                             APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
TITLE OF INVENTION: Complementary peptide ligands from the human genome
TITLE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
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Pred. No. 3.3e+02;
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Sequence 2605, Application US/09572404B GENERAL INFORMATION:
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44.48;
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ORGANISM: Homo Sapiens
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Best Local Similarity
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Best Local Similarity
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3 YNT-SQYD 9
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2 YNSPSQYE 9
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2 YNSPSOYE 9
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US-09-667-365-604
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    LENĞTH: 11
                          TYPE: PRT
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APPLICANT: KAWABE, TAKUMI
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING G2 CELL CYCLE
TITLE OF INVENTION: ARREST AND SENSITIZING CELLS TO DNA DAMAGING AGENTS
TITLE FOF INVENTION: ARREST AND SENSITIZING CELLS TO DNA DAMAGING AGENTS
FILE REFERENCE: 087533/0276411
CURRENT APPLICATION NUMBER: US/09/667,365
CURRENT FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 1948
SOFTWARE: PATENTIN VET: 2.1
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LOCATION: 9
OTHER INFORMATION: Xaa is any amino acid residue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Glucose Dehydrogenase; TITLE OF INVENTION: Glucose Dehydrogenase; FILE REFERENCE: 0230-0170P; CURRENT APPLICATION NUMBER: US/09/958,231 CURRENT FILING DATE: 1999-04-08; PRIOR PILING DATE: 1999-04-08; PRIOR FILING DATE: 1999-04-08; PRIOR FILING DATE: 2000-01-18; NUMBER OF SEQ ID NOS: 16; SEQ ID NO 5; SEQ ID NOS: 16
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    2000-09-21
                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                              36.18;
44.48;
CURRENT FILING DATE: 2000-NUMBER OF SEQ ID NOS: 1948
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 348
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Best Local Similarity 44.4
Matches 4; Conservative
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Matches 5; Conservative
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| LFHSPSOYE 9
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2 TYSTT-YD 8
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US-09-667-365-156
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GENERAL INFORMATION:
APPLICANT: SUGANUMA, MASASHI
APPLICANT: SUGANUMA, MASASHI
APPLICANT: KAWABE, TAKUMI
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING G2 CELL CYCLE
TITLE OF INVENTION: ARREST AND SENSITIZING CELLS TO DNA DAMAGING AGENTS
FILE REFERENCE: 087533/0276411
CURRENT APPLICATION NUMBER: US/09/667,365
CURRENT FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 1948
SOFTWARE: PATENTIN Ver. 2.1
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                                    OTHER INFORMATION: Description of Artificial Sequence: Synthetic COTHER INFORMATION: peptide US-09-667-365-156
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US-09-667-365-604
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Pred. No. 4e+02;
2; Mismatches 0;
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Pred. No. 4e+02;
2; Mismatches 0;
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                                                                                                                                           35.2%;
62.5%;
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62.5%;
ORGANISM: Artificial Sequence
                                                                                                                    Query Match
Best Local Similarity 62.30,
Thes 5; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 703-816-400
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: peptide US-08-143-311B-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1100 NOR:
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
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14, Apri
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28, Appl
28, Appl
5276016
16, Appl
16, Appl
13, Appl
13, Appl
17, Appl
17, Appl
17, Appl
                                                                                                               February 21, 2002, 17:18:30 ; Search time 12.46 Seconds (without alignments) 19.866 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 368,
Sequence 216,
Sequence 280,
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Sequence 133,
Sequence 7, Ap
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Sequence 370,
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Sequence 28,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                                Compugen Ltd
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US-08-758-417A-216
US-08-167-788A-280
US-08-465-391A-280
US-08-464-538B-280
US-08-463-759B-133
US-08-671-355A-133
US-08-669-304-7
US-08-669-304-7
US-09-120-365-28
US-09-1515-039-28
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US-08-540-412-37
US-08-361-517-17
US-09-051-342-37
US-09-051-759-37
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PCT-US95-08156-37
US-08-465-391A-334
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PCT-US96-00996-13
                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-143-311B-14
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US-09-186-723-16
            GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                             212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                           Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Issued_Patents_AA:*
                                                                                                                                                                                      US-08-753-851-16
61
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Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                 length: 0
length: 11
                                                                                                                                                                                                                                                            BLOSUM62
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq
Maximum DB seq
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                                                                                                                                                                                                                            Sednence:
                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                                                    Run on:
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1, Appli
18, Appl
18, Appl
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Sequence
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/143,311B
FILING DATE: 29-OCT-1993
CLASSIFICATION: 436
PRIOR APPLICATION NUMBER: 07/973,339
FILING DATE: 30-OCT-1992
CLASSIFICATION: 436
APPLICATION NUMBER: 07/669,730
FILING DATE: 15-MAR-1991
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-50
                       US-08 463-076E-371
PCT-US96-1263-5
US-08-72-258-67
US-08-465-965-1
US-08-465-966-1
US-08-465-966-1
US-08-125-099-18
US-09-125-099-18
US-09-125-098-18
US-08-039-137-25
US-08-039-137-25
US-08-0465-391A-335
US-08-465-391A-335
US-08-465-391A-355
US-08-465-391A-355
US-08-465-391A-355
US-08-465-391A-355
US-08-465-391A-355
US-08-465-391A-355
US-08-465-391A-355
US-08-464-538B-332
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APPLICANT: HALE, LAURA P.
APPLICANT: TELEN, MARILIN J.
APPLICANT: LIAO, HUA-XIN
TITLE OF INVENTION: AN ADHESION MOLECULE
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-143-311B-14; Sequence 14, Application US/08143311B Patent No. 5863540; GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-0CT-1996
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Best Local Similarity
Matches 4; Conserv
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APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                           Length 11;
                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
                         100.0%; Score 61; DB 2; L/
100.0%; Pred. No. 7.8e-05;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PAIGN APPLICATION DATA:
APPLICATION UNMBER: US 08/544,404
FILING DATE: 10-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/161,739 FILLING DATE: 03-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
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09-MAR-1994
                                                                                                                                                                                                                                                                                      Sequence 368, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
                                                                                       11; Conservative
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                                         Query Match
Best Local Similarity
Matches 11; Conserva
                                                                                                                                   1 LTYNTSQYDTY 11
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US-09-042-353-368
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Gaps
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Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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Pred. No. 1.6e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
                                    FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
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FILING DATE: 10-OCT-1995
                      WO PCT/US96/16433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 216, Application US/08758417A Patent No. 6300129 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 02-Dec-1996
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 941113834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 368:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.6%;
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STATE: California
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                                                                                                                                                                                                                                       NAME: Apple, Randolph T. REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     9 amino acids
PRIOR APPLICATION DATA: APPLICATION NUMBER: V
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Gaps
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TITLE OF INVENTION: Peptides and Compounds That Bind to the TITLE OF INVENTION: IL-1 Receptor NUMBER OF SEQUENCES: 405
CORRESPED NDERCES: ADBRESS:
ADBRESSEE: Townsend and Townsend and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STAREE: California
                                                                                                                                                                                                                                                                                            Length 11;
                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                          Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/465,391A FILING DATE: 05-JUN-1995 CLASSIFICATION: 514
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FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5786331V1e1, Vern
REGISTRATION NUMBER: 32,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/373,474 FILING DATE: 0.1-FEB-1995 CLASSIFCATION: 514 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 280, Application US/08465391A; Patent No. 5786331; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yanofsky, Stephen D.
Baldwin, David
Jacobs, Jeff W.
                     TELECOMMUNICATION INFORMATION: TELEPHONE: 415-496-2300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovy, Phillipe R.
Leahy, Ellen M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Barrett, Ronald W
  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                       LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                           TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 11 amino acids amino acids
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Best Local Similarity 50.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415-326-2422
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                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-190-788A-280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                            4 NTSQYDTY 11
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2 NSSWYDSF 9
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US-08-465-391A-280
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APPLICANT:
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APPLICANT:
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APPLICANT: Yanofsky, Stephen D.
APPLICANT: Barrett, Ronald W.
APPLICANT: Balayin, David N.
APPLICANT: Jacobs, Jeff W.
TITLE OF INVENTION: Peptides and Compounds That Bind to the TITLE OF INVENTION: IL-1 Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.6%; Score 26; DB 4; Length 9; 80.0%; Pred. No. 1.6e+05; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                              NAME: Serafin, Andrew T.

REGISTRATION NUMBER: 41,303

REFERENCE/DOCKET NUMBER: 014643-009030US

TELEPHONE: (415) 576-0200

INFORMATION FOR SEQ ID NO: 216:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                 PILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/165,699
                                                                                                                                                                                 FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
                                                                                                                                                                APPLICATION NUMBER: US 08/053,131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 216:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,567
FILING DATE: 05-WAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 280, Application US/08190788A Patent No. 5608035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IMP PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 9 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 80.۰۰
کرد 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
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US-08-190-788A-280
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Gaps
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Patent No. 5880096
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen D.
TITLE OF INVENTION: Peptides and Compounds That Bind to the TITLE OF INVENTION: IL-1 Receptor
NUMBER OF SEQUENCES: 392
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 11;
       Indels
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SUFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,076E
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
ATTONEY/AGENT TOTAL
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Two Embarcadero Center, Eighth Floor
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Patent No. 5876931
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Snyder, Joseph R. REGISTRATION NUMBER: 39,381
REFERENCE/DOCKET NUMBER: 16528A-001850US
TELECOMMUNICATION INFORMATION:
     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                           3,
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 370:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.6%;
50.0%;
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     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: peptide US-08-463-076E-370
                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS:
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Best Local Similarity
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STATE: Georgia
                                         4 NTSQYDTY 11
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2 NSSWYDSF 9
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                                                                                                                                               US-08-463-076E-370
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                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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     Matches
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APPLICANT: Leahy, Ellen M.
APPLICANT: Leahy, Ellen M.
TITLE OF INVENTION: Peptides and Compounds That Bind to the TITLE OF INVENTION: IL-1 Receptor
TITLE OF INVENTION: IL-1 Receptor
                                                                                                               DB 1; Length 11;
                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,538B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 26; DB 2;
Pred. No. 71;
                                                                                                            Score 26; DB 1
Pred. No. 71;
3; Mismatches
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                                                                                                                                                                                                                                                                                                          Sequence 280, Application US/08464538B
Fatent No. 5861476
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Baldwin, David
APPLICANT: Jacobs, Jeff W.
APPLICANT: Boyy, Phillipe R.
APPLICANT: Leahy, Ellen M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUIOR PAPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: SMICH, WIlliam M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1652
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEPAX: 415-326-2422
                                                                                                            42.6%;
50.0%;
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                                                                                                        Query Match 42.6
Best Local Similarity 50.0
Matches 4; Conservative
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TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
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STRANDEDNESS: single
                                 ; MOLECULE TYPE: peptide US-08-465-391A-280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: peptide US-08-464-538B-280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          San Francisco
California
                    linear
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Best Local Similarity
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2 NSSWYDSF 9
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APPLICANT: Peter Stougaard
APPLICANT: Ole Cai Hansen
TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A
TITLE OF INVENTION: METHOD OF PRODUCING SAME AND USE OF SUCH ENZYME
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: Hunton & Williams
STREET: 1900 K Street, N.W.
                                                                                                                                                                                                                                                                                                                              Length 10;
                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,304
FILING DATE: 12 July 1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.4e+02;
2; Mismatches 4
                                                                                                                                                                                                                                                                                                                                Score 24; DB 3;
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REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101 CON
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.3%; Score 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,910
FILING DATE: 7 June 1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08669304
Patent No. 6251626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 28,562
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
                                                     TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 133
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                39.3%;
40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (202) 955-1926
TELEFAX: (202) 778-2201
TELEX: NO. 651626e
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stanislaus Aksman
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 40.0.
                                                                                                                                          LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: peptide US-08-669-304-7
                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A. ZIP: 20006-1109
                                                                                                                                                                                                                                                                                                                                                                                                               1 LTYNTSQYDT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LKYRTKRYSS 10
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                                                                                                                                                                                                                                                                   US-08-871-355A-133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 133, Application US/08871355A
Patent No. 6015669
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                              FILING DATE: 03-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                             APPLICATION NUMBER: US/08/637,759B FILING DATE: 03-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/871,355A FILING DATE: 09-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 133
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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Best Local Similarity
Matches 4; Conserv
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ZIP: 30309-3450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LTYNTSQYDT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE:
; HYPOTHETICAL: N
US-08-637-759B-133
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Query Match
Best Local Similarity
Matches 6; Conserv
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US-09-515-039-28
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LENGTH: 6
                                                                                          SEQ ID NO 28
LENGTH: 11
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APPLICANT: Peter Stougaard
APPLICANT: Ole Call Hansen
TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A
TITLE OF INVENTION: METHOD OF PRODUCING SAME AND USE OF SUCH ENZYME
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hunton & Williams
                       Gaps
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                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,304
FILING DATE: 12 July 1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 24; DB 4; I
Pred. No. 1.6e+02;
0; Mismatches 1;
 Pred. No. 1.6e+02;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APIGLICANT: NATOTI, Shunji
TITUE OF INVENTION: NEW PROTEASE
FILE REFERENCE: 32290-1144749
CURRENT_APPLICATION NUMBER: US/09/120,365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28,562
ER: 320.000003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,910
FILLING DATE: 7 June 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                               Sequence 14, Application US/08669304 Patent No. 6251626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 28, Application US/09120365
; Patent No. 6103514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Stanislaus Aksman
REGISTRATION NUMBER: 28,562
RELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 955-1926
TELERAX: (202) 778-2201
TELEX: No. 6251626
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Hunton & Williams
STREET: 1900 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.3%;
80.0%;
 80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 11 amino acids
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 80.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 20006-1109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-08-669-304-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                       7 QYDTY 11
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                                                                           11 11
2 QYQTY 6
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US-08-669-304-14
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US-09-120-365-28
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Gaps
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FILE OF T-4 RECEPTORS AND ACT AS IMMUNGENS
NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/568,616
FILING DATE: 16-AGC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 314,507
FILING DATE: 15-FEB-1989
APPLICATION NUMBER: 48,148
FILING DATE: 11-AMY-1987
APPLICATION NUMBER: 878,586
FILING DATE: 26-JUN-1986
FILING DATE: 03-JUN-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 23.5; DB 4;
Pred. No. 1.9e+02;
0; Mismatches 1;
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Pred. No. 1.9e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Patent No. 5276016
; APPLICANT: PERT, CANDACE B.;RUFF, WILLIAM R.;FARRAR,WILLIAM L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INCORNATION:
APPLICANT: Natori, Shunji
TITLE OF INVENTION: NEW PROTEASE
FILE REFERENCE: 32290-144749
CURRENT FILITING DATE: 2000-03-06
ERALIER APPLICATION NUMBER: US/09/515,039
CURRENT FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 101
SEQ ID NO 28
                         9-333 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 28, Application US/09515039 Patent No. 6214599
CURRENT FILING DATE: 1998-07-22
EARLIER APPLICATION NUMBER: JP 9
EARLIER FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 10.1
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                           ; TYPE: PRT; ORGANISM: Sarcophaga peregrina
US-09-120-365-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Sarcophaga peregrina
US-09-515-039-28
                                                                                                                                                                                                                                                    38.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.5%;
60.0%;
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Best Local Similarity 60.0
Matches 6; Conservative
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5276018-3
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Gaps
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Query Match

37.7%; Score 23; DB 6; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 2; Indels
                                                                           5 TSQYDT 10
| | | | | |
1 TDNYDT 6
                                                                                                                    qq
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RESULT 15
US-08-377-309-16
Sequence 16, Application US/08377309A
Patent No. 5965528
GENERAL INFORMATION:
APPLICANT: WURGILEA,
TITLE OF INVENTION: RECOMBINANT HUMAN ALPHA-FETOPROTEIN AS
TITLE OF INVENTION: AN IMMUNOSUPPRESSIVE AGENT
FILE REPERBENCE: 06727/005001
CURRENT APPLICATION NUMBER: US/08/377,309A
UUMBER OF SED ID NOS: 16
SEO ID NO 16
LENGTH: 9
TYPE: PRT
TREE: PRT
TYPE: PRT

CORGANISM: Homo sapiens
US-08-377-309-16

; Query Match

37.7%; Score 23; DB 2; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.6e+05;
Matches 5; Conservative 1; Mismatches 3; Indels

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Gaps

2 TYNTSQYDT 10 :| || || 1 SYICSQQDT 9 ò

Search completed: February 21, 2002, 17:20:21 Job time: 111 sec